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Sequence 106, App
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Sequence 27026, A
Sequence 458, App
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence 22534, Application US/09252991A
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APPLICANT:
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FILE REFERENCE:
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CURRENT FLING DATE:
1999-02-18
FRIOR APPLICATION NUMBER: US/09/252,991A
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LIDPESQVGTTDRAGVKDVILESALTTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA 301
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ORGANISM: Pseudomonas aeruginosa
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                                                 IMDALFTGLIAIHGLKASDVNGPLINSRIGSIYIVKPKWHGPAEVAFICELFSRVEDVLG 421
                                                                                                        LPQNTMKIGIMDEERRITVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG 480
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Bacent No. 6506384

GENERAL INFORMATION:
APPLICANT: Laal, Suman
APPLICANT: Laal, Suman
APPLICANT: Belisle, John T

ITLE OF INVENTION: EACH DETECTION OF MYCOBACTERIAL DISEASE
FILE REFERENCE: 32004-169276
CURRENT FILING DATE: 1997-12-31

CURRENT FILING DATE: 1997-12-31

NUMBER OF SEQ ID NOS: 106

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT ; ORGANISM: Mycobacterium tuberculosis US-09-396-347F-106
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US-09-396-347F-106
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                                                                                                                                                                                           Length 739;
                                                                                                                                                                                                                            Indels
                                                                                                                                                                                        Score 2289; DB 2;
Pred. No. 4.1e-213;
0; Mismatches 184;
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Patent No. 6562958
GENERAL INFORMATION:
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                                                                                                                                                                                        60.1%;
     (718) 884-6600
                                                     2
 TELEPHONE: (718) 884-660
TELEFAX: 718/601-1099
TELEX: 620428
INPORMATION FOR SEQ ID NO: 2
SEQUENCE CHRAACTERISTICS:
LENGTH: 739 amino acids
TYPE: amino acids
                                                                                                                                                                                                                          Conservative
                                                                                                                  TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-836-943-2
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US-09-328-352-7603
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Best Local
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: PIN PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836,943

FILING DATE: 08-MAY-1997

CLASSIFICATION: 435
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APPLICANT: Eikmanns, Bernhard
APPLICANT: Eikmanns, Bernhard
APPLICANT: Eshm, Hermann
TITLE OF INVENTION: DNA WHICH REGULATES GEN
TITLE OF INVENTION: CORYNEFORM BACTERIA
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Firm of Karl F. Ross, PC
STREET: 5676 Riverdale Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC
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NAME: Myers, Jonathan
REGISTRATION NUMBER: 26,963
REFERENCE/DOCKET NUMBER: 20357
TELECOMMUNICATION INFORMATION:
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Patent No. 5965391
GENERAL INFORMATION:
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CITY: Bronx
STATE: New York
COUNTRY: USA
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                                                                                     SEO ID NO 5503
LENGTH: 3892
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APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-018A
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7603
LENGTH: 729
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                                                                                                                               Length 729;
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                                                                                                                              ; Score 2225; DB 4;
; Pred. No. 6.6e-207;
97; Mismatches 185;
                                                                                        ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7603
                                                                                                                                 59.4%;
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432; Conservative
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APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION:
TITLE OF INVENTION: BAUNANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT ABPLICANTON NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                         3.6%; Score 139; DB 4; Length 3892;
21.6%; Pred. No. 0.0043;
tive 78; Mismatches 300; Indels 228;
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US-09-328-352-5503
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RESULT

RESULT 6 US-09-328-352-5503 ; Sequence 5503, Application US/09328352

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3498 AAANQ-FIDTLARHRARRGLTS----VSLGWGLWHEASGLTGGLADIDRDRMS--RAGI 3549
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APPLICATION NUMBER: US/08/237,919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-008-237-919-2
'Sequence 2, Application US/08237919
'Patent No. 5610281
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ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DO
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ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B080;
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 VODGOLVVAL-PDKSTGLAN---
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CITY: Boston
STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 DDSVPLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHG 235
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                                                                                                   APPLICANT: Betlach, Mary C.
APPLICANT: Betlach, Mary C.
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: Tang, Li
TILE CE INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 30062-20029, 00
CURRENT APPLICATION NUMBER: US/09/428,517
CURRENT FILING DATE: 1999-10-28
EARLIER APPLICATION NUMBER: 60/120,254
EARLIER PELIJNG DATE: 1999-02-16
EARLIER FILING DATE: 1998-02-16
EARLIER FILING DATE: 1998-02-16
EARLIER FILING DATE: 1998-02-16
EARLIER FILING DATE: 1998-02-16
EARLIER FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Recombinant; OTHER INFORMATION: Oleandolide PKS
US-09-428-517-3
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3.5%; Score 135; DB 3; Length 3816;
Best Local Similarity 21.3%; Pred. No. 0.01;
Matches 190; Conservative 112; Mismatches 297; Indels 29
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             Sequence 3, Application US/09428517
Patent No. 6251636
GENERAL INFORMATION:
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GENERAL INCORMATION:
APPLICANT: Brenner, Michael B
APPLICANT: Brenner, Maryn L
APPLICANT: Brenner, Maryn L
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Modulating Heterotypic E-cadherin Interactions with T lymphocy
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks P.C.
STREET: 600 Atlantic Avenue 3712 A----PMPTDEALHLFDRATELGDPVLLPMRLNEAALEDRAAD---GTLPPLLSGLVRVR 3602 579 ------TIP--LAKELAWAPD---EIREEVDNNCOSILGYV-----VRWV 612 613 DQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRASLBRMAPLVDRQN 672 307 LPDKNMFTINRNTGVISVVTTGLDRESFPTY--TLVV------QAADLQGEGL--ST 353 142 YGTDVIPETDGAEKGPTYNKV--RGD-----KVIAYARKFLDDSVPLSSGSFGDATGFT 193 -- PGQFAGYTGAAESPTSV 229 3663 FRDIGFDSLTAVELRNRINAETGLRLPGTLVFDYPN----PSALADHLLELLAP----91 LPEPDDFTI-----TTSGVDAEITTTAGPQLVVPVLNARFALNAANARWGSLYDAL 3713 ----ATQPTAAPL---LABLERVEQLLSAAASPGGPASAVDEETRTLIATRLA 3758 STAWVPSPTAATLH-----ALHYHQVDVAAVQQGLAGKRRATIEQLL---673 AGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRREFKARAA 725 3.4%; Score 128; DB 1; Length 878; 22.0%; Pred. No. 0.004; cive 66; Mismatches 210; Indels 2

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APPLICANT: Cepek, Karyn
TITLE OF INVENTION: Methods and Compositions for Modulating Heterotypic E-cadherin
TITLE OF INVENTION: Interactions with T Lymphocytes
TITLE OF INVENTION: Interactions with T Lymphocytes
CURRENT APPLICATION NUMBER: US/09/798, 267
CURRENT FILING DATE: 2001-03-02
PRIOR FILING DATE: 1994-05-03
PRIOR FILING DATE: 1994-05-03
PRIOR APPLICATION NUMBER: PCT/US 95/05518
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                                                                                                                                                                                                       307 LPDKNMFTINRNTGVISVVTTGLDRESFPTY--TLVV------QAADLQGEGL--ST 353
                                                                                                                                                                                                                                              142 YGTDVIPETDGAEKGPTYNKV--RGD-----KVIAYARKFLDDSVPLSSGSFGDATGFT 193
                                                                                                                                                                                                                                                                                                                             - PGOFAGYTGAAESPISV 229
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                                                                                                                                                                   91 LPEPDDFTI-----TTSGVDAEITTTAGPQLVVPVLNARFALNAANARWGSLYDAL
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                                                                                                                                Gaps
                                                                                                                                Indels 200;
                                                                                       3.4%; Score 128; DB 4; Length 878; 22.0%; Pred. No. 0.004; ive 66; Mismatches 210; Indels 2
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BRICA REPLICATION NUMBER: US 08/732,429
PRIOR FILLING DATE: 1996-11-01
NUMBER OF SEQ ID NOS: 9
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Patent No. 6406870
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               194 VQDGQLVVAL-PDKSTGLAN--
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                                                                                                                  Best Local Similarity 22.. Matches 134; Conservative
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                                 , MOLECULE TYPE: protein US-08-732-429-2
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amino acid
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APPLICANT: Cepek, K
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Best Local
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279 DAADKVLGYRNWLGLN--KGDLAAAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGGRSLMF 336
                                                                                                                                                                                                                                                                                              -----EDVLGLPQNTMKIGIM 431
                                                                                                                                                                                                                                                                                                                                                                           432 DEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKGTMKSQPWILAY 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methods and Compositions for Modulating Heterotypic E-cadherin Interactions with T {\rm Lymphocytes}
                                                                                                                                                                                                               337 VRNVGHLMTNDAIVDTD-GSEVFEGIMDALFIGLIAIHGLKASDV--NGPLINSRIGSIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLHALHYH------QVDVAAVQQGLAGK----RRATIEQLLTIPLAKELAWAPDEI
                                                                                                                                                                          ------kiwieinpotgaistraeldredfehvkn--styta------
                                                                                   ZIF: 02210
COMPUTER READBLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/732,429
FILING DATE: herewith
                                                                                                                                                                                                                                                                                              394 IVKPK-----MHG----PAEVAFICEL-FSRV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Wolf, Greenfield & Sacks P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                              ----DYKINLKIMDNQNKDQVTTLEVSVCDCEG
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                                                          LLINHGLHIEILIDPESQVGTTDRAGV-
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APPLICATION NUMBER: 08/237,919
FILING DATE: 3 May 1994
ATTORNEY/ACENT INFORMATION:
NAME: Plumer, Elizabeth R
REGISTRATION NUMBER: 36,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08732429
Patent No. 6300080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: B0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       878 amino acids
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT:
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GENERAL INFORMATION:
APPLICANT:
ATTLE OF INVENTION: Methods and Compositions for Modulating Heterotypic TITLE OF INVENTION: E-cadherin Interactions with T Lymphocytes NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks P.C.
STREET: 600 Atlantic Avenue
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22.0%; Pred. No. 0.004;
live 66; Mismatches 210;
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; PRIOR FILING DATE; 1996-11-01; NUMBER OF SEQ ID NOS: 9; SOTWARE: Patentin version 3.0; SEQ ID NO 3; LENGTH: 878; TYPE: PRT ORGANISM: HOMO Sapiens US-09-798-267-3
                                                                                                                                                                                                  Query Match
Best Local Similarity 22.0%
Matches 134; Conservative
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STATE: MA
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ZIP: 02210
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APPLICANT: Cepek, Karyn
TITLE OF INVENTION: Methods and Compositions for Modulating Heterotypic E-cadherin
TITLE OF INVENTION: Interactions with T Lymphocytes
FILE REFERENCE: L0560/7008ERP
CURRENT APPLICATION NUMBER: US/09/798,267
CURRENT APPLICATION NUMBER: US 08/237,919
PRIOR FILING DATE: 1994-05-03
PRIOR FILING DATE: 1995-05-03
PRIOR FILING DATE: 1995-05-03
PRIOR FILING DATE: US 08/732,429
PRIOR FILING DATE: US 08/732,429
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3.4%; Score 128; DB 4; Length 878;
Best Local Similarity 22.0%; Pred. No. 0.004;
Matches 134; Conservative 66; Mismatches 210; Indels 200;
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TER: US 08/732,429
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Patent No. 6406870
GENERAL INFORMATION:
    PatentIn version 3.0
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; SOFTWARE: Patentin vers
; SEQ ID NO 2
; LENGTH: 878
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-798-267-2
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22.0%; Pred. No. 0.004;
ive 66; Mismatches 210; Indels 200;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTERS: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05518
FILING DATE: herewith
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                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/237,919
FILING DATE: 3 May 1994
ATTORNEY AGENT INFORMATION:
NAME: Plumer, Elizabeth R
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 612-720-2441
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 878 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 22.0
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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10640 AGVIKMVQALRHGVLPKTLHVDEPTDQVDWSAGSVELLTEAVDWPERPGRLRRAGVSAFG 10699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----QHLIRQALAD--ARLT----- 10582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 VLNARFALNAANARWGSLYDAL-YGTDV---IPETDGAEKGPTYNKVRGDKVIAYARK-- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 FLDDSVPLSSGSFG----DATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLINHGLHI------EILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDA 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----RNVGHLMTNDAIVDTDGSEV--FEGIMDALFTG--LIAIHGLKASDVNGPL 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INSRIGSIYIVKPKWHGPAEVAFTCELFSRVEDVLGLPQNTMKIGIMDEERRTTVNLKAC 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRDAGVI----DIVLRLTGIEPEPGSGGSDGGAADPGAEPEASI---DDLDAEA---LI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.4%; Score 128; DB 3; Length 11877;
20.7%; Pred. No. 0.34;
tive 85; Mismatches 319; Indels 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 11877;
                                                                                                                                                            APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TILLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----PWILAYED--HNVD--AGLA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10242 RMALGPRNTMTSSNEQLVDALRASLKENEELRKES-----
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                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/105,537A CURRENT FILING DATE: 1998-06-26 NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         445 IKAAADRVVFINTGFLDRTGDEIHT----
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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 11877
TYPE: PRT
ORGANISM: Streptomyces venezuelae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 20.7
Matches 172; Conservative
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OY 421LPQNTWKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDR 462	: :       : :	CY 463 TGDEIHTSNEAGPMVRKGTMKSQPWILAYEDHNVDAGLAAGFGGRAQVG	DD 95.2 SGVADGVKCEVQAAIABQLATILVVAQAGDLHAHASLAAGAAAVAVVEGASKGAQAG 1007 QY 512 KG-MWIMIELMADKVETKIAQPRAGASTAWVPSPTAATLHALHYHQVDVAAVQGLAGKR 570	AAARQQAAGAVVQLPHRHALRALAEQVAFIAVVQQ APDEIREEVDNNCQSILGYVVRWVDQGVGCSKVPDIHDVAL	QY 630 Db 1101	RRREFKARAAE 726    :   :   : RRRADLOVVQAD 1175	878-	; Sequence 2, Application US/U93208/8A ; Patent No. 611659 ; GENERAL INFORMATION: ; APPLICANT: ASHLEY, Carv	BETLACH, Melanie C. BELLACH, Mary C. MCDANEL, Robert TANG, Li	: RECOMBINANT NARBONOLIC 0622002120 N NUMBER: US/09/320,878A E: 1999-05-27	; EARLIER APPLICATION NUMBER: CIP OF 09/141,908 ; EARLIER FILING DATE: 1996-08-28 ; EARLIER APPLICATION NUMBER: CIP OF 09/073,538 ; EARLIER FILING DATE: 1998-05-05	APPLICATION N FILING DATE: APPLICATION N	FILING DATE: 1999-02 APPLICATION NUMBER: FILING DATE: 1998-0	APPLICATION N FILING DATE: OF SEQ ID NOS:	; SOFIWARE: Patentin Ver. 2.0 ; SEQ ID NO 2 ; LENGTH: 3739 ; TYPE: DRT	. 불등	3.3%; Score 126.5; DB 3; Length 3 Similarity 21.4%; Pred. No. 0.066;	; Conservative 87; Mis LPGTDIDPDSFWAGVDKVVADL1	: :       : :	CY 81 RQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPVLNARFALNAANARWGSLYDA 140	Db 1595 GRTYCRAGGFLDEAGEFDADFFGISPREALAMDPQQRLLLETSWEAVEDA 1644
DPAVAARALVDSRTAMEHRAVAVGDSREALRDALRMPEGLVRGTVTDPGRVAFVFPGQGT 10819	REBUDINACQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATL 636		ALSOQUENTATION ISADVARSDERNYFUNDKŲNAGUVAIKFNAFNNIUS 088 AVMVSLAKVWQHHGIIPEAVIGHSQGBIAAAVVAGALTLUDDA 10920	ULT 14 09-252-991A-21798 equence 21798, Application US/09252991A	GENERAL INFORMATION: PARCO J. Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS	107196.136 DAIN WIMBER: US/09/252,991A DAIR: 1999-02-18 ON NUMBER: US_60/074,788	FALOR FILING DAIE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142	LENGTH: 1650 TYPE: PRT ORGANISM: Pseudomonas aeruginosa	3.3%; Score 127; DB 4; Length 1650; 20.2%; Pred. No. 0.015;	VALIVE 110; MISMACCAES 349; INCELS 242; GADS 3  YDEVNNEALPGTDIDPDSFWAGVDKVVADLTPONQALLNARDEL S9	GNIMANAVEDVQKIDAQKAASIDQAILVVQVAAKQVEIDAALADQFALALAQALDK 438 QAQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTGGVDAE-ITTTAGPQLVV 118    :	QAQVAPGGDFAAVGGVDAPC-RQFQFAVAGQQAATVVQVGGAQAQRLLATEGAATVV 494 PVLNARFALNAANARWGSLYDALYGTDVIPETDG-AEKGPTYNKVRGDKVIA 169	: : :	YARKFLDDSVPLSSGSFGDATGFTVQDGQLVVAL 203 :::   :	PDKSTGLANPGQFAGYTGAAESPTSVLLINHG		: :	321	PGGGQFTLPGRSLMFVRNVGHLWINDALVDTDGSEVFEGIMDALFTGLIALHGL 375	GLAGORORTGAGEGPATVVQARGARRQAFADORALVVQHAAEAHAQAVLAVEPTAVAV 831	-KASDVNGPLINSRTGSIXIVXPKMHGPAEVAFTCELFSRVEDVLG 420

GIDPTSLQGQQVGVFAGTNGPHYEPLJRNTAEDLEGYVGTGNAAS 1689	VODGOLVVALPDK	IMSGRVSYTLGLEGPAVTVDTACSSSLVALHLAVQALRKGECGLALA 1736	AGVKDVILESAITTIMDFEVAAVDAADKVLGYRNWLGLNKGDLAAAVDK 304	1737 GGVIVMSTPTTFVEFSRQRGLAEDGRSKAFAASADG-FGPAEGVGWLLVERLSDARR 1792	305 DGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDALVDTDGSE 356	GHRVLAVVRGSAVNQDGASNGLTAFNGPSQQRVIRRALADARLTTADVD 1842	357 VFEGIMDALFTGLIALHGLKASDVNGPLINSRTGS 391	:::	IYIVKPKAHGPAEVAFTCELFSRVEDVLGLPQNTMKIGIMDEERRITVNLKACIKAAA 449	IKMVQAMRHGVLPKTLHVDRPSDQIDWSAGTVELLTEAMDWPRKQEGGLR 1947	DRVVFINTGFLDRTGDEIHTSMEAGPMVRKGTMKSQPMILAYEDHNVDAGLAAG 503			1 I.DAQIGRLAAFASQGRTDAADPGAVARVLAGGRAQFEHRAVALGTGQDDLA 2047	AVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIREEVDN 599	2048 AALAAPEGLVRGVASGVGRVAFVFPGQGTQWAGMGAELLDVSKEFAAAMAE 2098		- CEAALAPYVDMSLEAVVRQAPGAPTLERVDVVQP-VTFAVMVSLAKVWQHHGVTPQ 2153	ADVRASLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILS 700	2154 AVVGHSQGBIAAAYVAGALSLDDAARVVTLRSKSIGAHLAGQGGMLS 2200
1645	194 VQ	1690 iM	254 AĞ	1737 G	305 DG	1793 NG	357 VF	1843	392 IY	1898 IK	450 DR	1948 -R	504 FS	1997 LD	561	2048 AA	009 NC	2099 -C	655 AD	2154 AV
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Search completed: November 21, 2003, 16:11:36 Job time : 18.6054 secs

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November 21, 2003, 15:50:31 ; Search time 44.8027 Seconds (without alignments) 2621.664 Million cell updates/sec
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3810
1 TDRVSVGNLRIARVLYDFVN......KARAAEKPAFSDRAGDDAAR 740
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Perfect score:
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Maximum DB seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ø			SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ПD	Description
-	3810	100.0	1	22	AAE05665	Mycobacterium tube
7	3810	100.0		22	AAU01900	M. tuberculosis Th
m	3804	8.66	2502	21	AAB00117	M. tuberculosis po
4	2289	60.1		16	AAR77501	Malate synthase.
S	2289	60.1		22	AAG93234	C glutamicum profe
9	2275	59.7		22	AAB79539	Corvnebacterium ol
7	2253	59.1		22	AAB79540	Corvnebacterium ol
00	991.5	26.0		22	ABG18357	Novel human diagno
σ	741.5	19.5		22	ABG25453	Novel human diagno

10 594.5 15.6 504 22 ABC18358 13 485.5 11.4 140 22 ABC18358 13.5 11.4 120 ABC18358 13.5 11.4 120 ABC18358 13.5 11.4 120 ABC18358 13.5 11.4 120 ABC18358 13.5 13.5 13.5 ABC18358 13.5 13.5 ABC18358 13.5 13.5 ABC18358 13.5 13.5 ABC18358 128.5 3.4 823 22 ABC1848 128.5 3.4 823 22 ABC18500 22 ABC1850	ಹ	ď	ı di	orot	ate s		ntibioticus	actococcus lact	tuberculosis a	vel human diagn	human	ъ.	E-cadhe	E-cadher	nezuelae pik	an liver per	de #4190 en	rotein #4020	uman brain ex	bone marrow	le #4010 e	n titin	RGS11	acid	. venezuela	S. venezuelae pik	Narbonolide syntha	S. venezuelae narb	Haemophilus paraga	. Chlamydia pneumoni	S. venezuelae macr	amoplanin	1)	ίd	honol 4 d
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## ALIGNMENTS

RESULT 1 AAE05665

Mycobacterial disease, infection, 88-kDa protein, tuberculosis, TB, early antigen; human immunodeficiency virus, HIV; secreted protein. Detecting a mycobacterial disease (tuberculosis) in individuals comprise assaying a biological sample for the presence of Mycobacterium tuberculosis 88 kDa secreted protein. Zolla-Pazner S, Belisle JT; (UVNY-) UNIV NEW YORK MEDICAL CENT. (COLS ) UNIV COLORADO STATE. AAE05665 standard; peptide; 741 AA 97US-0001984. 97US-0034003 Mycobacterium tuberculosis 24-SEP-2001 (first entry) WPI; 2001-424324/45. 31-DEC-1997; 02-JAN-1997; US6245331-B1 12-JUN-2001. AAE05665; Laal S, THE SECTION OF THE SE

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                                                              The present invention relates to a method for early detection of active mycobacterial disease or infection comprises assaying a biological fluid sample for the presence of early antibodies specific for an 88-kba Mycobacterium tuberculosis (Mt) protein or immune complexes consisting of an 88-kba Mycobacterium tuberculosis protein antigen complexed with an antibody specific for the antigen. The method is useful for the early and rapid detection of mycobacterial disease, particularly tuberculosis, in individuals at heightened risk of developing tuberculosis. This individuals include human immunodeficiency virus (HtV)-infected subjects or other immunocompromised individuals. The method is a rapid and the present sequence is a Mt 88 kba secreted protein early antigen, used in the exemplification of the invention.
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anti-Mycobacterium tuberculosis antibodies or M. tuberculosis antigen-antibody complex
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                                                                                                                                                                                                                                                                         100.0%; Score 3810; DB 22;
100.0%; Pred. No. 4.7e-316;
ive 0; Mismatches 0;
                                        Claim 14; Column 121; 96pp; English.
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Best Local Similarity 100.
Marches 740; Conservative
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consisting of a His tag for purification, antigen MtB81 and antigen Moc. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease, ADS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccinating against Mycobacteria infections in mammals using fusion proteins comprising combinations of heterologous antigens
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                                                                                                                                                                                                                                                                                                                                                      TDF14; antigen, vaccine, tuberculosis; AIDS; His tag; MtB81; MO2; acquired immunodeficiency disease.
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/label= Histidine_tag
/label= Wickel chelating region used for the fusion protein"
9..749
/label= MtB81_region
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                         722 KARAAEKPAPSDRAGDDAAR
  KARAAEKPAPSDRAGDDAAR
                                                                                                                                                                                                                                                                                                              M. tuberculosis TbF14 fusion
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Binding-site
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OY  61 AQIDKWHERRVIEDIDMDAYRQFLTEIGYLLPEDDDFTITTSGVDAEITTTAGPOLVVPV 120  69 AQIDKWHERRVIEDIDMDAYRQFLTEIGYLLPEDDDFTITTSGVDAEITTTAGPOLVVPV 128  69 AQIDKWHRRRVIEDIDMDAYRQFLTEIGYLLPEDDDFTITTSGVDAEITTTAGPQLVVPV 128  CY  121 LNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP 180  129 LNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP 188  CY  181 LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI 240  DD  189 LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI 248  CY  241 LIDPESQVGTTDRAGYKDVILESAITTIMDFEDSVAAVDAADKVLGYRNMLGLNKGDLAA 300	249 LIDEESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLAKGGDLAA 301 AVDKDGTAFLRVLNRDRNYTAPGGGFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEG 303 AVDKDGTAFLRVLNRDRNYTAPGGGFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEG 304 AVDKDGTAFLRVLNRDRNYTAPGGGFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEG 305 AVDKDGTAFLRVLNRDRNYTAPGGGGFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEG 306 INDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKAHGPAEVAFTCELFSRVEDVLG 421 LPQNTMKLGIMDEBRRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG 422 LPQNTMKLGIMDEBRRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG 423 LPQNTMKLGIMDEBRRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG 424 LPGNTMKLGIMDEBRRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG 425 LPQNTMKLGIMDEBRRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG 426 LPQNTMKLGIMDEBRRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG 427 LPQNTMKLGIMDEBRRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG 438 TMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTWTELMADMVETKIAQPRAGASTAW 489 TMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTWTELMADMVETKIAQPRAGASTAW 641 VPSFTAATLHALHYHQVDVAAVQGGLAAGFSGRRATTFILALALHYHQVDVAAVQGGLAGKRRATTFILALHTBLALHALHYHQVDVAAVQGGLAGKRRATTFILALHTBLALHALHYHQVDVAAVQGGLAGKRRATTFILALHTBLALHALHYHQVDVAAVQGGLAGKRRATTFILALHTBLALHALHYHQVDVAAVQGGLAGKRRATTFILALHTBLALHALHYHQVDVAAVQGGLAGKRRATTFILALHTBLALHALHYHQVDVAAVQGGLAGKRRATTFILALHTBLALHALHYHQVDVAAVQGGLAGKRRATTFILALHTBLALHALHYHQVDVAAVQGGLAGKRRATTFILALHTBLALHTHALHYHQVDVAAVQGGLAGKRRATTFILALTFILALTHALHYHQVDVAAVQGGLAGKRRATTFILALTFILALTHALHYHQVDVAAVQGGLAGKRRATTFILALTFILALTHALHYHQVDVAAVQGGLAGKRRATTFILALTFILALTFILALTHALHYHQVDVAAVQGGLAGKRRATTFILALTFILALTTALALHYHQVDVAAVQGGLAGKRRATTFILALTFILALTTALTHALHYHQVDVAAVQGGLAGKRRATTFILALTFILALTTALTHALHYHQVDVA	549 601 609 661 721 729 8011 3 800117	XX XX XX XA AAB00117; XX XX X0

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.999 AVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDALVDTDGSEVFEG
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                                                        Polypeptides comprising an immunogenic portion of Mycobacterium tuberculosis antigens Mtb-81 or Mtb-67.2 or variants that differ by substitutions, additions, insertions and/or deletions but which still react with antigen specific antisers or T-cells are described. Also described are polymorleotides encoding the polypeptides. The polypeptides, expression vectors expressing the polypeptides or comprising an antisense polymorleotide, or an antigen presenting cell comprising a sequence encoding the polypeptides are useful for determining the presence or absence of M.:tuberculosis in whole blood, serum, sputum, plasma, saliva, cerebrospinal fluid or urine in a patient infected with human immunodeficiency virus (HIV):
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portion of M. tuberculosis antigens Mtb-81 and Mtb-67.2, use diagnosis, treatment and monitoring therapy of tuberculosis
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Pred. No. 9.3e-315;
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                         IMDALFIGLIAIHGLKASDVNGPLINSRIGSIYIVKPKMHGPAEVAFICELFSRVEDVLG
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Senoh A, Ikeda M,
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2000JP-0159162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ
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larity 61.3%; Pred. No. 3.1e-186;
Conservative 90; Mismatches 184;
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KARAAEKPAPSDRAGDDAAR 2438
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                                                                               Protein;
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                                                                                                                                               entry)
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                                                                                                                                                                                                                                                            Cornyeform glutamicum
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N-PSDB; AAT05501.
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Best Local Simi
Matches 444;
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed profile acids, but was obtained in electronic format directly from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 EMSKNGRIFTRELNKDRVYIGRNGTELVLHGRSLLFVRNVGHLMQNPSIL-IDGEEIFEG
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61.3%; Pred. No. 3.1e-186;
ive 90; Mismatches 184;
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Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation procein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diacid; carbohydrate; aromatic compound; vitemmin; cofactor; polyketide; diagnosis; Corynebacterium diphtheriae; evolutionary study.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sugar
or
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                                                               Corynebacterium glutamicum SMP protein sequence SEQ ID NO:594
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AAB79539 standard; Protein; 739
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99DE-103180
99DE-1032237
99DE-1032237
99DE-1032328
99DE-1032924
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99DE-1032974
99DE-1035974
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                                                                                                                                                                            Corynebacterium glutamicum
                                           (first entry)
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N-PSDB; AAF71656.
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08-JUL-1999;
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                                           30-APR-2001
                                                                                                                                                                                                                      04-JAN-2001
                      AAB79539;
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09-JUL-1
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standard; Protein; 712

AAB79540 AAB79540;

AAB79540 RESULT

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AAB79243 to AAB 79633 which are involved in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors [II] for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic amino acid (preferred), a purine or pyrimidine base, or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The presence of [I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of corpusational diphtheriae in a subject. (I), (II), (III) or host cells containing them are used to map genomes of enganisms related to containing them are used to map genomes of organisms related to containing them are used to map genomes of organisms related to in evolutionary studies, in determining SMP protein regions required for for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH).
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Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonprotelinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleoside; nucleoside fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; diol; diagnosis; Corynebacterium diphtheriae; evolutionary study.
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                                                                 Corynebacterium glutamicum SMP protein sequence SEQ ID NO:596.
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99DE-1031413.
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99DE-1031420.
99DE-1031424.
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                                                                                                                                                                                                        Corynebacterium glutamicum
                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pompejus M, Kroeger B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-061975/07.
N-PSDB; AAF71657.
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                                                                                                                                                                                                                                                                                      23-JUN-2000;
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09-JUL-1999;
09-JUL-1999;
09-JUL-1999;
09-JUL-1999;
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                                                                                                                                                                                                                                                                                 61 AQIDKWHRRRVIEPIDMDAYRQFLTBIGYLLPBPDDFTITTSGVDABITTTAGPQLVVPV 120
                                                                                                                                                                                                                                                                                                           MLIDDYHRNN-SGTIDQEAYEDFLKEIGYLVEEPEAAEIRTQNVDTEISSTAGPQLVVPI 138
                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIDPESQVGTIDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA 300
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                                                                                                                                                                                                                            TDRVSVGNIRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLIPQNQALLNARDELQ
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                                                                                                                                                                                                                                                                                                                                                          259 QIDPVHPIGKADKTGLKDIVLESAITTIMDFBDSVAAVDAEDKTLGYSNWFGLNTGELKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          660 SLERMAPLVDRONAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPQNTMKIGIMDEERRITVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPSPTAATLHALHYHQVDVAAVQQGL-AGKRRATIEQLLTIPLAKELAWAPDEIREEVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCOSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRA
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                                                                                                                                                                          Length 739;
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metabolism and oxidative phosphorylation (SMP) proteins given in ABB79243 to AAB 79633 which are involved in carbon metabolism and captured are involved in carbon metabolism and central program of the control of the control of glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleoside, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a contactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of containing them are used to map genomes of organisms related to one fine the map genomes of organisms related to in evolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein regions required metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP), NADPH).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NN-SGTIDQEAYEDFLKEIGYLVEEPEAAEIRTQNVDTEISSTAGPQLVVPILNARFALN 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIMDEERRITVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKGTMKSQPWI 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVRWVDQGVGCSKVPDIHDVALMEDRATIRISSQLLANWIRHGVITSADVRASLERMAPL 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 RRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPVLNARFALN 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 AANARWGSLYDALYGTNAIPETDGAEKGKEYNPVRGQKVIEWGREFLDSVVPLDGASHAD 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 ATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEILIDPESQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIAIHGLKASDVNGPLINSRTGSIYIVKPKMHGPAEVAFTCELFSRVEDVLGLPQNTMKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAWVPSPTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 VEKYNITDGKLAAHIGDSVYRLKNRESYRGFIGNFLDPBAILLETNGLHIBLQIDPVHPI
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AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.1%; Score 2253; DB 22;
61.2%; Pred. No. 3.5e-183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 61.2
Matches 438; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence . 712 AA;
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Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                            Novel human diagnostic protein #18348.
          ABG18357 standard; Protein; 1190 AA.
                                                                                                                    2000US-0540217.
2000US-0649167.
                                                                                                         30-MAR-2001; 2001WO-US08631
                                                                                                                                                           WPI; 2001-639362/73.
                                                                                                                                                Liu C,
                                                                                                                                                                                                                                                                                                                                             1190 AA
                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                 N-PSDB; AAS82544
                                                                                   WO200175067-A2
                                                                        Homo sapiens.
                                                                                                                    31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                             biodiversity
                                                                                                                                                 Drmanac RT,
                                18-FEB-2002
                                                                                              11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                              Sequence
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                      ABG18357;
RESULT 8
ABG18357
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Tang YT;

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The invention relates to isolated polymuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, colymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The control of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques contentifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a cod supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical cod isorders involving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations contexposes of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human of mannowing and produces of the invention.

Contexpositic amino acid sequences of the invention.

Contexpositic amino acid sequences of the invention.

Contexpositic amino acid sequences of the invention.
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.0%; Score 991.5; DB 22; Length 1190; ilarity 53.1%; Pred. No. 3.6e-75; Conservative 66; Mismatches 97; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                          Claim 20; SEQ ID No 48716; 103pp; English.
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18-FEB-2002
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DDSVPLSSGSFGDATGFTVQDGQLVVALPD-KSTGLANPGQFAGYTGAAESPTSVLLINH 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #25444
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N-PSDB; AAS89640.
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23-AUG-2000;
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disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of date and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412 FSRV--EDVLGLPQNTMKIGIMDEERRITVNLKACIKAAADRVVFINTGFLDRTGDEIHT
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food supplement; medical imaging; diagnostic; genetic disorder
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Best Local Similarity 60.3%; Pred. No. 4.5e-54;
Matches 146; Conservative 34; Mismatches 53; Indels
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N-PSDB; AAS82545.
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Human; chromosome mapping; gene mapping; gene therapy; forensic;
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           Drmanac RT,
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                               The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of dan and products dependent on DNA and amino acid sequences. ABG00010 ABG30377 represent novel human dan calculation, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                     69 RRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPVLNARFALN 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNPGPVKDKAAYKSFLRELGYLVPQPERVTVETTGIDSEITSQAGPQLVVPAMNAKYALN 258
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food supplement, medical imaging, diagnostic, genetic disorder.
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            Claim 20; SEQ ID No 48717; 103pp; English.
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50.9%;
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2000US-0649167.
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Best Local Similarity 50.95
Matches 115; Conservative
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23-AUG-2000;
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The invention relates to isolated polynucleotide (1) and polypeptide (11) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome conjunction and probability and in recombinant production of (11). The polynucleotides are also used in diagnostics as expressed sequence tags for for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (11) or to treat disease states involving (11). (11) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (11) and its binding partners are useful in medical inaging of sites expressing (11). (1) and (11) are useful in medical inaging of sites expressing (11). (1) and (11) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and call sequences. ABG00010-ABG00377 represent novel human amino acid sequences of that and products dependent on DNA and amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 LRIARVLYDFVNNEALPGIDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQIDKWHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1641;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.4%; Score 585.5; DB 22; Length 42.4%; Pred. No. 2.6e-40; ive 46; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 48715; 103pp; English.
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                                                                               WPI; 2001-639362/73.
Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1641 AA;
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                                                                                                                           N-PSDB; AAS82543
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(first entry)

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Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; ostecarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hyperthrision; hyperthridism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                               Human ORFX protein sequence SEQ ID NO:5996,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, SEQ ID 5996; 1037pp; English
                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000; 2000US-206132P. 29-AUG-2000; 2000US-228716P.
                                                                                                                                                                                                                                                                                                                                29-MAY-2001; 2001WO-US10836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABN18759.
                                                                                                                                                                                                                                                                 WO200192523-A2.
                                                                                                                                                                                                                                 Homo sapiens.
                 24-JUN-2002
                                                                                                                                                                                                                                                                                                06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chair reaction (PCR) primars, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical maging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and anno acid sequences. Agglowers of the invention.

Context The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the the. WiPo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 RRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPVLNARFALN 128
343 SNPGPVKDKAAYKSFLRELGYLVPQPERVTVETTGIDSEITSQAGPQLVVPAMMARYALN 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 LRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQIDKWHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 LRIDANFKRFVDEEVLPGTGLDAAFWRNFDEIVHDLAPENRQLLAERDRIQALDEWHR
                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 441;
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llarity 55.9%; Pred. No. 3.4e
Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 48714; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP03007 standard; Protein; 130 AA.
                                                                                                                                                                                                                                               Tang YT,
                                                                                                                                                               31-MAR-2000; 2000US-0540217.
                                                                                                                                                                                                                                                                               2001-639362/73
                                                                                                                                                                                                                                             Liu C,
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Matches 81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   441 AA;
                                                                                                                                                                                                              (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                               WPI; 2001-639362,
N-PSDB; AAS82542
                                                              WO200175067-A2.
                                                                                                                               30-MAR-2001;
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                                                                                                11-OCT-2001
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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN1575 to ABN27252 encode the human ORFX or proteins given in ABP00010 to ABN1505. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide squences can be used in gene therapy ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders related to organizansplantation, cardiovascular diseases, disorders related to organizansplantation, cardiovascular diseases, disorders related to organizatorace disease, various immune deficiencies and disorders, infectious disease, autoimmune thypoiditis, myasthenia gravis, graft-versus-host disease, autoimmune inflammatory eye disease. ORFX proteins are also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 AA;
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264 AITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAVDKDGTAFLR-VLNRDRNYTAP 322
                                                                                                                                                                                                                                                                                                                                              AA016702 standard; Protein; 533
                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli aceB protein.
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2001US-306867P.
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N-PSDB; AAL52112.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
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           144 TDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVPLSSGSFGDATGFTVQDGQLVVAL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 PDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEILIDPESQVGTTDRAGVKDVILES 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 IQQQQDIDN-GTLPDFISETASIRDADWKIRGIPADLEDRRVEITGPVERKMVINALNAN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----THFTPORNKLLAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter sequence joined to the coding sequence of the E.coli aceb gene at a unique Sall site. This sequence was then joined by the 3' sequence of exon 5 of sheep growth hormone gene. Minor sequence modification around the initiation codon of the bacterial aceB gene was made by site-directed mutagenssis. The construct was transferred to transgenic mice and the mice were analysed for expression of malate synthase. The value for expression (imples product formed/mg See AAAQ3177-Q43183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene expression cassette for high level expression of bacterial and/or plant genes - comprises inducible promoter and 3'-non-coding sequence of growth hormone exon 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Construct MTAceB2 consists of the sheep metallothionein-Ia gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99;
                                                                                                                                                                                                                 Growth Hormone; metallothionein Ia; inducible promoter;
bacterial gene expression; malate synthase; glyoxylate cycle;
transgenic animal.
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                                                                                                                                                                                                  E.coli malate synthase expressed from MTAceB2 construct
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                                                                                                                     AAR37585 standard; Protein; 533
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(first entry)
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                                          LNARFALNA 129
                                                                LNARFALNA 130
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                                                                                                                                                                                                                                                                  Escherichia coli.
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                                                                                                                                                                                                                                                                                        WO9218635-A1
                                                                                                                                                                                                                                                                                                                                   13-APR-1992;
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29-JUL-1993
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Best Local Simi
Matches 120;
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AAR37585
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111 VKVFMADFEDSLAP------DW---NK-----VIDGQINLRDAVNGTISYTNE 149
                                                                                                                                                                                      150 AGKIYQLKPNPAVLICRVRGLHLPEKHVTWRG----EAIPGSLFDFALYFFHNYQALLAK 205
                                                                                                                                                                                                                                                                                                                               380 VNGPLINSRIGSIYIVKPKWAHGPAEVAFICELFSRVEDVLGLPQNIMKIGIMDEERRITIV 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---HNVDA----GLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAWVPSPTA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises a method of preparing L-amino acids. The method involves fermenting microorganisms of Enterobacteriaceae family that produce the desired L-amino acid, in which the aceB (malate synthase A) agene is eliminated. The method is useful for preparing L-amino acids (e.g. L-threonine). The L-amino acids produced by the method of the invention are useful in human medicine and in the pharmaceuticals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enzyme; L-amino acid preparation; malate synthase A; aceB; L-threonine; human medicine; pharmaceutical industry; foodstuffs; animal nutrition.
                                                                                                                  323 GGGOFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEGIMDALFT-GLIAIHGLKA--SD
                                                                                                                                                                                                                                                                                                                                                                                                                                      206 GSGP-----YFYLPKTQSWQEAAWWSEVFSYAEDRFNLPRGTIKATLLIETLPAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 OMDEILHALRDHIVGLNCGRWDYIFSYIKTLKNYPDRVLPDROAVTMDKPFLNAYSRLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 KTCHKRGAFAMGGMAAFIPSKDEEHNNQ-VLNKVKAD----KSLEANNGHDGTWIAHPGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        440 NLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMV---RKGTMKSQPWLLAYED---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 GSGP-----YFYLPKTQSWQEAAWWSEVFSYAEDRFNLPRGTIKATLLIETLPAVF 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 KTCHKRGAFAMGGMAAFIPSKDEEHNNQ-VINKVKAD----KSLEANNGHDGTWIAHPGL 371
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industry, the foodstuffs industry and in animal nutrition. The present amino acid sequence represents the Escherichia coli aceB protein.
                                                                                                                                                                                                                                                                          Query Match 5.0%; Score 189.5; DB 24; Length 533; Best Local Similarity 22.7%; Pred. No. 3.1e-07; Matches 120; Conservative 67; Mismatches 253; Indels 89; Gaps.
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Sequence 7, Appli Sequence 10434, A Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 4, Appl Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 15, Appli

Sequence 15, A

Sequence Sequence Seguence Sequence

Sequence

Sequence 33, Appl Sequence 33, Appl Sequence 33, Appl Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 7, Appli

Sequence 6, Appli Sequence 37319, A Sequence 32438, A Sequence 2, Appli

us-09-688-672a-2.rapb

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AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTAGPQLVVPV
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US-09-272-975-2

Sequence 2, Application US/09272975

Publication No. US20030027774A1

GENERAL INPORMATION:
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: TUBERCULOSIS ANTIGENS AND METHODS
TITLE OF INVENTION: TUBERCULOSIS ANTIGENS AND METHODS
TITLE OF INVENTION: USBRECULOSIS ANTIGENS AND METHODS
TITLE OF INVENTION: 101021.474

CURRENT APPLICATION NUMBER: US/09/272,975

CURRENT FILING DATE: 1999-03-18

NUMBER OF SEQ ID NOS: 63

SEQ ID NO 2

EBNORTH 748

LENGTHAR: 748
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US-10-9864-761-37319
US-10-986-2438
US-09-864-2833
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US-09-986-3846-33
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 740; Conservative 0; Mismatches
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; ORGANISM: Mycobacterium tuberculosis
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Sequence 6988, Ap
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1 TDRVSVGNLRIARVLYDFVN......KARAAEKPAPSDRAGDDAAR 740
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APPLICANT: MAXAGAM, SALOSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TEBA, MASATO
APPLICANT: SENOH, AKCHIRO
APPLICANT: OZAKI, AKCO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILER REFERENCE: 249-125
CURRENT FILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 6988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-738-626-6988; Application US/09738626; Sequence 6988, Application US/09738626; ENDLication No. US20020197605A1; GENERAL INFORMATION: APPLICANT: NAKAGAWA, SATOSHI
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AVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEG 360
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                                                                                                                                                                             309 AVDKDGTAFLRVLNRDRNYTAPGGGPTLPGRSLMFVRNVGHLMTNDAIVDTDGSBVFBG
                                                                                      LIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA
                                                                                                                                                                                                                                                         369 IMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKMGPAEVAFTCELFSRVEDVLG
                                                                                                                                                                                                                                                                                                                                                                                                                            489 TMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMMTWTELMADMVETKIAQPRAGASTAW
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                                                              LIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA
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; Publication No. US20030027774A1
; GENERAL INFORMATION:
; APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hodds, Michael J.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: TUBERCULOSIS ANTIGENS AND METHODS
; TITLE OF INVENTION: OF USE THEREFOR
; FILE REFERENCE: 2.10121.474
; CURRENT FILING DATE: 1999-03-18
; NUVBER OF SEQ ID NOS: 63
; SEQ ID NO S8
; LENGTH: 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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11arity 100.0%; Pred. No. 0;
Conservative 0; Mismatches.
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US-09-272-975-58
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Best Local Similarity
Matches 740; Conserv
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US-09-272-975-58
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Length 530;

MASAHIRA

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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-562
CURRENT APPLICATION NUMBER: US 10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9582
LENGTH: 530
                                                                                                                                                               ORGANISM: Streptomyces avermitilis US-10-156-761-9582
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Best Local Simil
Matches 124;
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                                                                                       Gaps
                                                                                     ;9
                                                        Length 739;
                                                                                     Indels
                                                        Query Match 60.1%; Score 2289; DB 10;
Best Local Similarity 61.3%; Pred. No. 4.3e-205;
Matches 444; Conservative 90; Mismatches 184;
    ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6988
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                                                                                                    -LIDPES 246
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                                                                                                                                            GRIVAAPGERRPELLKERRRQAIRLAAGSALDFPLATAGVRADASWRVAAPAGLTDRRV
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                                                                                                                                                                                                                                                                                                                                                                                                    365 LFTGLIAIH-GLKASDV-NGPLINSRIGSIYIVKPKMHGPAEVAFTCELFSRVEDVLGLP
                                                                                                                                                                                                                                                     93 EITGPPDRRTAVNALNSKARVWWADFEDATSP------TWDNIIGGQL-----
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                                                    124;
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                                                                                                    197 GQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI---
4.8%; Score 184; DB 15;
21.9%; Pred. No. 4e-08;
ive 74; Mismatches 245;
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Sequence 9538, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISHIKAWA, JUN
HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
HATTORI, MASAHIRA
                          Similarity 21.9
24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
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KESULI 4.
US-10-156-761-9582.
Sequence 9582, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, UUN
APPLICANT: SHIRAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SARAKI, YOSHIYUKI

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49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3153 LHDLAGLRGGESVLVHSAAGGVGMAAVQLARHWDAEVFGTASKGKWDVLAAQGLDEEHIG 3212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3270 GVVGADGVPDIRYVAFD---LAEAGAERIGOMLDEIMALFDAGVLRLPPLRAWPVRRAHE 3326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SG----VAPDLAAELGALGAEVTVAACDVANRKALLEDI--PPEHPVTGIVHTAGVL 3438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3439 DDGVVSGLTPERVDTV-LKPKVDAALTLESVÍGELDLÜPALFVÍFSSAASMLGGPGGGSY 3497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A----PMPTDEALHLFDRATELGDPVLLPMRLNEAALEDRAAD---GTLPPLLSGLVRVR 3602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1603 HRPSARAGTATAAPATGPEAFARELAAAPDPRRALKDLVRGHVALVLGHSGPEAIDAEQA 3662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALNAANARWGSLYDALYGTDVIPETD--GAEKGPTYNKV-----RGDKVIAYARKFL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDSVPLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---VDAADKVL--GYRNWLGLNKGDL---A 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGSIYIVKPKMHGP-----AEVAF-TCELFSR-----VEDVLGLPQNTM-----KIGIM 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 SLMFV---RNVGH-LMTNDAIVDTDGSEVFEGIMDALFTGLIAIHGLKASDVNGPLINSR 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRASLERMAPLVDRQN 672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 TMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMW----TMTELMADMVETKIAQPRAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| :: || | :: || AAANQ-FIDTIJARHRARRGLTS-----VSLGWGLWHEASGLTGGLADI DRDRMS--RAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 PG----TDIDPD-SFWAGVDKTVADLIPQNQALLNARDELQAQIDKWHRRRVIEPID---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STAWVPSPTAATLH-----ALHYHQVDVAAVQQGLAGKRATIEQLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Recombinant OTHER INFORMATION: Oleandolide PKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TIP--LAKELAWAPD---EIREEVDNNCQSILGYV---
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3816;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        3.5%; Score 135; DB 11;
llarity 21.3%; Pred. No. 0.04;
Conservative 112; Mismatches 297;
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PRIOR APPLICATION NUMBER: 60/106,100
PRIOR FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 3
LENGTH: 3816
TYPE: PRT
CREATURE: PRT
CREATURE: PRT
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 190; Conserv
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OY 595 BEVDNNCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLR 648	OY 649 HGVITSADVRASLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELIL 699	700 SGAQQPNGYTEPILHRRREFKARAAEKPAPSDRA 734	:     :     :	·····································	; Sequence 539, Application US/10080170 ; Publication No. US20030129601A1	ACTERIAL GENOMICS AS A TOOL FOR	ITS FOR THE DIAGNOSIS, BACTERIOSES	CURRENT APPLICATION NUMBER: US/10/080,170 CURRENT FILING DATE: 2002-06-10 PRIOR APPLICATION NUMBER: 60/270,123	) PRIOR FILING DATE: 2001-02-22 ) NUMBER OF SECONDOS: 652	. Facement ver. 2 539 1624 RT	H	Query Match 3.4%; Score 130; DB 16; Length 1624;	Pred. No. 87; Mismato	Qy 153 ÅEKG-PIYNKVRGDKVIAYARKFLDDSVPLSSGSFGDAIGFIVQDGQLVVALPDKST 208	916 ADKGTATFSDIANDVAKSYG-FWLGDAF-ASGGSVGYDHKAMGITAR96	QY 209 GLANPGQFAGYTGFAESPISVLLINHGLHI-ELLIDPESQVGTIDFAGVKDV 259	260 -ILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAVDKDGTAFL	:       : :       : :       : :       : :       :	Qy 311 RVLNRDRNYTAPGGGFTLPGRSLMFVRNVGHLMTNDAIVDTGSEVFEGI 361	Db 1044DYDRSLISEGGGVYSREQKAIPLSAQVRAVLGIDGSVDGGAAEMAPPNLIRAILRAP 1100	362 MDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKMHGPAEVAFTCELFSRVEDVLGL 42	IKAESESDADVGDRAN	Qy 422 PQNTMKIGIMDEERRITTVNLKACIKAAADRVVFINTGFLDRTGDEIHT 46:	EVNI	Qy 470 SMEAGPMVRKGTMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTWTELMADMVET 527	Db 1187 KILIDSLVSAĞTVKADERTÖLLESMTDEVAQLVLADN 122	VPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQ 		OY 5/1 LDTITE-LAKELAWAFDEIKEEVDNNCQSIDGIVVKWVDQGVGCSKVFDINDVALMBUAAI 93
CY 673 AGDVAYRPMAPNFDDSIAFLAAQELILSCAQOPNGYTEPILHRRREFKARAA 725 	RESULT 7 IIS-10-329-079-45	; Sequence 45, Application US/10329079 ; Publication No. US20030198981A1	; GENERAL INFORMATION: ; APPLICANT: FARNET, Chris ; APPLICANT: ZAZOPOULOS, Emmanuel	; APPLICANT: STAFFA, ALFredo ; TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDE ; FILE REFERENCE: 3002-11US	CURRENT APPLICATION NUMBER: US/10/329,079 CURRENT FILING DATE: 2002-12-24	Nowher of SEQ 1D NOS: 00 7 SOFTWARE: Patentin version 3.0 7 SEQ ID NO 45	LENGTH: 5245   TYPE: PRT   TYPE: PRT   CRGANISM: Strebtomyces refuineus	US-10-329-079-45 Query Match 3.5%; Score 132.5; DB 12; Length 5245;	u)	OY 70 RVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVV 118	119 PULNARFALNAANARWGSLYDALYGTDVIPETDGAEKGFTYNKVR-GDKVIAYARKFLDD		Qy 178 SVPLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAB 224	Db 4205LNSRANRLARLLAGRGAGPEDTVAVLLP-RGAGLITALVAVQKAGAAYVPLDAE 4257	225 SPTSVLLINHGLHIEILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDA	4258 LPTGRIAHMLDDAKPVLTVTLTGMRDALPAGAGFVVCLDDPATEAALAGI	AAF 43	336 FVRNVGHLMINDAIVDTDGSEVFEGIMDALFIGLIAIHGLKA	Db 4353 LVRSAARYRGAAGTVLLHGSPAFDLTVTTLFTPLVAGGCIVVADLDAAEGDAPNRPDLLK 4412	Oy 384HOPAEVAFICE 410	Db 4413 VIPSHLAFLDGIASWAAPAADLVVGGEQLTGARLARLRAAHPGMRVYNDYGPTEATVSCA 4472	Qy 411 LFSRVEDVLGLPQNTMXIGIMDEERRTTVNLKACIKAAADRVVFIN 456	Db 4473 DFV-LEPGDELPADAVPIGRPLAGHRLFVLDERLRPvPAGVPGELYIAGVGVA 4524	OY 457 IGFLDRIGDEIHTSMEAGPWVRKGIWKSQPWILAYEDHNVDAGLAAGF 504	Db 4525 RGYLGRPGMTAERFVGCPFGGPGBRMYRTGDLARWRPDGNLEY 4567	OY 505 SGRAQVGKGMWTWTELMADMVETKIAOPRAGASTAWVPSFTAATLHAL 552	Db 4568 LGRGDGQLKVRGFRIEPGEIEAALLDRPEIGQAAVVLRGERLVAYVAAPEA 4618	OY 553 HYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIR 594	DD 4619EFUFAALKEGLAAKLFKXMVFAA1VKLDALFLAFGGKLDHKALFEFFAFALAFHUKK 46/5

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APPLICANT: Cepek, Karyn
TITLE OF INVENTION: Methods and Compositions for Modulating Heterotypic E-cadherin
TITLE OF INVENTION: Interactions with T Lymphocytes
FILE REFERENCE: LO0560/70010ERP
CURRENT APPLICATION NUMBER: US/10/165,049
CURRENT FILING DATE: 2002-06-07
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    744 TRDNVYYYDEEGGGEEDQDFDLSQLHRGLDARPEVTRNDVAPTLMSVPRYLPRPANPDEI 803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        560 -----LIIATDNGSPVATG----TGTLL---LILSDVNDNAPIPEPRTIFFC 599
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22.0%; Pred. No. 0.016;
iive 66; Mismatches 210;
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PRIOR APPLICATION NUMBER: USSN 08/237,919
PRIOR FILING DATE: 1994-05-03
PRIOR APPLICATION NUMBER: USSN 08/237,919
PRIOR PILING DATE: 1994-05-03
PRIOR PILING DATE: 1995-03-03
PRIOR PILING DATE: 1996-11-01
PRIOR PILING DATE: 1996-11-01
PRIOR FILING DATE: 1996-11-01
PRIOR FILING DATE: 2001-03-01
NUMBER: OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
LENGTH: 878
                                                                                                                                                                                                      Sequence 2, Application US/10165049
Publication No. US20020192724A1
GENERAL INFORMATION:
APPLICANT: Brenner, Michael
APPLICANT: Cepek, Karyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (800)..(808)
OTHER INFORMATION: HAV tripeptide
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NAME/KEY: misc feature
LOCATION: (2225). (2295)
OTHER INFORMATION: transmembrane
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Best Local Similarity 22.0
Matches 134; Conservative
                                             594 REEVDNNCQS 603
                                                                            804 GNFIDENLKA
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                                                                                                                                                                                                                                                                                 Sequence 48, Application US/09905983

Retent No. US20020045591A1

GENERAL INFORMATION:

APPLICANT: Geiger, Benjamin

APPLICANT: Geiger, Benjamin

APPLICANT: Sadot, Avri

APPLICANT: Sadot, Enhat

IIILE REFERENCE: 01/2236

CURRENT APPLICATION NUMBER: US/09/905,983

CURRENT APPLICATION NUMBER: US/09/905,983

CURRENT FILING DATE: 2001-09-28

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin version 3.1

SEQ ID NO 48

LENGTH: 878
                                                                                 1326 -RETPEIRSHQLRREIVTTMLINDLVDTAGITYAFRIAEDVGVTPI-----DAVRTYVAT 1379
  ----LATELPDQDVFASRLPRYFPTALRE---- 1325
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                                           LRISSQLLANWLRHGVITSADVRASLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQ 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              354 TATAVITVTDINDNPPIFNPTTYKGQVPENBANVVITTLKVTDADAPNTPAWBAVYTILN 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------PGQFAGYTGAAESPTSV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLINHGLHIEILIDPESQVGTTDRAGV------KDVILESAITTIMDFEDSVAAV 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 DAADKVLGYRNWLGLN--KGDLAAAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMF 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337 VRNVGHLMTNDAIVDTD-GSEVFEGIMDALFIGLIAIHGLKASDV--NGPLINSRIGSIY 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    548 TLHALHYH------QVDVAAVQQGLAGK----RRATIEQLLTIPLAKELAWAPDEI 593
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22.0%; Pred. No. 0.016;
ive 66; Mismatches 210; Indels 200;
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                                                                                                                                 ELILSGAOOPNGYTEPILHRRRREFKARAAEKP-APSDRAGDDAAR 740
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1279 GLTSPELATLMAHVKLGLKEEV--
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Best Local Similarity 22.0
Matches 134; Conservative
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; ORGANISM: Homo sapiens
US-09-905-983-48
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US-09-905-983-48
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Db 560LIIATDNGSPVATGTGTLLLILSDVNDNAPIPEPRTIFFC 599	OY 394 IVKPKMHGPAEVAFTCEL-PSRV	Qy 432 DEERRITYVLKACIKAAADRVVFINTGFLDRIGDEIHTSMBAGPMVRKGTMKSQPWILAY 491	OY 492 EDHNVDAGLAAGFSGRAQVGKGMWIMTELMADNVETKIAQPRAGASTAWVPSPTAA 547	OY 548 TLHALHYHQVDVAAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEI 593	Qy 594 REBUDNNCQS 603        ::       ::         ::	Query Match Best Local S	<pre>172; Conservative 85; Mismatche 9 LRIARVLYDFVNNEALPGTDIDPDSFWAGVDE  </pre>	DAEITTTAGPQLVVP   :  RRRADRRQEPMAIVG	Qy 120 VLNARFALNAANARWGSLYDAL-YGTDVIPETDGAEKGPTYNKVRGDKVIAYARK 173 ::	QY 174 FLDDSVPLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSV 229	Qy 230 LLINHGLHI:BILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDA 280  10397 RGTDVGVYVGCGYQDYAPDIRVAPEGTGGVV-VTGNSSAVASGRIAYSLGLEGPAVTVDT 10455	Qy 281 ADKVLGYRNWLGLNKGDLAAAVDKDGTAFLRVLNRDRNYTAPGGGQFTLFGRSLMFV 337
Db 600 ERNPKPQVINIHDADLPPNTSPFTAELTHGRVPNWTIQYNDPTQESIILKPKMALEVG 657	Qy 432 DEERRITVNLKACIKAAADRVVFINTGFLDRIGDEIHTSMEAGPMVRKGTWKSQPWILAY 491  Db 658DYKINLKLMDNQNKDQVTTLEVSVCDCEGAAGVCRKAQP 696	QY 492 EDHNVDAGLAAGFSGRAQVGKGWWTWTELMADWVETKIAQPRAGASTAWVPSPTAA 547	QY 548 TLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEI 593	Qy 594 REEVDNNCQS 603  Db 804 GNFIDENLKA 813	ESULT 11 S-10-165-049 S-quo-165-049 S-grant on Fibration GENERAL INF APPLICANT: APPLICANT: TITLE OF ITITLE	3 . 3.48;	Best Local Similarity         22.0%;         Pred. No. 0.016;           Matches         134;         Conservative         66;         Mismatches         210;         Indels         200;         G           91         LPEPDDFTI        TISGVDAEITTTAGPQLVVPVLNARFALNAANARWGSL	307 LPDKNMFTINKNTGVISVVTTGLDRESFPTYTLVVQAADLQGEGLST 35 142 YGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVPLSSGSFGDATGFT 19	DD 354 TATAVITYTDINDNPPIRNPTTYKGOVPENBANVVITTLKVTDADAPNTPAWEAVYTILN 413  QY 194 VQDGQLVVAL-PDKSTGLANPGQPAGYTGAAESPTSV 229	230 LLINHGLHIEILIDPESQUGTTDRAĞVKDVILESAITTIMDFEDSVAAV	279 DAADKVLGYRWHGLNKGDLAAAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMF	DD 526 SNWLEINPOTGAISTRAELDREDFEHVKNSTYTA 559 QY 337 VRNVGHLMTNDAIVDTD-GSEVFEGIMDALFTGLIAIHGLKASDVNGPLINSRTGSIY 393

10582

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-AGFSGRA 508

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-SWEVFERAGIDPASV 10396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10583 ---SSDVDVVEGHGTGTRLGDPIEAQALLATYGQGRAPGQPLRLGTLKSNIGHTQAASGV 10639
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                                                                                                                                                                                                                                                                                                                                              INSRIGSIYIVKPKWHGPABVAFICELFSRVEDVLGLPQNIMKIGIMDEERRITVNLKAC 444
PLDDSVPLSSGSFG----DATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSV 229
                                                                                                                                                                      A---DKVLGYRNWLGLNKGDLAAAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFV
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                                                                                    -----EILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDA
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Publication No. US20030087405A1
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Alao, L.
TITLE OF INVENTION UNMERS: US/09/836,821
CURRENT APPLICATION NUMBER: US/09/836,821
CURRENT PILING DATE: 2001-04-17
PRIOR PRILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
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                                      10349 FLDDAAGFDAAFFGISPREALAMDPQQRQLLEA
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Best Local Similarity 20.7
Matches 172; Conservative
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LENGTH: 11877
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US-09-836-821-6
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                                                             0498 SQQAMAADGRIKGFASAADGLAWGEGVAVLLLERLSDARRKCHRVLAV-----VRGSA 10550
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                         ---RNVGHLMTNDAIVDTDGSEV--FEGIMDALFTG--LIAIHGLKASDVNGPL 384
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                                                                                                             INSRIGSIYIVKPKMHGPAEVAFTCELFSRVEDVLGLPQNTMKIGIMDEERRITVNLKAC
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                                                                                                                                                 -----ARLIROALAD--ARLT-
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APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Abe, L.
TITLE OF INVENTION: LibA encoding methywycin and pikromycin
TILE OF INVENTION: 600.438031
CURRENT APPLICATION NUMBER: US/09/860,846
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
                                                                                                                                                                                                                                                                                                                                                                     509 QVGKGMWTMTELMADMVETKIAQPRAGASTA-W-VPSPTAATL
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
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Patent No. US20020164742A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
US-09-860-846-6
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US-09-860-846-6
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                             Sequence 49, Application US/10271889
Publication No. US2030194784A1
GENERAL INFORMATION:
APPLICANT: Liu, H.
APPLICANT: Liu, H.
TAPLICANT: Zhao, L.
TILLE OF INVENTION: DNA Encoding Methymycin and Pikromycin;
TILLE OF INVENTION: DNA Encoding Methymycin and Pikromycin;
FILE REFERENCE: 600.582US1
CURRENT APPLICATION NUMBER: US/10/271,889
CURRENT FILING:DATE: 2002-10-15
FRIOR PELING:DATE: 2001-05-18
FRIOR PELING DATE: 2001-05-18
FRIOR PELING DATE: 2001-05-18
FRIOR PELING DATE: 2001-05-18
RESULT 15
US-10-271-889-49
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vyvgcgyodyapdirvapegtggyv-vtgnssavasgriaysigiegpavtvbt 10455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQIDKWHR
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                                                                                                                                                                                                                                                                                                                                                          3.4%; Score 128; DB 12; Length 11877;
20.7%; Pred. No. 1.2;
ive 85; Mismatches 319; Indels 256; Gaps
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NN NUMBER: US 09/836,821
E: 2001-04-17
NN NUMBER: US 09/105,537
E: 1998-06-26
NOS: 55
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Search completed: November 21, 2003, 16:38:09 Job time : 32.8617 secs

- protein search, using sw model OM protein

November 21, 2003, 15:57:31; Search time 15.4376 Seconds (without alignments) 4609.825 Million cell updates/sec Run on:

Title: Perfect score:

US-09-688-672A-2 3810 1 TDRVSVGNLRIARVLYDFVN......KARAAEKPAPSDRAGDDAAR 740

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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	S15387	SYKVMA	B82519	SYCSM2	T30289	D75581	E82589	B86807	C70867	A90770	E85632	B85547	F90696	HOECL	F70720	I38344
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	3.9	3.8	3.6	3.6	3.6	3.6	3.6	ш Ю	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.3
	149	144.5	139	138	137.5	135.5	135.5	134.5	130	129.5	129.5	129	129	128.5	128.5	127.5
-	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1
F70722
probable glcB protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence revision 17-Jul-1998 #text change 22-Oct-1999
C;Accession: F70722
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holrovd, S
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A. Hitle. Designshowing the bieles: Of Managhantanian takes and the second of

A,Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A,Reference number: A70500; MUID: 98295987; PMID: 9634230
A,Reference number: A70722
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Residues: 1-741 <COL>
A,CLOSS-references: GB: Z78020; GB: AL123456; NID: g3261625; PIDN: CAB01465.1; PID: e257679; A,Gene: g1cB

ö 240 61 AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV 120 121 INARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP 180 300 122 LNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP 181 LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI 241 9 61 2 TDRVSVGNLRIARVLYDFVNNBALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ 62 AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDABITTTAGPQLVVPV 1 TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI LIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA Gaps . 0 Length 741; Indels Query Match
100.0%; Score 3810; DB 2;
Best Local Similarity 100.0%; Pred. No. 3.7e-246;
Matches 740; Conservative 0; Mismatches 0; 182 241 121 181 ò a ઠ g  $\delta$ g  $\delta$ g  $\delta$ 

LIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA 301 301 AVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEG 360 242 g ò Db IMDALFIGLIAIHGLKASDVNGPLINSRIGSIYIVKPKOHGPAEVAFICELFSRVEDVLG 420

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R; Parkhill, J: Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, October 1997
A; Reference number: Z22833
A; Reference number: Z22833
A; Accession: T44752
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Rocession: T44752
A; Residues: 1-731
A; Residues: 1-731
A; Residues: 1-731
A; Residues: EMBL:ALO08609; PIDN:CAA15459.1
A; Residues: Cosmid B1788
C; Genetics:
A; Note: glc8
C; Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase
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IMDALFIGLIAIHGLKASDVNGPLINSRIGSIYIVKPKMHGPAEVAFICELFSRVEDVLG
                                                 LPQNTWKIGIMDEERRITVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPWVRKG
                                                                                                        TMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQFRAGASTAW
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                                                                                                                                                                                                    COSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRAS
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                           LPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG
                                                                                    TMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAW
                                                                                                                                           VPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIREEVDNN
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82.0%; Pred. No. 5.7e-200;
ive 54; Mismatches 72;
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Cigreides Perudomonas aeruginosa
Cigreides Perudomonas aeruginosa
Cibate: 15-8ep-2000 #sequence_revision 15-8ep-2000 #text_change 31-Dec-2000
CiAccession: H8358m, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, X.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Rutes complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Rocession: H83586
A;Accession: H83586
A;Status: preliminary
A;Molecule Lype: DNA
A;Residues: 1-725 < STO>
A;Cross-references: GB-AE004485; GB:AE004091; NID:g9946332; PIDN:AAG03871.1; GSPDB:GN001
C;Genetics:
A;Gene: glcB; PA0482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 INARFALMAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 LSSGSFGDATGFTVQDGQLVVALPDKS-TGLANPGQFAGYTGAAESPTSVLLINHGLHIE
                                                                                                                                                                                         ASTAWVPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIRE
                                                                                                                                                                                                                                                                           DVRASLERMAPLVDRQNAGDVAYRPNAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHR
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                                                                                 EDVLGLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGP
                                                                                                                       EDVLGLPQGTLKVGIMDEERRTTLNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGP
                                                                                                                                                                 MVRKGTMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAG
EVFEGIMDALFIGLIAIHGLKASDVNGPLINSRIGSIYIVKPKMHGPAEVAFICELFSRV
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69.1%; Pred. No. 2.2e-163;
ive 77; Mismatches 139;
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Best Local Similarity 69.1:
Matches 502; Conservative
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mailer synthase G (PA0482) [imported] - Agrobacterium tumefaciens (strain CS8, Cereon) C.Species: Agrobacterium tumefaciens G.Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C.Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C.Dacession: P9784 B. Patrick C. Paris, F.; Mollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A.; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tun A; Reference number: A97359; MUID:21608551; PMID:11743194 A; Status: preliminary A; Scotte: DNA A; Residues: 1-744 < KUR.
                                                                                                                                                                                                                                                                                                                                                                                   PRPNWTPEBIQRELDNNAQGILGYVVRWVDQGVGCSKVPDINNIGLMEDRATLRISAQHM 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANWIRHGVITSADVRASLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQ 703
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       VDPEIAVVAGPQLVVPVMNARYALNAANARWGSLYDALYGTDAISDADGAEKGRGYNPKR 184
                                                                                                                                                       224 ESPTSVLLINHGLHIEILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADK 283
                                                                                                                                                                                                                                                                                                        305 VLVYGNWLGLMRGDLTEÅVSKGGNTFTRRINPDRYYTAPDGSALTLPGRSLMLVRNVGHL 364
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                                                       GDKVIAYARKFLDDSVPLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAA
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A,Gene: AGR C 78
A,Map position: circular chromosome
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AH2582
malate synthase G [imported] - Agrobacterium tumefaciens (strain CS8, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AH2582
C;Accession: AH2582
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Residues: 1-744 <KUR>
A;Residues: 1-744 <KUR>
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                                                                                  EEVSKGGSTFTRIMNPDRVYTRADGSELTLHGRSLLFVRNVGHLMTNDAILDKDGNEVPE
                                                                                                                                                                                 362 GIQDGLFTSLIAIH-----DLNGNTSRKNSRTGSVYIVKPKWHGPEEAAFTNELFGRVED
                                                                                                                                                                                                                                                                                      VLGLPRNTLKVGIMDEERRTTVNLKACIKAAKDRVVFINTGFLDRTGDEIHTSMEAGAVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDAEITTTAGPQLVVPVLNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTVNKVR
                                                  AAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFE
                                                                                                                                                    GIMDALFIGLIAIHGLKASDVNGPLI--NSRTGSIYIVKPKMHGPAEVAFTCELFSRVED
                                                                                                                                                                                                                                                   VLGLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMV
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a gene encoding malate synthase in Coryneba
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Relate: Synthase (EC 4.1.3.2) - Corynebacterium glutamicum
C./Species: Corynebacterium glutamicum
C./Species: Corynebacterium glutamicum
C./Species: Corynebacterium glutamicum
C./Species: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-May-2000
C./Accession: 140715; 140836
R./Richellogy 140, 3099-3108, 1994
A./Ritle: Malate synthase from Corynebacterium glutamicum: sequence analysis of the A/Reference number: 140715; MUID:95111631; PMID:7812449
A./Ricession: 140715
A./Status: preliminary; translated from GB/EMBL/DDBJ
A./Ricession: 14039
A./Richelle Lype: DNA
A./Ricession: 1739 < RES>
A./Cross_references: EMBL:X78491; NID:9530011; FIDN:CAA55243.1; PID:9530012
R./Lee, M./Archiol: Biotechnol. 4, 256-263, 1994
A./Ritle: Molecular characterization of aceB, a gene encoding malate synthase in A/Recession: 140836
A./Status: preliminary; translated from GB/EMBL/DDBJ
A/Rolecule Lype: DNA
A/Rolecule Lype: DNA
A/Rolecule Lype: DNA
A/Rolecule Cype: DNA
A/Rolec
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                                                                                                                                                                                RFALMAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVPLSS
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                     DKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPVLNA
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VSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQI
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AF3299

Mal3299

Mal3291

C; Species: Brucella melitensis

C; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002

C; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002

C; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002

C; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002

C; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002

R; DelVacchio, V; G; Kapatral, V; Redkar, R; J; P.H; Hagius, S; O'Callaghan, D:; Letess Proc. Natl. Acad. Scil. U.S.A. 99, 443-448, 2002

A; Title: The genome sequence of the facultative intracellular pathogen Brucella melitens

A; Reference number: AD3252; PMID:11756688

A; Residues: preliminary

A; Molecule type: DNA

A; Residues: 1-728 *kUR>

A; Cross-references: GB:AE008917; PIDN:AAL51561.1; PID:g17982281; GSPDB:GN00190

A; Experimental source: strain 16M

C; Genetics:

A; Gene: BME10380

A; Map position: I

C; Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase
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    ELSPKNRELLAKRDALQEKIDGWYRENG-APSDFDAYEAFLKEIGYLLPEGPGFKVETNN 124
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                                                                                                                                                VLGYRNWLGLNKGDLAAAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHL
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                                                              EVAFICELFSRVEDVLGLPQNTMKIGIMDEBRRTTVNLKACIKAAADRVVFINTGFLDRT
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.larity 61.8%; Pred. No. 1.2e-146;
Conservative 97; Mismatches 174; Indels
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A,Molecule type: DNA
A,Residues: 1-727 <STO>
A,Residues: 1-727 <STO>
A,Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05852.1; GSPDB:GNO(
A,Experimental source: strain C-125
C,Gene: BH2133
                                                                                                                                                                                                                                                                                                                                                                EGKIKKKRINEDRSYTAPNGETFSLPGRSLMFVRNVGHLMTTPVIRTQSGEEVPEGILDG
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S51788

Malate synthase (EC 4.1.3.2) isoenzyme G - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 23-Aug-1995 #sequence_revision 13-Mar-1997 #text_change 01-Mar-2002
C;Accession: 551789; F65083
C;Accession: 1.; Pellicer, M.T.; Badia, J.; Aguilar, J.; Baldoma, L.
Eur. J. Biochem. 224, 541-548, 1994
A;Title: Molecular characterization of Escherichia coli malate synthase G.
                                                                                                                                                                                     WHRRRVIEPIDWDAYROFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPVLNARF
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                                                                                                        Score 2256.5; DB 2;
Pred. No. 1.5e-142;
; Mismatches 184;
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Best Local Similarity 60.7%
Matches 439; Conservative
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Cipacies: Bacillus halodurans
Cipaces: Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
Cipacession: E8316
R.Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.;
Nucleic Acids Res. 28, 4317-4331, 2000
A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A.Reference number: A83650; MuID:20512582; PMID:11058132
A.Accession: E8316
A.Status: preliminary
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Ba3916

malate synthase BH2133 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Pactes: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: E8316
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                                                                                                                                          QIDPVHPIGKADKTGLKDIVLESAITTIMDFEDSVAAVDAEDKTLGYSNWFGLNTGELKE
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                                                                                         Indels
                                 oxo-acid-lyase
                                                          Score 2289; DB 2; Pred. No. 1.1e-144; 90; Mismatches 184;
                                 coenzyme A;
C,Genetics:
A,Gene: aceB
C,Keywords: carbon-carbon lyase;
                                                           60.1%;
larity 61.3%;
Conservative 9
                                                          Query Match
Best Local Similarity
Matches 444; Conserv
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A;Reference number: S51788; MUID:95010032; PMID:7925370 A;Accession: S51788 A;Status: preliminary	Oy 717 RRE 719  Db 717 LRE 719
A; Residues: 1-723 cMOL. A; Residues: 1-723 cMOL. A; Residues: 1-723 cMOL. A; Residues: 1-723 cMOL. A; Cross-references: EMBL:X74547; NID:9517246; PIDN:CAA52639.1; PID:9517247 A; Cross-references: EMBL:X74547; NID:9517246; PIDN:CAA52639.1; PID:9517247 B; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A; Title: The complete genome sequence of Escherichia coli K-12. A; Accession: F65083 A; Accession: F65083 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Rosidues: 1-723 cBLAP. A; Cross-references: GB:AE000380; GB:U00096; NID:91789344; PIDN:AAC76012.1; PID:91789348; A; Residues: 1-23 cBLAP. A; Cross-references: GB:AE000380; GB:U00096; NID:91789344; PIDN:AAC76012.1; PID:91789348; A; Gene: glob C; Genetics: A; Gene: glob C; Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase	RESULT 10 817774 malter synthase (EC 4.1.3.2) - Neurospora crassa C;Species: Neurospora crassa C;Species: Neurospora crassa C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-May-2000 C;Accession: 817774 R;Sandeman, R.A.; Hynes, M.J.; Fincham, J.R.S.; Connerton, I.F. Mol. Gen. Genet. 228, 445-452, 1991 A;Nitle: Molecular organisation of the malate synthase genes of Aspergillus nidulans and A;Reference number: 817773; MUID:91375430; PMID:1832736 A;Accession: 817774 A;Accession: 517774 A;Relevence number: Branch and A;Residues: 1-542 cSAN> A;Residues: 1-542 cSAN> A;Residues: 1-542 cSAN> A;Residues: EMBL:X56672; NID:92974; PIDN:CAA39994.1; PID:92975
Query Match Best Local Similarity 58.0%; Pred. No. 9.7e-136; Matches 419; Conservative 115; Mismatches 174; Indels 15; Gaps 5;	Aintrons: 447/3 C,Superfamily: malate synthase C,Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase
QY 4 VSVGNLRIARVLYDFVNNBALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQI 63 ::	Query Match 5.4%; Score 205.5; DB 2; Length 542; Best Local Similarity 24.4%; Pred. No. 6.6e-06; Matches 135; Conservative 64; Mismatches 205; Indels 149; Gaps 33;
QY 64 DKWHRRRVIEPIDMDAXRQFLTEIGYLLPEPDDPTITTGGUDAEITTTAGPQLVVPVLNA 123	QY 194 VQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEILIDPESQVGTTDR 253
QY 124 RFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVPLSS 183	QY. 254 AGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAAVD-KDG 306  103 KMVVNALNSDVYTYMADFEDSSAPTWANMVNGQVNLYDAIRRQIDFKQG 151
QY 184 GSFGDATGFTVQDGQLVVALPD-KSTGLANPGQFAGXTGAAESPTSVLLINHGLHIEILI 242	QY 307 TAFLRVLNRDRNYTAPGGGGFTLPGRSLMFVRNVG-HLMTNDAIVDTDGSEVFEGIMDAL 365  152 PKEYK-LRTDRTLVR-TRFRGWHLEEKHVIIDGEPVGGSLFD 193
QY 243 DPESQVGTTDRAGVKDVILESALTTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAV 302	Qy 366 FTGLIAIHGLKASDVNGPLINSRTGSIYIVKPROWHGPAEVAFTCELFSRVEDVLGLPQNT 425
QY 303 DKDĞTAFLRVLNRDRNYTAPGGGĞFTLFGRSLMFVRNGHLMTNDAIVDTDGSEVFEGIM 362 : :  :  :	Qy 426 MKIGIMDEBRRITVNLKACIKA-AADRVVFINTGFLDRTG-DEIHTSMEAGPWV 477  :
OY 363 DALFTGLIAIHGLKASDVNGPLINSRTGSIXIVKPKMHGPAEVAFTCELFSRVEDVLGLP 422	QY 478RKGTMKSQPW1LAYEDHNVDAGLAAGFSGRAQVGKGMWIMT 518
OY 423 ONTWKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKGTM 482	QY 519 ELMADMVETKIAQPRAGASTAWVPSPTAATLHALHYHQVDVAAVQQGL 566 :
QY 483 KSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTWTELMADMVETKIAQPRAGASTAWVP 542	QY 567 AGKRATIEQLLTIPLAKELAWAPDEIREEVDNNCQSILGYVVRWVDQGVGCSKVPDIHD 626 : :   :
QY 543 SPTAATLHALHYHQVDVAAVQGGLAGKRRATIEQLLTIPLAKELAWAPDEIREEV 597	Qy 627 VALMEDRATLRISSQLLANWLRHGVITSADVRASLERVAPLVDRQNAGDVAYRPMA 682
QY 598 DNNCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADV 657	OY 683 PNFDDSIAFLAAQ 695 Db 500 NKFNLAAQYFASQ 512
658	RESULT 11 D91245 malate synthase A [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)

89;

Length 533; Indels

Score 190.5; DB 2; Pred. No. 6.4e-05; 67; Mismatches 241;

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A,Cross-references: GB:AE005174, NID:g12518944, PIDN:AAG59206.1, GSPDB:GN00145; UWGP:ZS6
A;Experimental source: strain 0157:H7, substrain EDL933
A;Genteise:
A;Gente: aceB
C;Superfamily: malate synthase
                                                                                                                                                                                                                                          159 YNKVRGDKVIAYARKFLDDSVPLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAG
                                                                                                                                                     5.0%;
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Best Local Similarity 22.8%
Matches 117; Conservative
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         1-533 <STO>
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: D91245
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterchemorrhagic Escherichia coli 0157:H7 and gency A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Recension: D91245
A;Rocession: D91245
A;Rocession: D91245
A;Rosidues: 1-533 <-HAX>
A;Rosidues: 1-533 <-HAX>
A;Rosidues: 1-533 <-HAX>
A;Rosidues: 1-533 <-HAX>
A;Cross-references: GB:BA000007; PIDN:BAB38355.1; PID:g13364408; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Superfamily: malate synthase
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K.; Apodaca,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 YGEQEKQILTAEAVEFLTELV------THFTPQRNKLLAARIQQQQDIDN-GTLPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 YTGAAESPISVLLINHGLHIEILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKPKMHGPAEVAFTCELFSRVEDVLGLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVF
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                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.0%; Score 190.5; DB 2; Best Local Similarity 22.8%; Pred. No. 6.4e-05; Matches 117; Conservative, 67; Mismatches 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGCVPI-----YGLMEDAATABISRTSIWQWIHH 464
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Manales Synthase (EC 4.1.3.2) - Salmonella enterica subsp. enterica serovar Typhi (strain malate synthase (EC 4.1.3.2) - Salmonella enterica serovar Typhi (species: Salmonella enterica serovar Typhi (species: Salmonella enterica serovar Typhi A,Note: this species has also been called Salmonella typhi (CjDate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 (speciession) AD1011 R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R; Parkhill, J.; Moule, S.; O'Gaora, P. (Conin, A.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. (Conin, A.) Bavis, P.; Davies, R.M.; Simmonds, M.; Skelton, J.; Stevens, K., A; Authors: Parky, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A; Reference number: ABD502; MUID:21534947; PMID:11677608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 AFIPSKDEEHNNQ-VLNKVKAD----KSLEANNGHDGTWIAHPGLA------DTAM 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 YLPKTQSWQEAAWWSEVFSYAEDRFNLPRGTIKATLLIETLPAVFQMDEILHALRDHIVG 271
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| : | : | : | : | | : | | 17 YGEQEKQILTABANEFLTELV------THFTPQRNKLLAARIQQQQDIDN-GTLPD
                                                                                     YTGAAESPTSVLLINHGLHIEILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAV
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C;Superfamily: T
C;Keywords: carl
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27;

Gaps

61

--PGQFAGYTGAAESPTSVLLINHGL---HIEILIDPESQVGTTDRAGVKDVILESAITT 267 KLPDFISETTSIRESNWOIRGIPADLQDRRVET-----TGPVERKMVINALNANVKVF 114 IMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAVDKDGTAFLR-VLNRDRNYTAPGGGQ 326 115 MADFEDSLAP------DW---NK-----VIDGQINLRDAVNGTISYTNEAGKI 153

213 62

12 TFTRPQGELEKQVLTAEAVEFLTELV-----TRFTPKRNKLLAARIQQQQDIDNG

TYNKVRGD----KVIAYARKFLDDSVPLSSGSFGDATGFTVQDGQLVVALPDKSTGLAN-

23.2%; Pred. No. 6.9e-05; ive 67; Mismatches 249; Indels 140;

Conservative

ò g 8 Вb  $\delta$ Db à g à g à g ò g ò g

Local Similarity

384 LINSRIGSIYIVKPRMHGPAEVAFTCELFSRVEDVLGLPQNTMKIGIMDEERRTTVNLKA 443 -----YFYLPKTQAWQBAAWWSBVFSYAEDRFNLPRGTIKATLLIETLPAVFQMDB 260

FTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEGIMDALFT-GLIAIHGLKA--SDVNGP

327

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malate synthase A VC0734 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 18 Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: H82287
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
R;Heidelberg, J.F.; Eisen, J.A.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Status: preliminary
A;Status: preliminary
A;Ressiques: 1-556 cHEI>
A;Coss-references: GB:AE004159; GB:AE003852; NID:g9655167; PIDN:AAF93899:1; GSPDB:GN001
A;Experimental source: serogroup 01; strain N16961; blotype El Tor
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: aceB
A;Map position: 91 min
C;Superfamily: malate synthase
C;Keywords: carbon-carbon lyase; coenzyme A; glyoxylate bypass; oxo-acid-lyase
                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 IQQQQDIDN-GTLPDFISETASIRDADWKIRGIPADLEDRRVEITGPVERKMVINALNAN 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 VKVFMADFEDSLAP-----DW---NK-----VIDGQINLRDAVNGTISYTNE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            323 GGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEGIMDALFT-GLIAIHGLKA--SD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 QMDEILHALRDHIVGLNCGRWDYIFSYIKTLKOVYPDRVLPDRQAVTMDKPFLNAYSRLLI 316
                                                                                                                                                                                                                                                                                                                                                                                                                                          263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380 VNGPLINSRIGSIYIVKPKMHGPAEVAFICELFSRVEDVLGLPQNIMKIGIMDEERRITV 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 GSGP-----YFYLPKTQSWQEAAWWSEVFSYAEDRFNLPRGTIKATLLIETLPAVF 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---HNVDA----GLAAGFSGRAQVGKGMWTWTELMADMVETKIAQPRAGASTAWVPSPTA 546
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                                                                                                                                                                                                                                                                                                                     144 IDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVPLSSGSFGDATGFTVQDGQLVVAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          440 NLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMV---RKGTMKSQPWILAYED---
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iive 67; Mismatches 253;
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A/Residues: 1-533 <BLAT>
A/Cross-references: GB:AE000474; GB:U00096; NID:g1790440; PIDN:AAC76984.1; PID:g1790444;
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417 GMRANIRVAVQYIEAWI-PGNGCVPI-----YGLMEDAATAEISRTSIWQWIHHEKTLSN

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-GVITSADVRASL-ERMAPLVD-----RONAG--DVAYRPM--APNFDDSIAFL 692 GKPVTKALFREMLAEEMRVIQDELGEHRYSSGRFDDAARLMEQITTSDDLIDFL 524

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-------GLADTAMAVFNEVLGEHKNQLFITRDEDAPITAÈQLLEPCEGERTEA 416 596 EVDNNCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRH----- 649

----TIPLAKELAWAP---DEIRE

NVDA---GLAAGFSGRAQVGKGMWTWTELMADMVETKIAQPRAGASTAWVPSPTAATLHA 551

321 KRGAFAMGGMAAFIPSKDVERNNQVLAKVKAD----KALEANNGHDGTWIAHP----

552 LHYHQVDVAAVQQGLAGKRATIEQLL--

261 ILHALRDHIVGLNCGRWDYIFSYİKİLKNHPDRVLPDRQVVTMDKPFLSAYSRLLIKTCH

444 CIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMV---RKGTMKSQPWILAYED--

210

malate synthase A in Escherichia g revision 31-Mar-1990 #text\_change 01-Mar-2002 E65208; 000592 Asylocute synthase (EC 4.1.3.2) A - Escherichia coli (strain K-12) C;Species: Escherichia coli (strain K-12) C;Species: Bscherichia coli C;Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text\_change 01-C;Accession: A32649; A30378; E65208; Q00592 R;Byrne, C. A32649; A30378; E65208; Q00592 R;Byrne, C. Sibre and Library, July 1988 A;Reference number: S05692 A;Accession: A32649 A;Rolecule type: DNA A;Residues: 1-533 aRR.>
R;Byrne, C.R.; Stokes, H.W.; Ward, K.A. Nucleic Acids Res. 16, 10924, 1988 A;Title: Nucleotide sequence of the aceB gene encoding malate synth A;Reference number: A30378; MuID:89083515; PMID:3060852 A;Molecule type: DNA A;Residues: 1-533 <BYR2> R;Blattner, F.R.; Plunkett III, G.; Bloch, -A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A;Title: The complete genome sequence of Es

C.A.; Perna, N.T.; Burland,

A)Reference number: A64720; MUID:97426617; PMID:9278503 A)Accession: E65208

Score 187; DB 2; Pred. No. 0.00012; 4.9%;

Mismatches 217; Indels 92; Gaps 23;	GTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAVDKDGTA 308          : : :           :		FLR-VLNRDRNYTAPGGG-QFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEGIMD-AL 365	NLRDAILGSISYINPDNGKRYELNANPAVLICRVRGLHLKEKHVIYNGLAIPGSLFDFAL 216	FTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKAHGPAEVAFTCELFSRVEDVLGLPQNT 425	: ::	MKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSNEAGPNVRKGTM 482		KSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWIWTELMADMVETKIAQPR 533 		AGASTAWVPSPTAATLHALHYHQVDVA-AVQQGLAGKRRATIEQLLTIPL-AKELAWA 589	DTAMAVFNEVLGERKNQLNVSRMADAPITAAELLAP 431	PDEIREEVDNNCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWL 647                           CDGSRSEHGMRHNIRVALQYIEAMI-SGNGCVPIYGLMEDAATAEISRASIWQWI 485		RHGVITSADVRASLERMAPLVDRQNAGDVAXRPMAPNFDDSIAFLAAQELI 698 				
116; Conservative 69;	249 GTTDRAGVKDVILESAITTI	118 GPTDRKMVINALNANVKVFM	309 FLR-VLNRDRNYTAPGGG-Q	157 NLRDAILGSISYTNPDNGKR	366 FTGLIAIHGLKASDVNGPLI	: : : : : : : : : : : : : : : : : : :	426 MKIGIMDEERRTTVNLKACI	:   ::   3.00		326 MDKPFLNAYSRLLIYTCHKR	534 AGASTAWVPSPTAATLHALH	382 NGHDGTWVAHPGLA	590 PDEIREEVDNNCOSILGY	432 CDGSRSEHGMRHNIRVALQY	648 RHGVITSADVRAS	486 QHGKTLDNGQVVTNELFRDY	699 LSGAQO-PNGYTEP 711	537 LTTSQELPNFLTIP 550	
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No.
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P13244 brassica na	Q43827 raphanus sa	P24571 cucurbita m	P77947 streptomyce	P08216 cucumis sat	P17815 ricinus com	P19927 escherichia	Q50612 mycobacteri	P39180 escherichia	P25062 halobacteri	Q8kft1 chlorobium	P17432 gossypium h
MASY BRANA	MASY RAPSA	MASY_CUCMA	MASY_STRAE	MASY_CUCSA	MASY RICCO	MBHL_ECOLI	SEA2 MYCTU	AG43 ECOLI	CSG HALVO	IF2 CHLTE	MASY_GOSHI
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## ALIGNMENTS

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                                                                                   Pfam; PF01274; Malate_Synthase; 1.
TIGRFAMs; TIGR01345; malate_syn_G; 1.
Transferase; 1)
Transferase; 1)
Transferase; 3D-structure.
Complete protectione; 3D-structure.
CATALYTIC BASE (BY SIMILARITY ACT SITE 63 83 CATALYTIC ACID (BY SIMILARITY SEQUENCE 741 AA, 80403 MW; A92P54E0FEBB7C64 CRC64;
                                                                                                                                                                                                    Indels
                                                                                                                                                                            100.0%; Score 3810; DB 1;
100.0%; Pred. No. 2.5e-241;
ive 0; Mismatches 0;
                                                      HAMAP; MF 00641; -; i.
InterPro; IPRO01465; Malate synthase.
InterPro; IPRO06253; Malate synthG.
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                                  TIGR; MT1885; -.
Tuberculist; Rv1837c;
F70722; F70722.
1N8I; 18-DEC-02.
1N8W; 18-DEC-02.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-:- SUBDATT: Monomer (By similarity).
-:- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
-:- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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Cole S.T., Edifineler K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnher T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.,
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82.0%; Pred. No. 4.3e-196;
Live 54; Mismatches 72; Indels 5;
                                                                                                                                                                                            GLCB OR ML2069 OR MLCB1788.27.
Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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638 638 CATALYTIC ACID (BY SIMILARITY)
731 AA, 80141 MW, 3878CADA45DB416C CRC64;
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Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
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                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.39)
GLCB OR ML2069 OR MLCB1788.27.
731 AA
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HAMAP, MF 00641, -; 1.
InterPro, IPR001465, Malate_synthase.
InterPro, IPR006555, Malate_synthG.
Pfam; PF01274; Malate_synthase; 1.
PRT;
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ACT_SITE 340
ACT_SITE 638
SEQUENCE 731 AA;
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597; Conserv
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LNARFALNAANARWGSLYDALYGTDTIPETEGAEKGSEYNKIRGDKVIAYARKFMDQAVP 181
                                                                                                                                                                                                                                                                       EVDNNCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSA 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PATHWAY: Glyoxylate bypass; second step.
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                                   ILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLA
                                                               AAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIV----DTDGS
                                                                                                 EVDNDCQSILGYVVRWVDQGIGCSKVPDIHNVALMEDRATLRISSQLLANWLRHGVITSE
                                                                                                                                    MVRKGTMKSQPWILLAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAG
                                                                                                                                                                                                           ASTAWVPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLIIIPLAKELAWAPDEIRE
                           EDVLGLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGP
                                                                                                                                                                        DVRASLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQOPNGYTEPILHR
                                                                                                                                                                                                                                                                                                                      LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPT-SVLLINHGLHIE
                                                                                                                          EVFEGIMDALFIGIIAIHGLKASDVNGPLINSRIGSIYIVKPKMHGPAEVAFICELFSRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization of a chromosomal locus that affects pathogenicity Rhodcoccus fascians.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhodococus fascians.
Bacteria, Actinobacteria; Actinobacteridae, Actinomycetales;
Corynebacterineae; Nocardiaceae; Rhodococcus.
NCBI_TaxID=1828;
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Goethals K.;
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
datate synthase G (EC 2.3.3.9).
GLCB OR VICA.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GILDALFTSLAGLHSLTPDNV---LSNSRTGSLYIVKPKWHGPDEVAFTAELFGRVEOVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLPINTLKVGIMDEERRTIVNLKACIQAASERVVFINTGFLDRTGDBIHTSMEAGPVVRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKVDAWHGEHAGAEYDRAAYKAFLKEIGYLLDEPADFQIHTSGVDTEITTTAGFQLVVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNARFALNAANARWGSLYDALYGTDVI PETDGAEKGPTYNKVRGDKVI AYARKFLDDSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSSGSFGDATGFTVQDGQLVVALPDKST-GLANPGQFAGYTGAAESPTSVLLINHGLHIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WVPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIREEVDN
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                                                     4.
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                                                                                                                                                                                                                                                                                                                                69.1%; Score 2634; DB 1;
69.0%; Pred. No. 1.6e-164;
iive 82; Mismatches 138;
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Matches 499; Conservative
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LSSGSFGDATGFTVQDGQLVVALPDKS-TGLANPGQFAGYTGAAESPTSVLLINHGLHIE 239
                                                                                                         240 ILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLA
                                                                                                                                                                                                                      300 AAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFE
                                                                                                                                                                                                                                                      302 BEVSKGGSTFTRIMNPDRVYTRADGSELTLHGRSLLFVRNVGHLMTNDAILDKDGNBVPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 IQIDPSSPVGQTDAAGVKDVLMEAALTTIMDCEDSVAAVDADDKVVIYRNWLGLMKGDLA
                                                                                                                                                                                                                                                                                                                                  GIMDALFTGLIAIHGLKASDVNGPLI--NSRTGSIYIVKPKWHGPAEVAFTCELFSRVED
                                                                                                                                                                                                                                                                                                                                                                                    362 GIQDGLFTSLIAIH-----DLNGNTSRKNSRTGSVYIVKPKMHGPEEAAFTNELFGRVED
                                                                                                                                                                                                                                                                                                                                                                                                                                            418 VLGLPQNTMKIGIMDEERRITVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           417 VLGLPRNTLKVGIMDEERRITVNLKACIKAAKDRVVFINTGFLDRTGDEIHTSMEAGAVV
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Environ. Microbiol. 4:799-808162002).
-i. CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate +
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Nelson K.E., Wehnel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Nelson K.E., Wehnel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Bartins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes I
Brinkac L., Beanan M., DeBoy W.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Mocstl D., Wedler H.,
Lauber J., Stjepandic D., Hobeisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Prīteobacteria, Gammaproteobacteria, Pseudomonadales;
Pseudomonadaceae, Pseudomonas.
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15-SEP-2003 (Rel. 42, Last sequence update)
Malate synthase G (EC 2.3.3.9).
GLCB OR PP0356.
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Q88QX8;
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PSEPK
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-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAINAARC 15692, PAOL;
MEDLINE=20437337; PubMed=10984043;
MEDLINE=20437337; PubMed=10984043;
MEDLINE=20437337; PubMed=10984043;
MISCHOR C.K., Pham X.-Q.T., Brwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PROI, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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CATALYTIC ACID (BY SIMILARITY).
3669670A9E38D391 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 725;
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HAMAP, MF 00641, -1, 1.

InterPro, IPR006253; Malate_synthag.

InterPro, IPR006253; Malate_synthag.

InterPro, IPR01246; Malate_synthag.

TIGRPAMS, TIGRO1345; Malate_syn G; 1.

TIGRPAMS, TIGRO1345; Malate_syn G; 1.

Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
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Local Similarity 69.1%; Score 2569; DB 1; Length 7
Local Similarity 69.1%; Pred. No. 2.9e-160;
les 502; Conservative 77; Mismatches 139; Indels
                                                                                                                                                              15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9)
                                                                                                                  PRT;
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                                                                                                                  STANDARD;
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Nature 406:959-964(2000)
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                                                                                                                                                                                                                                                                                      GLCB OR PA0482.
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MASZ PSEAE
Q91636;
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            GLCB OR FC2.4
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MASZ PSEFL
AC 005137; DO MAYZ-2000
DT 30-MAYZ-2000
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                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to the malate synthase family, GlcB subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ
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CATALYTIC ACID (BY SIMILARITY)
8363F218E6116AE1 CRC64;
                                                                                                                                                                                                                                    TIGR; PP0356; -.
HAWAP; MF 00641; -; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
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67.1%; Pred. No. 1.9e-158;
iive 95; Mismatches 139;
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TIGR; PP0356; -.
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631 631 CZ
725 AA; 78346 MW;
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ACT_SITE 340 3
ACT_SITE 631 6
SEQUENCE 725 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- PATHWAY: Glyoxylate bypass; second step.
-:- SUBUNIT: Monomer (By similarity).
-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-:- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate
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R EMBL; Y11998; CAA72726.1; -...

R HSAP, P13304; DEV

R HAMAP, MF 00641; -; 1.

DR InterPro; IPR001455; Malate_synthase.

DR InterPro; IPR001523; Malate_synthase, 1.

DR TIGRFAMS; TIGR01345; malate_synthase; 1.

TIGRFAMS; TIGR01345; malate_syn G; 1.

""-ansferase; Glyoxylate bypass; Tricarboxylic acid cycle.

""-ansferase; Glyoxylate bypass; Tricarboxylic acid cycle.

""-ansferase; Glyoxylate bypass; Tricarboxylic ACID (BY SIMILARITY).

""-ansferase; Glyoxylate bypass; Tricarboxylic ACID (BY SIMILARITY).

""-ansferase; Glyoxylate bypass; Tricarboxylic ACID (BY SIMILARITY).

""-ansferase; Glyoxylate bypass; Tricarboxylic ACID (BY SIMILARITY).

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""-ansferase; Glyoxylate bypass; Tricarboxylic ACID (BY SIMILARITY).

""-ansferase; Glyoxylate bypass; Tricarboxylic ACID (BY SIMILARITY).

""-ansferase; Glyoxylate bypass; Tricarboxylic ACID (BY SIMILARITY).
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Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Artiguenave F.M., Delecu M., Vilagines R., Danglot C.; "A functional glyoxylate bypass is mandatory for utilization alkanes by Pseudomonas fluorescens."; Submitted (MAR-1997) to the EMBL/Genbank/DDBJ databases.
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                                                                                 30-MAY-2000 (Rel. 39; Created)
30-MAY-2000 (Rel. 39, Last sequence update)
115-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.3).
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725
STANDARD;
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us-09-688-672a-2.rsp

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AE016857; AAO54024.1;
PSPTO0480; -.
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725 AA;
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ACT_SITE 631
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-!- SUBJUIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                            EEVAKGGKTFTRIMNPDRVYTGVDGQDVTLHGRSLLFVRNVGHLMTIDAILDKAGNEVPE
                                                                                                                                             SLERMAPLVDRONAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRRE
    IQIDASTPVGQTDAAGVKDVLMEAALTTIMDCEDSVAAVDADDKVVIYRNWLGLMKGDLA
                                                                             GIMDALFIGLIALHGLKASDVNGPLINSRIGSIYIVKPKMHGPAEVAFICELFSRVEDVL
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                            AAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFE
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Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Daugherty S.,
Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
White O., Fraser C., Collmer A.;
"Complete sequence of Pseudomonas syringae.";
"Complete sequence of Pseudomonas syringae.";
submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G 1 (EC 2.3.3.9).
GLCB1 OR GLCB-1 OR PSPTO0480.
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                                                                     340 CATALYTIC BASE (BY SIMILARITY)
631 CATALYTIC ACID (BY SIMILARITY)
79143 MW, F1993264E8083660 CRC64;
TIGR; PSPT00480; -.
HAMAP; MF 00641; -; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
                                                                                                                                            Match 65.3%; Score 2489; DB 1; Length 7 Local Similarity 65.3%; Pred. No. 4.8e-155; es 473; Conservative 97; Mismatches 150; Indels
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              IMDALFTGLIAIHGLKASDV - - NGPLINSRTGSIYIVKPKWHGPAEVAFTCELFSRVEDV
                                                                                          LGLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVR
                                                                                                                                                                                                                                                AWVPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIREEVD
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SEQUENCE FROM N.A.

MEDLINE=21608551, PubMed=11743194;

MEDLINE=21608551, PubMed=11743194;

MUREDLINE=21608551, PubMed=11743194;

Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Houmiel K., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.;

Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
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-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  731 AA
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                                                                                                                                                      STRAIN=MAPP303099;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
Machine T., Kadmura Y., Sato S., Asamizu B., Kato T., Kimura T.,
Machine A., Kiyokawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
-:- CATALYIIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate +
                                                                                                                                                                                                                                                                                                                                                                                            -!- PATHWAY: Glyoxylate bypass; second step.
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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63.4%; Score 2416; DB 1; Length 721;
Best Local Similarity 64.4%; Pred. No. 2.8e-150;
Matches 467; Conservative 86; Mismatches 164; Indels
Malate synthase G (EC 2.3.3.9).
GLCB OR MLR4664.
Rhizobium loti (Mesorhizobium loti).
Bacteria, Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
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CATALYTIC ACID (BY SIMILARITY).
65376311A7E1BFDF CRC64;
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InterPro; IPR001465; Malate_synthase.
InterPro; IPR006253; Malate_synthG.
Pfam; PP01274, Malate_synthase; 1.
TIGRFAMS; TIGR01345; malate_syn_G; 1.
Transferase; Glyoxylate_bypass; Tricarboxylic acid cycle;
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SEQUENCE 721 AA;
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                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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CATALYTIC ACID (BY SIMILARITY)
69F304D5D6F8EFFB CRC64;
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InterPro; IPR001465; Malate_synthase.
InterPro; IPR006253; Malate_synthG.
Pfam; PF01274; Males_synthase; 1.
TIGRFAMS; TIGR01345; malate syn G; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
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92; Mismatches 165; Indels
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EMBL; AE007947; AAK85871.1; ALT INIT.
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PIR; F97364; F97364.
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ACT_SITE 346
ACT_SITE 637
SEQUENCE 731 AA;
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606 AQGILGYVVRWVDQGVGCSKVPDINNIGLMEDRATLRISAQHMANWLRHGVVTBAQIIKT 665
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                                                                                                                                                                                   63 IDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPVLN
                                                                                                                   LERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQOPNGYTEPILHRRREF
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-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 RVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQ
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HAWAP; MF 00641; -; 1.
InterPro; IPRO0145; Malate synthase.
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Pfam; PF01274; Malate synthase; 1.
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TIGR12
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
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Garcia de los Santos A., Hynes M.F.;
"Malate synthase gene from Rhizobium leguminosarum.";
submitted (CTL-2001) to the EMBL/Genbank/DDBJ databases.
-- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0937\(\bar{n}\);
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9).
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SEQUENCE FROM N.A.
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the Buropean Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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; Pred. No. 4.6e-146;
94; Mismatches 169; Indels 5;
                                                                                                                                                            REMIL, ALSTITE; CAC41449.1;
RAMAP; MF 00641; 1.1

INTERPRO; IPR006253; Malate synthase.
InterPro; IPR006253; Malate synthase.

R InterPro; IPR006253; Malate synthase; 1.

R TIGREAMS; TIGRO145; malate synthase; 1.

Transferase; Glyoxylate bypass; Tricarboxylic acid cycle; Complete proteome.

ACT SITE 338 338 CATALYIC BASE (BY SIMILARITY).

ACT SITE 629 629 CATALYIC ACID (BY SIMILARITY).

SEQÜENCE 723 AA; 78853 MW; A0E95E8A5164BBS8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          338 338 CATALYTIC BASE (BY SIMILARITY)
629 629 CATALYTIC ACID (BY SIMILARITY)
723 AA; 78853 MW, AOE95E8A5164BB58 CRC64;
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62.9%;
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Best Local Similarity 62.9%
Matches 455; Conservative
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15-SEP-2003 (Rel. 42, Last annotation update)
18 Malate synthase G (EC 2.3.3.9)
19 GLCB OR R00662 OR SMC02581.
20 Shizoblum melliloti (Sinochizoblum melliloti).
21 Rhizoblum melliloti (Sinochizoblum, Ensity Alphaproteobacteria; Rhizoblales;
22 STRAIN=1021;
23 NCBH TAXID=382;
24 NCBH TAXID=2139650; PubMed=11481430;
25 STRAIN=1021;
26 STRAIN=1021;
27 MEDLINE=2139650; PubMed=11481430;
28 MEDLINE=2139650; PubMed=11481430;
28 MEDLINE=2139650; PubMed=11481430;
28 Acapela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
24 Robite T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
25 Godrie T., Goffeau A., Kahn D., Wainelle B., Ramsperger U.,
26 Robite T., Portefelle D., Vandenbol M., Weidner S., Galibert F.;
27 Ranald C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
28 Ranard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
28 Ranard C., Thebault B., Vandenbol M., Weidner S., Galibert F.;
29 Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).
20 -- CATALIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate +
IDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAA
                                                                                                         PONTMKIGIMDEERRITVNLKACIKAAADRVVFINTGFLDRIGDEIHTSMEAGPMVRKGI
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|362 MDAAITGLIALYDIGPS---GRRKNSRIGSMYVVKPKWHGPEEVAFAVEIFSRVEDALGL
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-!-PHWAY: Glyoxylate bypass; second step.
-!-SUBUNI: Monomer (By similarity).
-!-SUBUNI: Monomer (By similarity).
-!-SUBUNIAR LOCATION: Cytoplasmic (By similarity).
-!-SIMILARITY: Belongs to the malare synthase family. GlcB subf
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-i-SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i-SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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                                                                                                                250 NADHPIGKTDPAHIADVVLESAISTIQDCEDSIAAVDAEDKVAVYRNWLGLMNGKLEDTF
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MEDLINE=22247441; PubMed=12271122;

Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,

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                                                                       DPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAV
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Brucellaceae; Brucella
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    -!- PATHWAY: Glyoxylate bypass; second step.

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115-SEP-2003 (Rel. 42, Last seq
15-SEP-2003 (Rel. 42, Last seq
Malate synthase G (EC 2.3.3.9)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=29461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BRUSU
                                                                                                                                                                                                                                                                                                                                                423
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                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIR-16M / ATCC 23456 / Biotype 1;
MEDLINE-20020109; Pubbed=11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: Glyoxylate bypass; second step.
-!- SUBDATT: Monomer (By similarity).
-!- SUBCELLUTAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 VEIEGLAVAPELVEFLAKEAAPGTGVEPEKFWKGFAAIIRDLAPKNRALLAKRDELQARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 DKWHRRRVIEPIDMDAYROFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPVLNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 DAWYKENRDKGYSQADYQQFLKDIGYLLPEGGAFSVSTTNVDPEITHIAGPQLVVPVMNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4,
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CATALYTIC ACID (BY SIMILARITY)
B1313A617979270D CRC64;
                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MF_00641; -; 1.
InterPro; IPR001465; Malate_synthase.
InterPro; IPR006253; Malate_synthG.
Pfam; PF01274; Malate_synthase; 1.
TIGRPAMS; TIGR01345; malate_syn_G; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                  15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (BC 2.3.3.9)
Brucella melitensis.
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                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                Brucellaceae, Brucella.
NCBL_TaxID=29459;
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636
628 AA;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- ENZYME REGULATION: Inhibited by oxalate, glycolate and ATP.
-!- PATHMAY: Glyoxylate bypass; second step.
-!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=ATCC 13059 / AS019;
Lee H.S., Sinskey A.J.;
"Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum.",
J. Microbiol. Biotechnol. 4:256-263(1994).
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                                                                                                                                                                                                                                                          [1] SEQUENCE FROM N.A., SEQUENCE OF 1-10, AND CHARACTERIZATION.
SEQUENCE FROM N.A., SEQUENCE OF 1-10, AND CHARACTERIZATION.
SEQUENCE 5311631, DubMed=7812449;
MEDLINE=95111631, PubMed=7812449;
Reinscheid D.J., Eikmanns B.J., Sahm H.;
"Malate synthase from Corynebacterium glutamicum: sequence analysis of the gene and biochemical characterization of the enzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 9
                               01-NOV-1995 (Rel. 32, Created)
15-SEP-2003 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.9).
GLCB OR ACEB OR CGL2329.
Corynebacterium glutamicum (Brevibacterium flavum).
Corynebacteria; Actinobacteria; Actinobacteriaes, Corynebacterines, Corynebacterines, Corynebacterines, Corynebacterines, Corynebacterines, Corynebacterium.
NCBI_TaxID=1718;
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REMEL; MAG68074.1; -

REMEL; AP07521; BAB9722.1; -

REMEL; AP07521; BAB9722.1; -

REMEL; P37330; 1D8C.

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CATALYTIC ACID (BY SIMILARITY)
72AA0663AE7C87F4 CRC64;
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61.3%; Pred. No. 5.8e-142;
ive 90; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [3]
SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
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355 355 CA
646 646 CA
738 AA; 82231 MW;
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Matches 444; Conservative 9
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INIT MET 0
ACT SITE 355
ACT SITE 646
SEQUENCE 738 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakagawa S.;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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EXNGRQMTRELNGDRIYTAPDGSTLTLKGHSLMLVRNVGHLMTNPAILDAEGNEVPEGIM 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       542
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SIMILARITY).
CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 728
                                                                                            EMBL; AE014458; AAN30550.1; -.
TIGR; BR1648; -.
HAMAP. MF 200641; -; I
InterPro; IPR001465; Malate synthase.
InterPro; IPR00553; Malate_synthG.
Ffam; PF01274; Malate_synthG.
Ffam; PF01274; Malate_synthase; I
ITGRPAMS; TIGRPAMS; Talate_synthase; I.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
60.7%; Score 2313; DB 1; Length 7
Best Local Similarity 61.6%; Pred. No. 1.5e-143;
Matches 443; Conservative 97; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                             CATALYTIC BASE (BY CATALYTIC ACID (BY F95669D002A14EDE
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636 636 C
728 AA; 79966 MW;
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ACT_SITE 345 3
ACT_SITE 636 6
SEQUENCE 728 AA;
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AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV 120

19

8 8

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STANDARD;

RESULT 14 MASZ\_CORGL ID MASZ\_CORGL

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and its and the statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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             GlcB subfamily
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CRC64;
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                                                                                                                                                                                                                                                                                                                          Length
              Belongs to the malate synthase family.
(By similarity).
                                                                                                                                                                                                                                                                                                                         59.7%; Score 2273; DB 1;
61.5%; Pred. No. 6.5e-141;
                                                                                                                                                                                                                                                                362 CATALYTIC BASE (BY 653 CATALYTIC ACID (BY 83491 MW; F9550473EC4E9A09
                                                                                                                                                                                                                                                                                                                                                    90; Mismatches
                                                                                                          entities requires a license agreement or send an email to license@isb-sib.ch)
  Cytoplasmic
                                                                                                                                                                    HAMAP; MF_00641; -; 1.
InterPro; IPR011465; Malate synthase.
InterPro; IPR06253; Malate_synthG.
Pfam; PF01274; Malate synthase; 1.
IIGRPAMs; TIGR01345; malate_syn_G; 1.
                                                                                                                                                       EMBL; AP005221; BAC19041.1; -.
  LOCATION:
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653 6
748 AA;
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ACT_SITE 362
ACT_SITE 653
  SUBCELLULAR
                 SIMILARITY:
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 SLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRRE
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                                                                                                                            LDGASHADVEKYNITDGKLAAHIGDSVYRLKNRESYRGFTGNFLDPEAILLETNGLHIEL
                                                                                                                                                                                                               AVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEG
                                              LNAR FALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP
                                                                                                    LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The entire genomic sequence of Corynebacterium efficiens YS-314.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate
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A., Nishio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi
Usuda Y., Sugimoto S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9).
GLCB OR MASZ OR CE2231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: Glyoxylate bypass; second step.
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Search completed: November 21, 2003, 16:04:15 Job time : 11.7256 secs

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OBZIWO Salmonella OBZIWO Salmonella OBZEG escherichia OBEDG secherichia OBEDG chortosteli OBEDG chortosteli OBEGE shewanella OBGGE shewanella OBGGE vibrio vuln OBGGI vibrio vuln OBGGI vibrio vuln OBGGI vibrio vuln OBGZI vibrio chol OBZZZ ralstonia SQRZZ ralstonia SQRZZZ ralstonia SQRZZZ ralstonia SQRZZZ reptomyce OBGZZZ reptomyce OBGZZZ reptomyce OBGZZZ reptomyce OBGZZZ reptomyce OBGZZZ reptomyce OBGZZZ ralstonia DECEDGI VERNING PROMINIO OBZZZZ PROMINIO OBZZZZ COCCOUS OBGENZZ COCCOUS OBCENZZ COCCOUS OBCENZZ COCCOUS OBCENZ C

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Sequence:

Searched:

Database

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SEQUENCE FROM N.A.
STRAIN=D188;
Goethals K., Van Montagu M., El Jaziri M., Holsters M.,
Goethals K.;
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69.0%; Pred. No. 2.2e-162;
live 82; Mismatches 138; Indels 4
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Nocardiaceae; Rhodococcus.
NCBI_TaxID=1828;
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01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
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Matches 499; Conservative
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Query Match
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Q91636 pseudomonas
Q98dk4 rhizobium 1
Q917w7 rhizobium m
Q92ta4 rhizobium m
Q92ta5 prucella me
Q94x13 brucella me
Q94x03 boronas ac
Q84x03 boronas had
Q84x04 boronas
Q94x06 senthomonas
Q94x06 xanthomonas
Q94x06 accordadi
Q97x33 caenorhabdi
Q17353 caenorhabdi
Q87x609 escherichia
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1 TDRVSVGNLRIARVLYDFVN.......KARAAEKPAPSDRAGDDAAR 740
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                                  GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
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6: Sp mamman:*
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Maximum DB seq length: 200000000
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AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV 120

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Result No.

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AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSSGSFGDATGFTVQDGQLVVALPDKS-TGLANPGQFAGYTGAAESPTSVLLINHGLHIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 ILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 BEVSKGGSTFTRTMNPDRVYTRADGSELTLHGRSLLFVRNVGHLMTNDAILDKDGNBVPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIMDALFIGLIAIHGLKASDVNGPLI - - NSRTGSIYIVKPKMHGPAEVAFTCELFSRVED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417 VLGLPRNTLKVGIMDEERRTTVNLKACIKAAKDRVVFINTGFLDRTGDEIHTSMEAGAVV
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                                                                                                                                                                        725 AA; 78659 MW; 3669670A9E38D391 CRC64;
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Last annotation update)
                                                                                                                                                                                                                     67.4%; Score 2569; DB 16;
69.1%; Pred. No. 3.7e-158;
iive 77; Mismatches 139;
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                                          InterPro; IPR001465; Malate synthase.
InterPro; IPR006253; Malate_synthG.
Pfam; PF01274; Malate_synthase; 1.
TIGRFAMs; TIGR01345; malate_syn_G; 1.
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EMBL; AE004485; AAG03871.1;
HSSP; P37330; 1D8C.
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Matches 502; Conservative
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                                                 LNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP 180
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STRAIS-ATCC 15692 / PAO1;
STRAIS-ATCC 15692 / PAO1;
SCOVER C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Strover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hunnagle W.O., Kowahlik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa.
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadacee, Pseudomonas.
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01-MRR-2001 (TrEMBLrel. 16, C;
01-MRR-2001 (TrEMBLrel. 16, Li
01-MRR-2003 (TrEMBLrel. 23, Li
Malate synthase G.
GLCB OR PA0482.
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Nature 406:959-964(2000).
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YKA 721
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656 DSLQRMAAIVDRQNVGDPLYRPWAPDFDKSIAFQAACDLVFKGTSQPNGYTEPVLHARRL 715
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                  ASLERMAPLVDRONAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21668550; PubMed=11743193; Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland B., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W.,
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Science 2941:2323-2328(2001).

EMBL; AE00899; AAL41078:1;

EMBL; AE007947; AAK85871:1;
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                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Malate synthase G.
GLCB OR ATUO047 GR AGR C 78.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales;
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InterPro; IPR006253; Malate synthG.
Pfam; PF01274; Malate synthase; 1.
IIGRPAMs; TIGR01345; malate_syn_G; 1.
                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                         Rhizobiaceae, Rhizobium.
NCBI_TaxID=176299;
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SEQUENCE FROM N.A.
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01-JUN-2002
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Matches 462;
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                                                                                                             SEQUENCE FROM N.A.

STRAIN=WAFF303099;

MEDLINE=21082930; PubMed=11214968;

Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,

Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,

Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,

Takeuchi C., Yamada M., Tabata S.;

"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVR
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                                              Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Phyllobacteriaceae, Mesorhizobium.
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Best Local Similarity 64.4%; Pred. No. 3.1e-148;
Matches 467; Conservative 86; Mismatches 164;
                                                                                                                                                                                                                                                                                                     EMBL; AP003004; BAB51267.1; -.
InterPro; IPR001465; Malate synthase.
InterPro; IPR006553; Malate synthG.
Pfam; PF01274; Malate synthase; 1.
TIGRPAMS; TIGR01345; malate_syn_G; 1.
                                Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                                     Mesorhizobium loti.";
DNA Res. 7:331-338(2000)
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                                                                                 NCBI_TaxID=381;
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                                                                                                                                                                        122 ARYALNAANARWGSLYDALYGTDAIPESDGAEKGKSYNPKRGEKVIAWVRDFLDTSAPLO 181
                                                                                                                                                                                                                    SGSFGDATGFTVQDGQLVVALPDKSTGLANPGQ-FAGYTGAAESPTSVLLINHGLHIEIL 241
                                                                                                                                                                                                                                         CRWKDVGSFAVKDGALVVRSIDGEQAMLTDGKHFAGYRGDAAAPTHILLKNNGIHIEIV 241
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                                                                                  IDKWHRRKVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTFAGPQLVVPVLN
                                               RVDKAKGLAIETVLHDFLVEEVLPGLAVDADKFFADFSAIVHDLAPKACALLAKRDELQVK
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MEDLINE=21396507; PubMed=11481430;
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRC-2003 (TrEMBLrel. 2), Last annotation update)
01-MAR-2003 (TrEMBLrel. 2), Last annotation update)
Probable malate synthase G protein (EC 4.1.3.2).
GLCB OR R00062 OR SMC02581.
GLCB OR R00062 OR SMC02581.
Shacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium.
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AKQA 722
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NCBI_TaxID=382;
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ARPATILLGKNGLHTEIŲIDPSTEIGKSDRAGISDVILESALTTIMDCEDSVAAVDAEDK
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                                                  GDKVIAYARKFLDDSVPLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAA
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY059637, AAL17965.1;
InterPro; IPR00465; Malate synthase.
InterPro; IPR005253; Malate synthase.
Ffam; PF01274; Malate synthase; 1.
TIGRPAMS; TIGR01345; malate synthase; 1.
SEQUENCE 723 AA; 79677 WW; 4E879906CFD64444 CRC64;
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Last annotation update)
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Garcia de los Santos A., Hynes M.F.;
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01-DEC-2001 (TrEMBL
01-MAR-2003 (TrEMBL
Malate synthase G.
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Best Local Similarity
Matches 464; Conserv
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Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
A Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,
Thalysis of the chromosome sequence of the legume symbiont
Sinorhizobium melliloti strain 1021.",
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
R EMBL, ALS91782; CAC41449.1.",
R InterPro; IPR006253; Malate synthase.
R InterPro; IPR006253; Malate synthase.
R PIGRFAMS; TIGR01345; malate synthase; I.
Figm. PF01274; Malate synthase; I.
Figm. PF01274; Malate synthase; I.
Figm. PF01274; Malate synthase; I.
Figm. PF01274; Malate synthase; I.
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Figm. PF01274; Malate synthase; I.
Figm. PF01274; Malate synthase; I.
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61.7%; Score 2351.5; DB 16.
Best Local Similarity 62.9%; Pred. No. 4.8e-144;
Matches 455; Conservative 94; Mismatches 169;
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                                                                                                                                                            SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=16M / ATCC 23456 / Biotype 1;

XI MEDLINE=20020109; PubMed=1175668ar R.J., Patra G., Mujer C., Los T.,

BA Lavanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,

A Ablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Golteman E.,

A Ablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Golteman E.,

A Haselkorn R., Kyrpides N., Overbeek R.;

A Haselkorn R., Kyrpides N., Overbeek R.;

The genome sequence of the facultative intracellular pathogen

RT Brucella melitensis.";

Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).

BR InterPro: IPR00486; Malate_Synthase.

DR InterPro: IPR00525; Malate_Synthase.

DR Ffan; PF01274; Malate_Synthase;

DR TIGRFAMS; TIGRO1345; malate_Synthase;

DR TIGRFAMS; TIGRO1345; malate_Synthase;

DR TIGRFAMS; TIGRO1345; malate_Synthase.
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                                                                                              Brucella melitensis.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Brucellaceae, Brucella.
NCBI_TaxID=29459;
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                                         Last sequence update)
Last annotation update)
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                             Created)
Q8YIR3
Q8YIR3
Q8YIR3
Q1-MAR-2002 (TrEMBLrel. 20, Cs
01-MAR-2002 (TrEMBLrel. 20, Ls
01-MAR-2003 (TrEMBLrel. 20, Ls
Malate synthase G (EC 4.1.3.2)
BMEI0380.
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SPTAATLHATHYHKIDVAAVQEKLKSRPRAKLDDILSVPVAVRPNWTPDDIQHEIDNNAQ
                                                      SILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRASLE
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Brucellaceae; Brucella.
NCBI_TaxID=29461;
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TRAIN=1330 / Biovar 1;
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                                                                                                                                                                                                                                                                                                                                                                                               607 GILGYVVRHIDQGVGCSKVPDINNVGLMEDRATLRISAQHIANWLYHGVVSEAQVMETMK 666
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QNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKGTM
                                                                                                                    KSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAWVP
                                                                                                                                                                            487 KQAAWIGAYEQWNVDIGLECGLSGHAQIGKGWWAMPDWMAAMLEQKIAHPKAGANTAWVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium efficiens.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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Last annotation update)
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01-MAR.2003 (TrEMBLrel. 23, Last seq.
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Malate synthase (EC 4.1.3.2).
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244 245 364

424 422 484 482 544 542 604 602 664 662 724

us-09-688-672a-2.rspt

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TOTAL SOURCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAIN=06.HI / CFT073 / ATCC 700928;

MEDLINE=22388234; PubMed=12471157;

MEDLINE=22388234; PubMed=12471157;

Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

Mesko D., Buckles B.L., Liou S.-R., Bouthn A., Hackett J., Stroud D.,

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

REBL, ABOLGF66; AANB211.;

N. Lyase; Complete protecome.

SEQUENCE 723 AA; 80440 MW; AAF740E5FE038F6F CRC64;
                            HEAINYAIMDKQLVVTLESGKMTRLKDETQFVGYQGSQGDPSVILLLHHGLHVEIQDA
                                                                                                                                                                                SWLSAYERSNVAAGLTCGFQGRAQIGKGMWAMPDLMNENMEQKGTQLEAGANTAWVPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         663 AKVVDEQNAGDPAXRPWADNLEQSVAFQAALELVIKGTEQPSGYTEPILHRRRLEFKQKI
                                                               FGDATGFTVQDGQLVVALPD-KSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEILIDP
                                                                                                                ESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAVDK
                                                                                                                                                                   DGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEGIMDA
                                                                                                                                                                                                                                                                                    423 TLKIGVMDEBRRTSLNLKACIEKVKERVVFINTGFLDRTGDEIHTSMEAGPMIRKGDMKS
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                                                                                                                                                                                                                   LFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKWHGPAEVAFTCELFSRVEDVLGLPQN
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01-MAR-2003 (TEMBLrel. 23, Created)

01-MAR-2003 (TEMBLrel. 23, Last sequence update)

01-MAR-2003 (TEMBLrel. 23, Last annotation update)

Malate synthase G (EC 4.1.3.2).

GICB OR C3705.

Escherichia coll 06.

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Escherichia.
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WHQXGNK-GPIDFSAYHSFLEEIGYLEPIPEHVTITTENVDDEIAAQAGPQLVVPVNNARY 125
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                      IMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKWHGPAEVAFTCELFSRVEDVLG
                                         LPONTMKIGIMDEERRITVNLKACIKAAADRVVFINTGFLDRIGDEIHTSMEAGPMVRKG
                                                                                      NCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRA
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                                                                                                                         TMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAW
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Malate synthase.
BH2131.
Bacillus halodurans.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubWed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.
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                                                                                                                                                                                                                                                 538 AA;
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SEQUENCE 538 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPVLNA
                                                                                                                         RFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVPLSS
                                                                                                                                                                                GSYQDVVAFKVVDKQLRIQLKNGKETTLRTPAQFVGYRGDTAAPTCILLKNNGLHIELQI
                                                                                                                                                                                                    DPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAV
                                                                                                                                                                                                                                                                              DALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKMHGPAEVAFTCELFSRVEDVLGLP
                                                                                                                                                                                                                                                                                                                                                         KSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAWVP
                                                                                                                                                                                                                                                                                                                                                                                              SPTAATLHALHYHQVDVAAVQQGLA----GKRRATIBQLLTIPLAKELAWAPDEIREEV
                                                                                                                                                                                                                                                                                                                                                                                                                                   DNNCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADV
                                                                                                                                                                                                                                                                                                                                                                                                                                              RASLERMAPLVDRONAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHR-R
                                                                                                                                                               GSFGDATGFTVQDGQLVVALPD-KSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEILI
                                                                                                                                                                                                                                                                                                                    QNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKGTM
                                                                                                                                                                                                                                                                                                                                                                           KSTPWIKAYERNNVLSGLFCGLRGKAQIGKGMWAMPDLMADMYSQKGDQLRAGANTAWVP
                                               4 VSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQI
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-077-2002 (TrEMBLrel. 22, Created)
01-077-2002 (TrEMBLrel. 22, Last sequence update)
01-077-2003 (TrEMBLrel. 23, Last annotation update)
Malate synthase.
Mis OR XAC0252 (XAC0254)
XALOLOMONAS axonopodis (pv. citri).
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales;
          Length 723;
                             15;
                             173; Indels
           DB 16;
          56.9%; Score 2168.5; DB 1
58.4%; Pred. No. 3.6e-132;
                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                             113;
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                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                     Similarity
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                            422;
          Query Match
Best Local S:
Matches 422
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RC STRAIN=306 / ATCC 13902 / XV 101;

RA da Silva A.C.R., Ferro J.A., Reinach E.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Quaggio R.B., Cannavan F., Cardozo J., Chambergo L.B.A.,

RA Cloarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Faria J.B., Ferraira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Faxia J.B., Ferreira A.M., S., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Mactins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Schubal J.C., Kitaijma J.P.,

RT "Comparison of the genomes of two Xanthomonas pathogens with differing

RT "Comparison of the genomes of two Xanthomonas pathogens with differing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
7.3%; Score 279.5; DB 10
Best Local Similarity 24.9%; Pred. No. 9.2e-10;
Matches 123; Conservative 59; Mismatches 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        465 LWQWLHHGQHLDDGTAIDQHLLQATLRALPARL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro, IPR004652; Malate_synthA.
Interpro; IPR001465; Malate_synthase.
Pfam; PF01274; Malate synthase; 1.
IIGRFAMS; TIGR01344; malate_syn_A; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 417:459-463(2002).
EMBL; AE011650; AAM35148.1;
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540 AA.

PRT;

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625 GLSRGTIKCTVLIEHLLATFQLHEIIHSLKDHVVGLNCGRWDFFCSHRHOISMTAPFMRN 684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420 GLPQNTMKIGIMDEERRITVNLKACIKAAADRVVFINTGFLDRIGDEIHTSMEAGPMVRK 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    685 YSLE----LIKTCHORGIHAMGGMAAHIPIKHDQIANDKAFALVTSDKOREVTDGHDGT 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307 TAFLRVLNRDRNYTAP-GGGQFTLPGR-SLMFVRNVGHLMTNDAI----VDTDGSEVFEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----LFDFGLFVFHNAKA-----LISKGSGP-YFYLPKLONAEBAQLWSDVFKFTEDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480 GTMKSOPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WVPSFTAATLHALHYHQVDVAAVQQGLAGKRRAT1EQLLT1FLA--KELAWAPDE1REEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----AVRNNISYTHPTTKKEYKLDEKHAVLMVRPRGWHLTEKHVQIHNQPTSGT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 IMDALFT-GLIAIHGLKASDVNGPLINSRTGSIYIVKPKWHGPAEVAFTCELFSRVEDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483 GPPDRKSVINALNSGANVFMTDFEDSNSPT------WRNOIEGOVNMYD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 206; DB 5; Length 90; Pred. No. 0.00013; S8; Mismatches 186; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Marchews J.,
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101848 MW; AAF64B820B82D1B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C.elegans: A platform
       D-GNGC--VP-IHN--LMEDAATAEISRAQLWQWLHHG 474
                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
BMBL; 2831216; CAB62784.1; --
HSSP, C53752; 1F61.
NormPep; C08F11.14; CE23529.
InterPro; IPRO00524; Isocit lyase.
InterPro; IPRO00524; Isocit lyase.
InterPro; IPRO00528; Malate_SynthA.
InterPro; IPRO06552; Malate_SynthA.
InterPro; IPRO01465; Malate_SynthA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGR01346; isocit lyase; Discretars; TIGRFAMS; TIGR01344; malate syn A; PROSITE; PS00161; ISOCITRATE LYASE; SEQUENCE 907 AA; 101848 NW: AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00463; ICL; 1.
Pfam; PF01274; Malate synthase;
ProDom; PD001857; Isocit_lyase_p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.4%;
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(TrEMBLrel. 13, I
(TrEMBLrel. 23, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 98; Conservative
                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                                                                         C08F11.14 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                             01-MAY-2000
                                                                                                                                                                                                       01-MAR-2003
                                                                                                                                                                               01-MAY-2000
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                                                                                                                                                                                                           STRAIN-ATCC 33913 / NCPPB 528;

STRAIN-ATCC 33913 / NCPPB 528;

MEDLINE-22022145; PubMed=12024217;

Ad Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

Ausgio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Alves L.M.C., do Amaral A.M., Berrollini M.C., Camargo L.B.A.,

Camarotte G., Cannavan F., Cardzoo J.C., Chambergo F. Ciaphna L.P.,

Rarau J.B., Ferranco M.C., Cursino-Santos J.R., El-Dorry H.,

Formignieri B.F., Franco M.C., Greggio C.C., Ferrol M.I.T.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

Locali B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machado M.J., Madeira A.M.B.N., Mayaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Perindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Spinola L.A.F., Takita M.A., Traumra R.E., Teixcira E.C., Tezza R.I.D.,

Spinola L.A.F., Takita M.A., Trauffi D., Tsai S.M., White F.F.,

Schubal J.C., Kitajima J.P.,

"Comparison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 AESPISVLLINHGLHIEILIDPESQVGTIDRAGVKDVILESAITTIMDFEDSVAAVDAAD 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 KVLGYRNWLGINKGDLAAAVDKDGTAFLRVLNRDRNYTAPGGGOFTL---PGRSLMFVRN 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 ----WRNLLA-GORTLAAAVRGELT------FDAPNGKHYALRPEHERAVLIVRP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340 VG-HLMTNDAIVDTDGSEVFEGIMDALFTGLIAIHG---LKASDVNGPLINSRTGSIYIV 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 NCGRWDYIFSYLKT-FRAHPDRVLPERGQVTMTQPFLKAYSELLIKTCHRRGAHAMGGMA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          506 GRAQVGKGMWTMTELMADMVETKIAQPRAGASTAWVPSPT------AATLHALH 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AELPAAL----QDRRIEI-----TGPTDPKMVINALNSGAKVFMADFEDSTAPT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 RGWHLDEKHVLI--DGQPMAGGLFDA---ALFAFHNARTLMAKD-RGP-----YLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396 KPKMHGPAEVAFICELFSRVEDVLGLPQNIMKIGIMDEERRITVNLKACIKAAADRVVFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342 AQIPINHDEAANEQAMARVRADKLREVSAGHDGTWVAHPALIPVAMAVFDEHMPTAHOHH
                                                                                                         Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 102;
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  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.8%; Score 258; DB 16; ilarity 26.4%; Pred. No. 2.3e-08; Conservative 54; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AE012119; AAM39556.1; -.
InterPro; IPR006252; Malate syntha.
InterPro; IPR001465; Malate synthase.
Pfam; PF01274; Malate synthase; I.
TIGRPAMS; TIGR01344; malate syn A; I.
  222,
01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 417:459-463(2002)
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Best Local Similarity
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                                                               Malate synthase.
                                                                                                                                                                             NCBI_TaxID=340;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            563 QLEGQINLYD------AVRNNISYTHPTTKKEYTLNEKHAVLKVRPRGWHLP 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDAIV----DIDGSEVFEGIMDALFT-GLIAIHGLKASDVNGPLINSRIGSIYIVKPKMH 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----NTEFNPRRLRLLSKRNQVQADINNSLWFPDFNKETEVLRSDQ--GWKG-AEIPRDL 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLINHGLHIEILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRN 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 WL--GLNKGDLAAAVDKDGTAFLRVLNRDRNYTAP-GGGQFTLPGR-SLMFVRNVG-HLM 344
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                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.2%; Score 198.5; DB 5; Length 968; 23.8%; Pred. No. 0.00044; tive 70; Mismatches 222; Indels 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Blanchard M., Kramer J., Gibson A.;
Blanchard M., Kramer J. elegans cosmid COSE4.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF026209; AAB71278.2; -.
HSSP; 053752; IF61.
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Last sequence update)
Last annotation update)
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InterPro; IPR006294; ISOCIL lyase.
InterPro; IPR0090918; ISOCIL_lyase_ph.
InterPro; IPR006225; Malate synthä.
InterPro; IPR001465; Malate_synthase.
                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-99069613; Pubmed-9851916;
                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Crt
01-MAY-2000 (TrEMBLrel. 13, Lat
01-MAR-2003 (TrEMBLrel. 23, Lat
Hypothetical 108.6 kDa protein.
CO5E4.9.
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Best Local Similarity 23.8
Matches 148; Conservative
                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 469
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                                                                                   017353
RESULT 15
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401 GPAEVAFTCELFSRVEDVLGLPQNTMKIGIMDEERRITVNLKACIKAAADRVVFINTGFL 460
                                                                                      653 SABEAQLWADVFKYTEDKLGLARGTIKCTVLIEHLLASFQLHEIIHALKDNIVGLNCGRW 712
                                                                                                                                                                                                                                -----GASTAWVPSPTAATLHALHYHQ 556
                                                                                                                                                                                                                                                                                                                            557 VDVAAVQQGLAGKRRATIEQLLTIP--LAKELAWA------PDEIREEVD--NNCQ 602
                                                                                                                                                                                                                                                                                                                                                                      ------GLVPLAKRVFDQMMPKPNQISKNLTRANCTKEDLTVIPEGTRTEAGFRHNIS 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                       858 VTLGYLDSWL-RGTGC--VPLYN---LMEDAATAEISRAQLWQWLHHDAXLEDGRTIDAG 911
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                                                                                                                                                                               713 DYIFSYİKİFQNHRKFLLPDRFQIGMTAPFWR-------NYSLEVIKACHLRĞ
                                                                                                                                     ---AGPMVRKGTMKSQPWILAYEDHNVDAGLAAGFSG
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Brevibacterium lac
B. flavum AK. Bre
AK wild type alpha
AK wild type alpha
B. lactofermentum
B. lactofermentum
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Feedback inhibitio
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                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium sp
Corynebacterium sp
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Propionibacterium
Methylophilus meth
Aspartokinase II.
Blifdobacterium lo
M. tuberculosis an
M. tuberculosis re
M. gonorrhoea emi
Listeria monocytog
H. pylori GHFO 774
Procein with aspar
Staphylococcus epi
Listeria monocytog
Human ORFX protein
Glycine max aspart
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//label= Histidine tag
/note= "Nickel chelating region used for purifying
fusion protein"
9..749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TbF14; antigen, vaccine; tuberculosis; AIDS; His tag; MtB81; Mo2; acquired immunodeficiency disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                             AAW06586
AAW61152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU01900 standard; Protein; 1172 AA
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/label= Mo2_region
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  Misc-difference 49
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Modified Corynebac
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C. Glutamicum meta
C. Glutamicum meta
C. Glutamicum prote
Corynebacterium gl
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                  GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                          of hits satisfying chosen parameters:
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Result

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The present invention relates to the isolation of Mycobacterium tuberculosis antigen polypeptides (e.g. Tb24) and the nucleic acids encoding them. The invention describes compounds and methods for the diagnosis of tuberculosis or for inducing protective immunity against tuberculosis. The compounds comprise at least one immunogenic portion of one or more Mycobacterium proteins and nucleic acid molecules encoding such polypeptides. The Mycobacterium proteins and nucleic acid molecules of Mycobacterium infection in patients and biological samples. The compounds of the invention and antibodies directed against the Mycobacterium infections and nucleic acid molecules may be used in vaccines for immunisation against Mycobacterium infections. The nucleic acids encoding the Mycobacterium proteins may be used in vaccines for immunisation against Mycobacterium polypeptide for MO-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An isolated polypeptide comprising a Mycobacterium antigen, e.g., from Mycobacterium tuberculosis, useful in a vaccine for enhancing an immune response to and inhibiting development of a Mycobacterium infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 RIVRNARKLDTVTFEEMLEMAACGAKVLMIRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VOKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
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                                                  Tuberculosis; Mycobacterium infection; gene therapy; anti bacterial; numunostimulant; MO-2.
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Pred. No. 3.8e-142;
8; Mismatches 34;
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                                                                                                                                       Location/Qualifiers
                Mycobacterium polypeptide for MO-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 17; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.8%;
                                                                                                                                                                                                                                                                                                                  26-FEB-2001; 2001WO-US05992
                                                                                                                                                                                                                                                                                                                                                  25-FEB-2000; 2000US-0185037
08-AUG-2000; 2000US-0223828
                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 85.1
Matches 338; Conservative
                                                                                                                                                                                           Misc-difference 305
                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-536638/59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 AA;
                                                                                                      Mycobacterium sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS12505
                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                         Campos-Neto A,
                                                                                                                                                                                                                                             WO200162893-A2
                                                                                                                                                                                                                                                                                 30-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
                                                                                                                                                                                                                                                                                                              consisting of a His tag for purification, antigen MtB81 and antigen Mo2. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease, AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   929 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1049 GRQDRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAGWRSHPGVTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       749 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAERLQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   989 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAERLQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRODRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAGMRSHPGVTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     809 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEEGRVVLVAGFQGVSQDTXDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         869 LEEGRVVLVAGFOGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIVENARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FCEALAAVGVNIELISTSEDORSRCCAATPNWTRPWSRCMKRSGSAATRRPRCTRGRDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                        Lodes ML;
                                                                                                                                                                                                            Vaccinating against Mycobacteria infections in mammals using fusion
                                                                                                                                                                                                                                                                                                 represents Mycobacterium fusion protein antigen TbF14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 2193; DB 22; Length 1172; 100.0%; Pred. No. 5.5e-195; ive 0; Mismatches 0; Indels 0;
                                                                                                                      Dillon DC,
                                                                                                                                                                                                                              proteins comprising combinations of heterologous antigens
                                                                                                                      McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU08233 standard; Protein; 421 AA.
                                                                                                                      Houghton RL,
                                                                                                                                                                                                                                                                Claim 3; Fig 3; 168pp; English.
                                   99US-0158338
99US-0158425
2000WO-US28095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424; Conservative
                                                                                     (CORI-) CORIXA CORP.
                                                                                                                                                        2001-290576/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1172 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 424; Conserv
                                                                                                                      Reed S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WACQ 1172
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                                                                                                                                                        WPI; 2001-290576,
N-PSDB; AAS03794
10-OCT-2000;
                                                  07-OCT-1999;
                                                                                                                                                                                                                                                                                                   The sequence
                                   07-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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AAU08233
ID AAUC
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AC AAUC
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180

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240 244

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120

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17; Gaps

34; Indels

22; Length 421;

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305 D----GTTD--ITFTCPRSDGPRAMELLKKWQQQGDWTNVLYDDQVGKVSLVGAGMKSH 357
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    185 RIVPNAQKLERLSFEEMLELAAVGSKILVLRSVEYARAFNVPMRVRSSYSNDPGTLIAGS 244
                                                                        245 MEDIPMEEAVLTGVATDKSEAKVTVLGIPDKPGEAAKVFRALADAEINIDMVLQNVSSVE 304
                                      241 IKDVPMEDPILIGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRR------RQHRHGAA
                                                                                                                 295 ERLQGRGRQDRHHLHLLPQTSGPPFWKNWTRSETRSASTQLLYDDHIGKVSLIGAGMRSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding modified aspartokinase without synergistic feedback inhibition by L-lysine and L-threonine for efficient production cL-lysine by coryneform bacterium fermentation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspartokinase; AK; lysine synthesis; feedback inhibition;
L-lysine; L-threonine; insensitive; product inhibition;
coryneform bacterium; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified Corynebacterium glutamicum aspartokinase, T311I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Wild-type Thr replaced with Ile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yonetani Y,
                                                                                                                                                                                         355 PGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                             358 PGVTAEFMEALRDVNVNVELISTSE 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 29-30; 33pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            Ā
                                                                                                                                                                                                                                                                                                                        AAB29607 standard; Protein; 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-APR-2000; 2000WO-JP02456.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-687179/67.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200063388-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                               AAB29607;
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                                                                                                  296 VLQNVSKVEKGKTDITFTCSRDVGPAAVEKLDSLRNEIGFSQLLYDDHIGKVSLIGAGMR 355
                      240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEEGRUVIVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAE---- 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                    296 RLQGRGRQDRHHLHLLPQTS---GPPPWKNWTRSETRSASTQLLYDDHIGKVSLLGAGMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 VQKYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLDLAAAVNPVPPAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a gene from a high temperature-resistant coryneform microbe that encodes a heat-resistant lysin biosynthetic enzyme enzyme has aspartate-semialdehyde dehydrogenase activity and can be used for growing amino acid-producing microbes. The present amino acid sequence corresponds to an enzyme of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A heat-resistant lysin biosynthetic system enzyme gene of a high temperature-resistant coryneform microbe
                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium thermoaminogenes lysin biosynthetic enzyme lysC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Heat-resistant; lysin biosynthesis; enzyme; coryneform;
aspartate-semialdehyde dehydrogenase; lysC.
                                                                                                                                                 SHPGVTATFCEALAAVGVNIELISTSEDQRSRCCAAT 389
                                                                                                                                                                       SHPGVTATFCEALAAVGVNIELISTSEIRISVLCRDT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.9%; Score 1248.5; DB 22
65.2%; Pred. No. 1.5e-107;
ive 58; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 21-22; 27pp; Japanese.
                                                                                                                                                                                                                                                                                  AAG64046 standard; Protein; 421 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium thermoaminogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99JP-0311148.
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                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AJIN ) AJINOMOTO KK.
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N-PSDB; AAH45374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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Best Local 8
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                                                                                                                            Best Local Similarity
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                                         VQKYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLELAAAVNPVPPAR
                                                                                             LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCELYTDVDGIFSADP
                                                                                                                           RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                     HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI
                                                                                                      --RRRRQHR
                               VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                              ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
                                                                                                                                                                                                                                                                                                                                           bacteria; chemical compound; L-amino acid; vitamin; lysC;
                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a aspartate kinase carrying T3111 mutation
                27;
 DB 21; Length 421;
56.0%; Score 1227.5; DB 21; Lengt
64.0%; Pred. No. 1.3e-105;
.ive 56; Mismatches 58; Indels
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                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium glutamicum.
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Query Match
Best Local Similarity 64.0
Matches 251; Conservative
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N-PSDB; ABZ77392.
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                                         The specification describes Coryneform bacteria which produce chemical compounds, which instead of a single copy of an open reading frame (ORF), gene or allale naturally present at a desired locus have at least two copies of the ORF, gene or allele, preferably in tandem arrangement. The modified bacteria are is useful for producing chemical compounds including L-amino acids, vitamins, nucleosides and nucleotides. The present sequence is encoded by a lysC gene, and represents an aspartate kinase carrying the T3111 mutation. Tandem duplications of the lysC gene are used to construct the bacteria of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
                                                                                                                                                                                                                                                                                                                                                                                    DB 24; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                 56.0%; Score 1227.5; DB 24; Lengt
64.0%; Pred. No. 1.3e-105;
.ive 56; Mismatches 58; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a wild-type aspartate kinase.
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Page 105-106; 109pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGAAERLQGRGROD-RHHLHLLP--OTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGTTDITFTCPRSDGRRAMEILKXLOVOG----NW-----TNVLYDDOVGKVSLV 349
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                                                                                                                                     L-lysine, has a
in question at
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                                                                                                                                                                                                                                                                                                                                                                                                                55.8%; Score 1224.5; DB 24; Lengt:
64.0%; Pred. No. 2.5e-105;
ive 55; Mismatches 59; Indels
                                                                                                                             Coryneform bacteria to produce chemical compounds e.g. least two copies of open reading frame, gene or allele particular desired site
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                                                        Thierbach
                                                                                                                                                                                              Claim 15; Page 102-103; 109pp; English.
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                                                          Moeckel
06-AUG-2001; 2001US-309877P.
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Best Local Similarity 64.0
Matches 251; Conservative
                                                          Kreutzer C,
                                                                                      WPI; 2003-278476/27.
N-PSDB; ABZ77391.
                                                                                                                                                                                                                                                                                                                                                                                   420 AA;
                           (DEGS ) DEGUSSA
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                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the isolation of novel Corynebacterium glutamicum genes (AAS96013.) AAS9612) encoding metabolic pathway (MP) proteins. The metabolic pathway proteins of the invention include enzymes involved in the lyaine and methionine biosynthetic pathways. The polynucleotide sequences of the invention of expression of for the large-scale production and/or andulation of expression of fine chemicals such as lysine and methionine. The sequences of the invention may be used to identify C glutamicum and related organisms e.g. C diphtheriae in a subject to detect diphtheria.

AAU71863-AAU71822 represent the novel C glutamicum metabolic pathway proteins of the invention.
                                                                                                                                                                                                              Kim J;
                                                                                                                                                                                                                                                                                                     Nucleic acids encoding metabólic pathway proteins from Corynebacterium glutamicum, useful for producing methionine and lysine in Corynebacterium and Brevibacterium -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Length 421;
                                                                                                                                                                                                              Haberhauer G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA----
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                                                                                                                                                                                                              Zelder O,
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                                                                                                                                                                                                              Schroeder H,
                                                                                                                                   09-MAR-2000; 2000US-187970P
23-JUN-2000; 2000US-0606740
                                                                                                       22-DEC-2000; 2000WO-IB02035
              Corynebacterium glutamicum.
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N-PSDB; AAS96084.
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                                                                                                                                                                                                                                Hwang B;
                                                                                                                                                                                (BADI ) BASF AG
                                           WO200166573-A2
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                                                                                                                                                                                                                                      The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, in the examplification of the invention.

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 EMDMLLTAGERISNALVAMAIESLGAEAQSFTGSQAGVLTTERHGNARIVDVTPGRVREA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                           Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQKYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLELAAAVNPVPPAR
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                                                                                                                                                                                                                                                                                                                                    Yokoi H;
                                                                                                                         Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.8%; Score 1224.5; DB 22; Length 421; 64.0%; Pred. No. 2.5e-105; ive 55; Mismatches 59; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; SEQ ID NO: 3781; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                     Ochiai K,
                                                                                                                                                                                                                                                                                                                                    H, Ando S, Hayashi M,
Ikeda M, Ozaki A;
                                                                                                  C glutamicum protein fragment SEQ ID NO: 3781.
                      AAG90027 standard; Protein; 421 AA
                                                                                                                                                                                                                                                                                                             (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                           99JP-0377484.
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03-AUG-2000; 2000JP-0280988.
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                                                                                                                                                             Corynebacterium glutamicum.
                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                    Mizoguchi F
Senoh A,
                                                                                                                                     organic acid synthesis.
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N-PSDB; AAH65246.
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                                                                                                                                                                                    EP1108790-A2.
                                                                                                                                                                                                                                                             16-DEC-1999;
                                                                       26-SEP-2001
                                                                                                                                                                                                            20-JUN-2001.
                                                                                                                                                                                                                                                                                                                                   Nakagawa S,
Tateishi N,
                                                 AAG90027;
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Best Local &
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 RESULT 8
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-----TNVLYDDQVGKVSLV 350
241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA-------RRRRQHR 290
                                                                                      245 MEDIPVEBAVLTGVATDKSEAKVTVLGISDKPGEAAKVPRALADAEINIDMVLQNVSSVE 304
                                                                                                                                                                                           291 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; putrine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
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                                                                                                                                                                                                                                                   348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
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                        HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a mutant version of the C. glutamicum asparto-kinase (AK) alpha submit. The mutation is at position 279 and is a corresponds to the substitution of a non-acidic amino acid, pref. Ala. This mutation causes removal of the enzyme from additional feedback inhibition. Inhibition by Thr is removed completely and the synergic inhibition of Lys and Thr is also removed. The new AK has increased heat stability.
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                                                                                                                                                                                                                                                                                                                                 Mutant, C. glutamicum, aspartokinase, AK; alpha; beta; subunit; substitution; non-acidic; amino acid; Ala; additional; enzyme; feedback inhibition; synergic inhibition; heat stability.
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                                                     305 DGTTDITFTCPRSDGRRAMEILKKLÓVQG-----NW
                                                                                                         351 GAGMKSHPGVTAEFMEALRDVNVNIELISTSE
                                                                                      348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Best Local Similarity 64.0
Matches 251; Conservative
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                                                                                                                                                                                                                                                                    (first
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAAF9534 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, including bases, nucleosides, nucleotides, includes acids, acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purline and pyrimidine bases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
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64.0%; Pred. No. 2.5e-105;
.ive 55; Mismatches 59; Indels
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99DE-1032926.
99DE-1033928.
99DE-1033006.
99DE-1033006.
99US-0140764.
99DE-1040765.
99DE-1040765.
99DE-1040766.
99DE-1040766.
99DE-1041380.
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Best Local Similarity 64.0
Matches 251, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kroeger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAF71765
                                                                                  12-AUG-1999;
27-AUG-1999;
27-AUG-1999;
                                                                                                                               27-AUG-1999;
27-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                              BADI ) BASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pompejus M,
                                                                                                                                                                                                                                                                                                                               03-SEP-1999
03-SEP-1999
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LEEGRVVLVAGFOGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                    DGTTDITFICPRADGRRAMEILKKLOVOG----NW-----TNVLYDDOVGKVSLV 350
                                                                                                                                                                                                                                               HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
             RIVPNAQKLEKLSFEEMLELAAVGSKILVLRSVEYARAFNVPLRVRSSYSNDPGTLIAGS
                                                                                      LDEGKICIVAGFOGVNKETRDVTTLGRGGSDTTAVALAAALNADVCEIYSDVDGVYTADP
                                                                                                                      RIVRNARKLDTVTFBEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                  241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA-
                                                                                                                                                                                                                                                                                                           348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                      GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
                                                                                                                                                                                                                                                                                                                                                                                                                         AAR71416 standard; Protein; 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93JP-0209775.
93JP-0209776.
94JP-0153876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94WO-JP01365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)

 glutamicum protein.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-106843/14.
N-PSDB; AAQ84970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsui H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9506114-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-AUG-1994;
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240
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                                                                                                                                        305 DGTTDITFTCPRADGRRAMEILKKLQVQG-----NW------TNVLYDDQVGKVSLV 350
                                                                                                                       291 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a mutant version of the C. glutamicum asparto-kinase (AK) alpha subunit. The mutation is at position 279 and corresponds to the substitution of a non-acidic amino acid, pref. Ala. This mutation causes removal of the enzyme from additional feedback inhibition. Inhibition by Thr is removed completely and the symercic inhibition of Lys and Thr is also removed. The new AK has increased heat stability.
                IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA-----RRRRQHR
RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                                                                                                                                                                                    Mutant; C. glutamicum; aspartokinase; AK; alpha; beta; subunit; substitution; non-acidic; amino acid; Ala; additional; enzyme; feedback inhibition; synergic inhibition; heat stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 15; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The mutant aspartokinase gene - used to produce AK which is removed from feedback inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 55.8%; Score 1223.5; DB 15; Lengt. Local Similarity 64.0%; Pred. No. 3.1e-105; Lengt. es 251; Conservative 55; Mismatches 59; Indels
                                                                                                                                                                                   379
                                                                                                                                                                                                                351 GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
                                                                                                                                                                                                                                                                                                                                                                                         AK alpha subunit T279A from clone ATCC 13869.
                                                                                                                                                                                   GAGMRSHPGVTATFCEALAAVGVNIELISTSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 22; 28pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93JP-0101450,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92JP-0110292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                           (first entry)
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N-PSDB; AAQ61599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
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Best Local S:
Matches 251
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181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Variant of phospho-enol pyruvate carboxylase - not substantially inhibited by aspartic acid, is used for efficient production of amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 55.8%; Score 1223.5; DB 16; Length 421; Best Local Similarity 64.0%; Pred. No. 3.1e-105; Matches 251; Conservative 55; Mismatches 59; Indels 27;
Phosphoenolpyruvate-carboxylase; Corynebacterium glutamicum.
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9 64

5 VQKYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLELAAAVNPVPPAR

VOKYGGSSVADAERIRRVAERIVATKKQGNDVVVVSAMGDTTDDLLDLAQQVCPAPPR

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                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                        124
                                                                                                                                                                                                                                                                                                                       121 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                                                                                                                                                                         184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 HGAAERLOGRGROD-RHHLHLLP--OTSGPPPWKNWTRSETRSASTOLLYDDHIGKVSLI 347
                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                        IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA------RRRRQHR
                                                                                                                                                                                                            5 VQKYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLELABAAVNPVPPAR
                                                                                                                                                                                                                                                          61 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
                                                                                                                                                                                                                                                                            181 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVVGS
                                                                                                                                                                                            1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
                                                                                                                                                            Gaps
inhibition, by substituting the respective alpha and/or beta subunit (ARR86307/08) residues Ala 279 and/or 30 with another amino acid, and homoserine dehydrogenase (HD) gene (AAT03321) which encodes an attenuated HD (AAR86306), by substituting the residues Leu 23 and/or Val 104 with another amino acid, esp. Phe or Ile.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant DNA encoding aspartokinase in Coryneform bacterium
                                                                                                                          55.8%; Score 1223.5; DB 16; Length 421; 64.0%; Pred. No. 3.1e-105; ive 55; Mismatches 59; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L-lysine; aspartokinase; lysC gene; coryneform bacterium;
Corynebacterium glutamicum; fodder; feedstuff.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yoshihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brevibacterium lactofermentum ATCC 13869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspartokinase alpha subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96JP-0325658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AJIN ) AJINOMOTO CO INC. (AJIN ) AJINOMOTO KK.
                                                                                                                                         1 Similarity 64.0
251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-416006/36.
N-PSDB; AAV41300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-DEC-1997;
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                                                                                                                            Query Match
Best Local S:
Matches 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
                                                                                                  Sequence
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                                                                                                                             LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
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                                                                                                                                                                                                                                                                                                                                           -----TNVLYDDQVGKVSLV 350
                                                                120
                                                                                                                                                                                                                                                                              HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
                                                                                                                                                            125 LDEGKICIVAGFOGVNKETRDVTTLGRGGSDTTAVALAAALNADVCEIXSDVDGVYTADP 184
   09
                                  64
                                                                                                                                                                                                               VQKYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLELAAAVNPVPPAR
                                                                                     IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA--------RRRRQHR
     VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                                  BLDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
                                                                                                                                                                                            RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coryneform bacteria with increased L-lysine prodn. efficiency are produced by integrating a Coryneform aspartokinase (AK) gene (AAT03326) which encodes an AK free of L-Lys and L-Thr feedback
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transformant coryneform bacteria homoserine dehydrogenase gene and free asparto:kinase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aspartokinase, homoserine dehydrogenase, L-lysine production, coryneform bacteria, feedback inhibition free, attenuated, ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "opt. substituted to remove L-Lys and L-Thr feedback inhibition"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum aspartokinase alpha-subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۲;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usuda
                                                                                                                                                                                                                                                                                                                                             GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                                    GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tanaka A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Pages 55-57; 77pp; Japanese.
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279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR86307 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95WO-JP00268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AJIN ) AJINOMOTO CO INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-320579/41.
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Misc-difference
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Yoshihara

Sugimoto M,

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The present invention describes a recombinant DNA autonomously replicable in cells of coryneform bacteria (CB), comprising a DNA sequence coding for an aspartokinase (AX) in which feedback inhibition by L-lysine and L-threonine is desensitised, a DNA sequence coding for a dinydrodipicolinate synthase (DHPR), a DNA sequence coding for dinydropicolinate synthase (DHPR), a DNA sequence coding for aspartate decarboxylase (DAMD) and a DNA sequence coding for aspartate aminotransferase (AAT). The present sequence coding for lysC from Brevibacterium lactofermentum. The DNA and related products from the present invention, can be used for improving L-lysine productivity by CB. The L-lysine produced can be used as a fodder
                                                                                                                                                                                                                                                             Recombinant DNA autonomously replicable in coryneform bacteria used to produce L-lysine, codes for e.g. aspartokinase, di:hydropicolinate reductase and synthase and di:amino-pimelate
                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 22-23; 59pp; English.
                                            97EP-0121443.
                                                                                   96JP-0325659
                                                                                                                         (AJIN ) AJINOMOTO CO INC
                                                                                                                                                               Araki M, Nakamatsu T,
                                                                                                                                                                                                        WPI; 1998-379060/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 AA;
                                                                                                                                                                                                                           N-PSDB; AAV40254,
                                                                                                                                                                                                                                                                                                                             decarboxylase
                                          05-DEC-1997;
                                                                                05-DEC-1996;
    22-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 RIVPNAQKLEKLSFEEMLELAAVGSKILVLRSVEYARAFNVPLRVRSSYSNDPGTLIAGS 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60
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                                                                        This is the wild-type alpha subunit of Brevibacerium lactofermentum CATCC 13689 (Corpubacterium glutamicum) aspartokinase, an enzyme involved in the biosynthesis of L-lysine, but which is subject to feedback inhibition. A claimed recombinant DNA molecule that is a utonomously replicable in coryneform bacteria comprises a DNA sequence coding for an aspartokinase in which feedback inhibition by L-lysine and L-threonine is desensitised, and a DNA sequence coding for a diaminopimelate decarboxylase. This mutant aspartokinase preferably has residue Ala-279 of the alpha subunit (see AAW68152) and residue Ala-30 of the beta subunit (see AAW68152) and residue Ala-30 of the beta subunit (see AAW68152) and maino acid that is not Ala and is not an acidic amino acid. The host coryneform bacteria are used in a claimed method for producing L-lysine, which is useful as a fodder additive. They show improvements in L-lysine yield without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                           55.8%; Score 1223.5; DB 19
64.0%; Pred. No. 3.1e-105;
iive 55; Mismatches 59;
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                                        Claim 2; Page 17-18; 50pp; English
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used in preparation of L-lysine
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                                                                                                                                  S VQKYGGSSLESAERIRNVABRIVATKKAGNDVVVVCSAMGDTTDELLELAAAVNPVPPAR
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                                                                                                     1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
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                                                        Gaps
                                                     27;
  DB 19; Length 421;
55.8%; Score 1223.5; DB 19; Lengt 64.0%; Pred. No. 3.1e-105; ive 55; Mismatches 59; Indels
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                                                     251, Conservative
                             Local Similarity
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Search completed: November 21, 2003, 16:03:11 Job time : 27.6707 secs

Brevibacterium lactofermentum, lysC, L-lysine, coryneform bacterium, aspartokinase, feedback inhibition, dihydropicolinate reductase, diaminopimelate decarboxylase, aspartate aminotransferase.

Brevibacterium lactofermentum

EP854189-A2

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1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
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ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SUSTRAKE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/311,731A
FLING DATE:
TILNG DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GAREY INFORMATION:
REFERENCE/POCKET NUMBER: 31,616
REFERENCE/POCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TVELED COMMUNICATION COMPANION: 617/720-3500
TELEGRAPA TALON COMPANION: 617/720-3500
TELEGRAPA TALON COMPANION: 617/720-3441
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
                                                                         US-08-532-828B-6
US-08-596-8
US-08-91-104-8
US-09-198-452A-1124
US-09-107-532A-6090
US-09-107-532A-6320
US-09-134-001C-4941
US-09-252-991A-22037
US-09-252-991A-22037
US-09-252-991A-2112
US-09-252-991A-2112
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US-09-108-452A-740
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US-09-997-686-114
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ORIGINAL SOURCE:
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Sequence 30, Appli
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Sequence 14, Appli
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Sequence 2, Appli
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                                                                                                                                                                                  ; Search time 8.9415 Seconds (without alignments) 2006.354 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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2193
1 VQKYGGSSVADAERIRRVAE......SAATRRPRCTRGRDGRWACQ 424
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-252-991A-29720
US-07-684-135A-2
US-09-072-596-227
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US-09-138-352-6511
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US-09-138-352-6511
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US-08-380-182-23
US-08-380-182-23
US-08-380-182-19
US-08-950-737-2
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                  Run on:
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<u>ښ</u>

Gaps

us-09-688-672a-4.rai

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305 DĠTTDITFTCPRADGRRAMEILKKLĠVQG-----NW------TNVLYDDQVGKVSLV 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 MEDIPVEEAVLTGVATDKSEAKVTVLGISDKPGEAAKVFRALADAEINIDMVLQNVSSVE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
                                                                                                                                                                                                                                                                                                                                                                           61 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTFGRLQTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 VOKYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLELAAAVNPVPPAR
                                                                                                                                                                                                                                                                                                                                                                                                                           65 EMDMLLTAGERISNALVAMAIESLGAEAQSFTGSQAGVLTTERHGNARIVDVTPGRVREA
                                                                                                                                                                                                                                                                    1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                                                                                                                                                                                 Gaps
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                                                                                                                                                               DB 1; Length 421;
                                                                                                                                                                                                               59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08700359; Sequence 9, Application US/08700359; Patent No. 5766925; GENERAL INPORMATION:
APPLICANT: SUGINOTO, MASAKAZU
APPLICANT: USUDA, YOSHIHIRO
APPLICANT: USUDA, YOSHIHIRO
APPLICANT: TANAKA, AKIKO
APPLICANT: TANAKA, AKIKO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK ...
STREET: 1755 c
CITY
                                                                                                                                                            Query Match
55.8%; Score 1223.5; DB 1
Best Local Similarity 64.0%; Pred. No. 1.1e-116;
Matches 251; Conservative 55; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Corynebacterium glutamicum
STRAIN: ATCC13869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: ATELNOTON
STATE: VA
COUNTRY: USA
CONFUTER: VA
ZIP: 22202
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: ISM PC COMPATIBLE
SOFTWARE: WS-DOS STAT EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,359
FILING DATE: 08-0CT-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/700,359
FILING DATE: 04-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 24,618
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US-08-532-828B-3
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                                                                                                                                                                                                                                                                                                                            185 RVVHNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNI PVHVRSSYADKPGTVIVGS 244
                                                                                 61 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
                                                                                                                                                                                        121 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                                       125 LDEGRIVLVAGFQGVSQDTRDITTLGRGGSDTTALAMAAALGADVCEIYTDVDGIFSADP 184
                                                                                                                                                                                                                                                                                                                                                                                                     241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAE---- 295
                                                                                                                                                                                                                                                                                                                                                                                                                                   245 IKDVPMEDPILITGVAHDRSEAKVTIVGIPDIPGYAAKVFRAVA------DADVNIDM 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 RLQGRGRQDRHHLHL---LPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAGMR 352
                                                                                                                                   65 ELDMLLTAGERISNALVAMAİESFGAQARSFTGSQAGVITTGTHGNAKIIDVTFTRLQFA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 VLÓNVSKVEDGKIDITFICSRDSGPIAVAKLGSLRDBIGFÍQLLÝDDHÍGKVSLÍGAGMR 355
5 VQXYGGSSVADADRIRRVAERIVQTKKQGNDIVVVVSAMGDTTDDLLDLAQQVCPEPPAR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   356 SHPGVTATFCEALAAVGVNIELISTSEIRISVLCRDT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 SHPGVTATFCEALAAVGVNIELISTSEDORSRCCAAT 389
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GENERAL INC. SOCIETA
GENERAL
APPLICANT: SUGIMOTO, Masakazu
APPLICANT: SUGIKOTO, Masakazu
APPLICANT: SUZUKI, Tomoko
APPLICANT: TANAKA, Akiko
APPLICANT: TANAKA, Akiko
APPLICANT: TANAKA, Akiko
APPLICANT: MATSUI, Hiroshi
TITLE OF INVENTION: MUTANT ASPARTOKINASE GENE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-764-0 PCT
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
APPLICATION NUMBER: US/08/532,828
RICHARD ATTORNEY
ATTORNEY ATTORNEY
COMPUTER: 27-APR-1995
FILING DATE: 27-APR-1995
FILING DATE: 27-APR-1995
FILING DATE: 27-APR-1995
FILING DATE: 17-APR-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08532828B Patent No. 5688671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
TOPOLGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARLINGTON
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STREET: 1'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-08-532-828B-3
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348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-209775
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-209776
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-153876
FILING DATE: 05-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F:
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-784-0 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAMONE: (703) 413-3200
TELECAMONE: (703) 413-3200
TELECAMONE: (703) 413-3200
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                                                                                                                                                                                                                                                                                                                                                                                                                                    : 421 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 64.09
Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-596-366-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 IKDVPMEDPILTGVAHDRSBAKVTIVGLPDIPGYAAKVFRAVA------RRRRQHR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
                                                                                                                                                                                                                                                                                                                                                                                               64
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Patent No. 5876981

GENEMATION:
APPLICANT: SUGINOTO, Masakazu
APPLICANT: SUZUKI, Tomoko

APPLICANT: MATSUI, Hiroshi
APPLICANT: IZUL, Katsura
ITILE OF INVENTION: ITS GENE, AND PRODUCTION METHOD OF AMINO ACID
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
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ADDRESSEE: P.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 RIVPNAQKLEKLSFEEMLELAAVGSKILVIRSVEYARAFNVPLRVRSSYSNDPGTLIAGS
                                                                                                                                                                                                                                                                                                                                                   1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                                   DB 1; Length 421;
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUDKESSEE: P.C., OFLVAK, MCCLELLAND, MAIER, & NEISTREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400 STATE: VIRGINIA
                                                                                                                                                                                                                                                              55.8%; Score 1223.5; DB 1; 64.0%; Pred. No. 1.1e-116; ive 55; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/596,366
FILING DATE: 29-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Pn-1
REFERENCE/DOCKET NUMBER: 1
TREECOMMUNICATION INFORMATION
TELEPHONE: 703-413-3000
TELEFRX: 703-413-2220
                                                                                                                                TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-700-359-9
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 64.0°
Matches 251; Conservative
                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22202,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIRGINIA
: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-08-596-366-6
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120
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                                                                                                                                                                                                                                                                                                                                                                                 121 LEEGRVVLVAGFOGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA-------RRRRQHR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 HGAAERLOGRGROD-RHHLHLLP--OTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 BLDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
                                                                                                                                                                                                                                                                                           65 EMDMLLTAGERISNALVAMAIESLGAEAQSFTGSQAGVLTTERHGNARIVDVTPGRVREA
                                                                                                                                                               5 VQKYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLELAAAVNPVPPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                           1 VQKYGGSSVADABRIRRVABRIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SUGIMOTO, Masakazu
APPLICANT: SUGIMOTO, Tomoko
APPLICANT: MATSUI, Tomoko
APPLICANT: MATSUI, Hiroshi
APPLICANT: IZUI, Katsuza
TITLE OF INVENTION: MUTANT PHOSPHOENOLPYRUVATE CARBOXYLASE,
TITLE OF INVENTION: ITS GENE, AND PRODUCTION NETHOD OF AMINO ACID
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER, & NEUSTADT,
                                                               27;
   DB 2; Length 421;
55.8%; Score 1223.5; DB 2; Length 64.0%; Pred. No. 1.1e-116; iive 55; Mismatches 59; Indels
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MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI
FOR PRODUCING L-LYSINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 DGTTDITFTCPRADGRRAMEILKKLQVQG-----NW-------TNVLYDDQVGKVSLV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 MEDIPVEEAVLTGVATDKSEAKVTVLGISDKPGEAAKVFRALADAEINIDMVLQNVSSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 LEEGRIVYLVAGFOGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27;
                                                                                                                                                                                        ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR COUNTY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 55.8%; Score 1223.5; DB 3 Best Local Similarity 64.0%; Pred. No. 1.1e-116; Matches 251; Conservative 55; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: JP 8-325659
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F: OBLON
REGISTRATION NUMBER: 24,618
TELEPHONE: 703-413-3000
TELEPRAX: 703-413-3220
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,908
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
                                                                                        ; Sequence 5, Application US/08985908
; Patent No. 6004773
; GENERAL INFORMATION:
APPLICANT: MASAYUL ARAKI, MASAKA;
; TITLE OF INVENTION: METHOD FOR PR.
NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                         US-08-985-908-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 1223.5; DB 2; Length; Pred. No. 1.1e-116; 55; Mismatches 59; Indels
SSEE: P.C.
F: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400
ARLINGTON
VIRGINIA
                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
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                                                                                                                                                                                                                                                                             PILING DATE:
CLASSIPICATION NOWIBER: US/08/98/,104
FILING DATE:
APPLICATION DATA:
APPLICATION NUMBER: US 08/596,366
FILING DATE: 29-APR-1996
APPLICATION NUMBER: UP 5-209775
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 5-209776
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-153876
FILING DATE: 05-UUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
NAME: OBLON, NORMAN F.
REGISTATION NUMBER: 24,618
                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 64.0%;
Matches 251; Conservative 59
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                                                                                                                 ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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               ADDRESSEE:
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                                                                                               COUNTRY:
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Sequence 5, Application US/08985916
Patent No. 6221636
GENERAL INFORMATION:
APPLICANT: ATSUSHI HAYAKAWA, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI
TITLE OF INVENTION: WETHOD FOR PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
COUNTRY: VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGAABRLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----TNVLYDDQVGKVSLV 350
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                                                                                                                                                                                                                                                                                                                                                                            COMPUTE: RELABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elem PC compatible
COMPUTER: Elem PC compatible
COMPUTER: Elem PC compatible
COMPUTER: DEADLE FLOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,916
FILING DATE: 05-DEC-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: UP 8-325658
ATORNEY/AGENT INPOMMATION:
NAME: US/MAMTION:
NAME: OSLOM
REGISTRATION NUMBER: 24,618
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351 GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       305 DĞTTDITFTCPRADGRRAMBILKKLÖVQĞ-----NW-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 24,618
TELEPHONE: 703-413-3000
TELEFAX: 703-413-220
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 64.09
Matches 251; Conservative
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                                                                                                           PARENT NO. 900597

PARENT NO. 900597

PARENT NO. 900597

APPLICANT: SEIKO HIRANO, MASAKAZU SUGIMOTO, EIICHI NAKANO,
APPLICANT: MASAKAZ IZUI, ATSUSHI HAYAKAWA, YASUHIKO YOSHIHARA, AND TSUYOSHI
APPLICANT: NAGAMATSU

TILLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER AND NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STRIE: VA
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STRING DATE: OC-DOS/MS-DOS
SOFTWARE: PREDLICHION DATA:
APPLICATION NUMBER: US/08/852,730
FILING DATE: OS-OV-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US-UN-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
NAME: NORMAN F. OBLON
NAME: NORMAN F. OBLON
TREDSCRAFTON NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IKDVPMEDPILIGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA------RRRRQHR 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGTTDITFTCPRADGRRAMEILKKLOVOG-----NW-----TUVLYDDOVGKVSLV 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.8%; Score 1223.5; DB 3; Length 64.0%; Pred. No. 1.1e-116; ive 55; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                             Sequence 14, Application US/08852730 Patent No. 6090597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 421 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 64.09
Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-852-730-14
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NS-09-252-991A-29720

Sequence 29720, Application US/09252991A

Sequence 29720, Application US/09252991A

Sequence 29720, Application US/09252991A

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AERUGINGSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINGSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

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SPIOR FILING DATE: 1998-02-18

SPIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                         30S DGTTDITFTCPRADGRRAMBILKKLQVQG-----NW------TNVLYDDQVGKVSLV 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 RIVRNARKLDIVIFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGIVVVGS 240
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185 RIVPNAQKLEKLSFEEMLELAAVGSKILVLRSVEYARAFNVPLRVRSSYSNDPGTLIAGS 244
                                                                                                                            291 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
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                                                                                                                                                                                                                                                                                                                                                                                  348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
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US-07-684-135A-2
; Sequence 2, Application US/07684135A
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Best Local Similarity 42.61
Matches 170; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. STREET: 1755 S. JEPFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 421;
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Best Local Similarity 63.8%; Pred. No. 2.8e-116;
Matches 250; Conservative 55; Mismatches 60;
                                                                                                                                                                                                                                                                                                 GENERAL INPORMATION:
APPLICANT: STGIMOTO, MASAKAZU
APPLICANT: GGAWA, YULI
APPLICANT: SUZUKI, TOMOKO
APPLICANT: TANAKA, AKİKO
APPLICANT: MANSIGUI, HİLOSHİ
TITLE OF INVENTION: MUTANT ASPARTOKINASE GENE
NÜMBER OF SEQUENCES: 24
351 GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS TEXT EDITOR
CURRENT APPLICATION NUMBER: US/08/532,828
FILING DATE: 27-OCT-1995
CLASSIFICATION 1435
PRIOR APPLICATION UNMBER: JP S-101450
FILING DATE: 27-APR-1993
ATTORNEY AGENT INPORMATION:
NAME: ADPRIANT INPORMATION:
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                                                                                                                                                                                                                                 Sequence 4, Application US/08532828B Patent No. 5688671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: NORWAN F. OBLON
REGISTRATION NUMBER: 24,618
REPERENCE/DOCKET NUMBER: 10-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acids
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 -ESVTWEQNLVVRGVAFEDEITRVTVFGLPNSLISLIFITLA----
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GENERAL INFORMATION:
APPLICANT: Schendel Frederick J. and
APPLICANT: Schendel Frederick J. and
APPLICANT: Flickinger, M. C.
TITLE OF INVENTION: Bacillus MGA 3 Aspartokinase
TITLE OF INVENTION: II Gene
NUMBER OF SEQUENCES: 2
CORRESPONDENCES: 2
CORRESPONDENCES: 2
APPRESED: Merchant & Gould
STREET: 3100 No. 5243039west Center
STREET: Minneapolis
STRATE: Minneapolis
COUNTRY: USA
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ZIP: 55402

ZOP: TEADDBLE FORM:
COMPUTER READDBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb
COMPUTER: No. 5243039thgate 386
OPERATING SYSTEM: DOS 4.0
CONTWARE: WordPerfect 5.0
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WordPerfect - 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/684,135A
FILING DATE: 19910412
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REJISTRATION NUMBER: 80,440
REFERENCE/DOCKET NUMBER: 600.216-US-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TEMPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 411 amino acids TYPE: AMINO ACID
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62 LDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTAL 121
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Sequence 227, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION REGG, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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CURENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,556

FILING DATE: 07-APR-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: MARX, DAVIG J.

REGISTRATION NUMBER: 31,392

REGISTRATION NUMBER: 31,210121.457

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-601

INFORMATION FOR SEQ ID NO: 227:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               AUDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAM 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
35.1%; Score 770; DB 4;
Best Local Similarity 100.0%; Pred. No. 6.5e-71;
Matches 156; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 222, Application US/09072596; Patent No. 6458366; GENERAL INFORMATION:
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Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
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Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Sequence 5225, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC.07
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR PELING DATE: 1997-08-14
NUMBER: OF SEQUENCE SEQUENCES SEGT4

SEQUENCE SEQUENCES SEGT4

NUMBER: OF SEQUENCES SEGT4

NUMBER: OF SEQUENCES SEGT4
                                                                                                                                                                                                                                                                                                          241 IKDVPMEDPILLTGVAHDRSEAKVTI-VGLPDIPGYAAKVFRAVARRRRQHRHGAAERLQG 299
                                                                                                                                                                                               LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 VDMIVQNVEEDGTTDFTFTVNRVDLAKAEKILNETA-----KN---IGAREVSTR----D 362
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                                                                                                                                 61 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
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                                                                                                                                                                                                                      181 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 VLKFGGSSVSDFKKIKMIAEMLKTRIEDGEELIVVVSAMGKTTDQLMMNVSSLTSTFKDQ
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                         1 VOKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
                                                               17 VOKYGGTSMGTPERILNVARRVKRWHDHGHKVVVVVSAMSGETNRLLALÁKAITETPDPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 HIGKVSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363 DIVKVSIVGVGMRSHAGVASKMFTALADEGINILMISTSE 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 35.69
Matches 138; Conservative
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US-09-134-001C-5225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM:
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Patent No. 654298
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Patent No. 654298
Patent No. 654298
Patent No. 654298
Patent No. 84029000
PILE OF INVENTION NUMBER: US/09/328,352
PILE REPRENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
NUMBER OF SEQ ID NOS: 8252
                         TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTAL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 LDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTAL 121
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APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.1%; Score 770; DB 4; Length 156; 100.0%; Pred. No. 6.5e-71; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                        Version #1.30
                                                                                    3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 EEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAM 156
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42.0%; Pred. No. 8.2e-68;
tive 73; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISCHATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPARE: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                       US/09/072,596
05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 622-490
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 amino acids
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Best Local Similarity 42.0%
Matches 168; Conservative
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Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-09-072-596-222
                                                                                                                                                    Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                               CITY: Seattle
STATE: Washingt
COUNTRY: USA
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US-09-328-352-6511
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LENGTH: 438
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November 21, 2003, 16:08:22 ; Search time 16.537 Seconds (without alignments) 4680.740 Million cell updates/sec
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2193
1 VQKYGGSSVADAERIRRVAE.....SAATRRPRCTRGRDGRWACQ 424
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1: /cgn2_6/ptodata/1/pubpaa/PCT_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/USO0_NEW PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 163, App	Sequence 3781, Ap	Sequence 24, Appl	Sequence 5, Appli	Sequence 2, Appli	Seguence 16, Appl	Sequence 12093, A	Sequence 227, App	Sequence 222, App	Sequence 290, App	Sequence 17, Appl	Sequence 8, Appli	Sequence 6, Appli	Sequence 23, Appl	Sequence 23, Appl
ΩI	US-09-793-306-163	US-09-738-626-3781	US-09-746-660A-24	US-10-226-136-5	US-10-067-974-2	US-10-067-974-16	US-10-156-761-12093	US-10-084-843-227	US-10-193-002-222	US-09-882-227-290	US-09-890-813-17	US-09-890-813-8	US-09-890-813-6	US-10-301-997-23	US-09-989-339-23
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% Query Match Length DB	421	421	421	421	421	421	430	156	156	394	564	555	260	262	449
% Query Match	73.7	55.8	55.8	55.8	55.5	55.2	52.2	35.1	35.1	30.7	17.2	16.2	16.0	14.3	14.2
Score	1615.5	1224.5	1224.5	1223.5	1217.5	1211.5	1144.5	770	770	673	377	356	350	314.5	310.5
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## ALIGNMENTS

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Sequence 163, Application US/09793366
; Sequence 163, Application US/09793366
; Sequence 163, Application US/09793366
; Patent No. US20020098200A1
; GENERAL INNORATION:
    APPLICANT: Campos-Neto, Antonio
    APPLICANT: Campos-Neto, Antonio
    APPLICANT: Ovendale, Pamela
    APPLICANT: Ovendale, Pamela
    APPLICANT: Corixa Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: MO-2 (aspartokinase)
US-09-793-306-163
RESULT 1
US-09-793-306-163
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291 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: POMPED-US, MATKUS
APPLICANT: POMPED-US, MATKUS
APPLICANT: SCHroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Gregor
APPLICANT: Kim, Jun-Won
APPLICANT: Kim, Jun-Won
APPLICANT: Kim, Jun-Won
APPLICANT: Kim, Jun-Won
APPLICANT: Lew, Heung-Schick
APPLICANT: Lew, Heung-Schick
APPLICANT: Lew Heung-Schick
APPLICANT: MTABACLIC PATHWAY PROTEINS
FILE OF INVENTION: ORRNBER: US/09/746,660A
FILE REFERENCE: BGI-121CP2
CURRENT APPLICATION NUMBER: US/09/746,660A
FILE REPERENCE: BGI-121CP2
CURRENT FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR PELLON NUMBER: 60/14101
PRIOR PELLON NUMBER: 60/14101
PRIOR PELLON NUMBER: 60/14101
PRIOR PELLON NUMBER: 60/148613
PRIOR PELLON NUMBER: 60/148613
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PRIOR PELLON NUMBER: 000-03-09
PRIOR PELLON NUMBER: DE 19931420.9
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 1090-07-08
PRIOR FILING DATE: 1008: 125
SOFTWARE PELLON VUMBER: 00.03-09
PRIOR FILING DATE: 1000-03-09
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                                                                                                         241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA-
                                                                                                                                                                                                                                                    305 DGTTDITFTCPRSDGRRAMEILKKLOVOG-----NW---
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64.0%; Pred. No. 6.9e-109;
live 55; Mismatches 59;
                                                                                                                                                                                                                                                                                                       GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                   351 GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Asherhauer, Gregor
APPLICANT: Lee, Heung-Schick
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Best Local Similarity 64.09
Matches 251; Conservative
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                                                                        LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCELYTDVDGIFSADP
                                                                                                         LEBGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
                                                                                                                                                                         RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   356 SHPGVTATFCEALAAVGVNIELISTSEIRISVLCRDT 392
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GENEKAL INFORMATION:
APPLICANT: MIZGGUCHI, HIROSHI
APPLICANT: MIZGGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: SENOH, AKKHIRO
APPLICANT: SENOH, AKKHIRO
APPLICANT: SENOH, AKKHIRO
APPLICANT: SENOH, AKKHIRO
APPLICANT: SENOH, AKKHIRO
APPLICANT: OZAKI, AKIO
TILE REFERENCE: 249-125
CURRENT FILING THE: 2000-12-18
PRIOR RILING DATE: 1999-12-16
PRIOR PELING DATE: 2000-14-07
PRIOR APPLICATION NUMBER: JP 90/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/159163
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET: 3.0
SEQ ID NO 3791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 3781, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION:
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Sequence 2, Application US/10067974

Publication No. US20030055232A1

Publication No. US2003005532A1

GENERAL INFORMATION:

APPLICANT: Li, Linia - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Veni - Ve
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         VQXYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLELAAAVNPVPPPAR
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Matches 250; Conservative
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US-10-067-974-2
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245 MEDIBVYERAVLTGVATDKSBAKVTVLGISBKPGBAAKVFRALADAEINIDMVLQNVSSVE
RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                            241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA------RRRRQHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR CITY: ARLINGTON STATE: VA
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/226,136

FILING DATE: 23-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KOBAYASHI, Masaki
YOSHIHARA, Yasuhiko
NAKAMATSU, TSUYOShi
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                         305 DGTTDITFTCPRSDGRRAMEILKKLÖVQG-----NW---
                                                                                                                                                                                                                                                                                                                                   GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                               GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/952,976
FILING DATE: 8-DEC-1997
APPLICATION NUMBER: UP 7-140614
FILING DATE: 07-ULL-1955
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-300
TELEPHONE: 703-413-220
FORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUGIMOTO, Masakazu
IZUI, Masako
HAYAKAWA, Atsushi
NAKANO, Eiichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/10226136
Publication No. US20030054506A1
GENERAL INFORMATION:
APPLICANT: OTSUNA, Seiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 421 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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Best Local Simi
Matches 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-10-226-136-5
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----ROHRHGAAERLQGRGRQDRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDDHIG 342
--TNVLYDDQVXKVSLV 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEEGRAVILVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---FTLPKTEGRKAIDALEKAKSVIGFDSLRYDDOÍG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 VQKYGGSSVADAEGIKRVAKRIVEAKKNGHQVVVVVSAMGDTTDELIDLAEQVSPMPSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 RIVRNARKLDTVTFBEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -EDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.2%; Score 1144.5; DB 1660.2%; Pred. No. 3.4e-101; tive 54; Mismatches 75;
    305 DGTTDITFTCPRXDGRRAMEILKKLQVQG-----NW
                                                                                                                                                                                                                                                   APPLICANT: ONURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, UUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SAFAKI, YOSHIVUKI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-39
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
                                                             348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE
                                                                                          351 GAGMKSHPGVTAEFMEALRDVNVNIELISXSE
                                                                                                                                                                                                ; Sequence 12093, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 227, Application US/10084843 Publication No. US20030143243A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 IDMVVQNVSAASTGLTDIS---
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Matches 239; Conserv
                                                                                                                                                             RESULT 7
US-10-156-761-12093
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US-10-084-843-227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                              APPLICANT: Li, Lhing-Yew
APPLICANT: Li, Lhing-Yew
APPLICANT: Li, Lhing-Yew
APPLICANT: Trei, Kelli J.
TITLE OF INVENTION: Polynucleotide Constructs for Increased Lysine Production
FILE REFERENCE: 1533.2640001
CURRENT APPLICATION NUMBER: US/10/067,974
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,183
PRIOR FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIVRNARKLDTVTFEEMLEMAACGAKVLMIRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 IKDVPMEDPILIGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA-------RRRROHR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 MEDIPVEEAVLTGVATDKSEAKVTVLGISDKPGEAAKVFRALADAEINIDMVLQNVSSVE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
                                 30S DGTTDITFTCPRADGRRAMEILKKLQVQG----NW-----TNVLXDDQVGKVSLV 350
          HGAAERLQGRGROD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Consensus Sequence of Protein Sequence Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 15; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.2%; Score 1211.5; DB 1563.5%; Pred. No. 1.2e-107; iive 55; Mismatches 61;
                                                                                    348 GAGMRSHPGVTATFCBALAAVGVNIELISTSE 379
                                                                                                           351 GAGMKSHPGUTAEFMEALRDVNVNIELISISE 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MISC_FEATURE
LOCATION: (380)
/ OTHER INFORMATION: May be either Thr or 1le
US-10-067-974-16
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                                                                                                                                                                                                                      ; Sequence 16, Application US/10067974; Publication No. US20030055232A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (317)..(317)
OTHER INFORMATION: May be either
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 either
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 63.5
Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MISC FEATURE
LOCATION: (345)..(345)
OTHER INFORMATION: May be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC_FEATURE LOCATION: (40)...(40)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: MISC_FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGTLOTAL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 OKYGGSSVADAERIRRVAERIVATKKQGNDVVVVSAMGDTTDDLLDLAQQVCPAPPPRE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 QKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
       AFFLICAVITY SACIONAL SKEIKY, Yasir A.W.

Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 35.1%; Score 770; DB 12; Length 156; Best Local Similarity 100.0%; Pred. No. 7.4e-66; Matches 156; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER REALDALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION ADATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNYY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 EEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAM 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 227:
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Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                  STATE: Washington
                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 98104-7092
APPLICANT:
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US-10-193-002-222
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62 LDMLLTAGERISNALVAMAIESLGAHARSFIGSQAGVITTGTHGNAKIIDVTPGRLQTAL 121
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                                                                                                                                                                      METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: Washington
COUNTRY: USE
ZIE: 93104-7092
COMPUTER: Bloppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: PREADLE FORM:
MEDIUM TYPE: POC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
FILING DATE: 10-Jul-2002
CLASSIFICATION NOWBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: AUNKNOWN>
PRIOR APPLICATION: AUNKNOWN>
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAXI, DAVID J.
REGISTRATION NUMBER: 31.392
REGISTRATION NUMBER: 31.392
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 290, Application US/09882227
Publication No. US20030158396A1
GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: Kleanthous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean-Prancois
APPLICANT: Ocomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 EEGRVVLVAGFOGVSODTKDVTTLGRGGSDTTAVAM 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 210121.417C9 TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 222:
US-10-193-002-222
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND ME
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 222:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
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203
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264 AIPVVTGFLGKGWKSGAVTTLGRGGSDLTATTIGKALGLREIQVWKDVDGVLTCDPNIYP 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | |:|||||: | |: || |: 86 VMKFGGSSVSSAARMAEVAGLILTFPEE--RPVVVLSAMGKTTNNLLLAGEKAVGCGVIH 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 ECMSTRIFSAYLNKIRVKARQYDAFDIGFITTDEFGNADILEATYPAVAKRIHGDWIQDP 263
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                                                                                                                                                                 325 KAEPVPYLTFDEAAELAYFGAQVLHPQSMRPARESDIPVRVKNSYNPKAPGTLIT---KA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----VS 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -------PSKLWSRELIQQASEL----DHVVEELEKIAVVNLLQNRSIIS 483
97 VMKFGGSSVASADRMKEVATLILSFPEE--RPIVVLSAMGKTTNKLLLAGEKAVSCGVIN 144
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                                                                                                                                                                                                                 125 RVVLVAGFOGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADPRIVR 184
                                                                                                                                                                                                                                              265 AIAIVIC'HLGRARKSCAVTTLGRGGSDLTATTIGKALGLPEIQVWKDVDGVLTCDPNIYP 324
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                                                                                                                                                                                                                                                                                                                                                                         244 VPMEDPILTGVAHDRSEAKVTIVGLPDIP--GYAAKVFRAVARRRRQHRHGAAERLQGRG 301
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                                                                                               145 VSSIBELCFIKDLHLRTVDQLGVDGSVISKHLBELEQLLKGIAMMKELTKRTQDYLVSFG
                                                            --DLAQQVCPAPPREL----DMLLTAG
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16.2%; Score 356; DB 10;
Best Local Similarity 29.9%; Pred. No. 2.7e-25;
Matches 101; Conservative 57; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09990813; Fublication No. US20020183486A1; Fublication No. US20020183486A1; GENERAL INFORMATION: BAPPLICANT E.I. du Pont de Nemours and Compa; TITLE OF INVENTION: Aspartate Kinase; FILE REFERENCE: BB1430 PCT; CURRENT PFLLING DATE: 2010-108-02; PRIOR APPLICATION NUMBER: 60/172944; PRIOR PLLING DATE: 1999-12-21; NUMBER OF SEQ ID NOS: 24; SOFTWARE: Microsoft Office 97; SEQ ID NOS: 24
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      Encoding No. US20030158396Alel Helicobacter Polypeptides in
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                                                                                                                                                                                                                                                                                                Length 394;
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                                                                                                                                                                                                                                                                                                Query Match 30.7%; Score 673; DB 12; Length 39-
Best Local Similarity 40.1%; Pred. No. 5.8e-56;
Matches 151; Conservative 83; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours and Company
TITLE OF INVENTION: Aspartate Kinase
TITLE OF INVENTION: Aspartate Kinase
FILE REPERENCE: B1430 PCT
CURRENT APPLICATION NUMBER: US/09/890,813
CURRENT APPLICATION NUMBER: 60/172944
PRIOR PILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: MICROSOFT OFFICE 97
TITLE OF INVENTION: Encoding No. US2003015813
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/047002
CURRENT APPLICATION NUMBER: US/09/882,227
CURRENT FILING DATE: 2001-06-15
PRIOR PELING DATE: 1997-07-29
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO-390
LENGTH: 394
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                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 564
TYPE: PRT
ORGANISM: Glycine max
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Best Local Simi
Matches 128;
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US-09-890-813-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 IPVVIGFLGKGWKSGAVITLGRGSDLTATIGKALGLREIQVWKDVDGVLTCDPNIYPH 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WAKFGGSSVSSARMAEVAGLILTFPEE--RPVVVLSAMGKTTNNLLLAGEKAVGCGVIH 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTAL-----EEGR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCELYTDVDGIFSADPRIVRN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 ARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDR-PGTVVVGSIKDV 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 PMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAERLQGRGRQD 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 RHHLHL------LPQTSGPPPWKNWTRSETRSASTQLLYDDHIGK------ 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 VSEIBEWNWVKSLHIKTVDELGLPXICNTSLYELEQLLKGIAMMKELTPRTSDYLVSFGE 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 155; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 560;
                                                   244 VPMEDPILTGVAHDRSEAKVTIVGLPDIP--GYAAKVF 279
                                                                                   381 RDMDKVVLTSIVLKSNVTMLDIVSTRMLGQYGFLARVF 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                 US-09-890-813-6

Sequence 6, Application US/08890813

Publication No. US20020183486A1

GENERAL INFORMATION:
APPLICANT: B.I. du Font de Nemours and Company
TITLE OF INVENTION: Aspartate Kinase
FILE REFERENCE: B81430 PCT
CURRENT APPLICATION NUMBER: US/09/890,813

CURRENT FILING DATE: 2001-08-02

PRIOR FILING DATE: 1999-12-21

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.0%; Score 350; DB 10
26.4%; Pred. No. 1e-24;
iive 76; Mismatches 15
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NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: UNSURE
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RESULT 14 US-10-301-997-23 ; Sequence 23, Application US/10301997

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200 MAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVVGSIKDVPMEDPILTGVAHDRS 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 BAKVTI-VGLPDIPGYAAKVFRAVARRRRQHRHGAAE------RLQGR-----GRQD 304
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                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41;
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14.3%; Score 314.5; DB 12; Length 262;
Best Local Similarity 33.9%; Pred. No. 8.7e-22;
Matches 87; Conservative 47; Mismatches 82; Indels 41;
                          CAL INFORMATION:
APPLICANT: Holden, David W.
TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
NUMBER OF SECUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,997
FILING DATE: 22-No. US20030148346A1-2002
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 28341/33996
                                                                                                                                                                                                                                               STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/527,431
FILING DATE: «UNARLOwn»
APPLICATION NUMBER: US/08/887,534
FILING DATE: «Unknown»
                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (312) 474-6300
(312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 262 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: (312) 474-6600
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION
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Publication No. US20030148346Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        ZIP: 60606
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                           CITY: Chicago
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US-09-989-339-23
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APPLICANT: Falco, Saverio Carl
APPLICANT: Famodu, Layo
APPLICANT: Famodu, Layo
APPLICANT: Ramaker, Michael
APPLICANT: Ramaker, Michael
APPLICANT: Ranaker, Michael
APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Tarczynski, Mitchell C.
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APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Tarczynski, Mitchell C.
CURRENT APPLICATION NUMBER: US/09/989,339
CURRENT APPLICATION NUMBER: 08/703,829
PRIOR PELLING DATE: 1996-08-27
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Microsoft Office 97
SOFTWARE: Microsoft Office 97
SOFTWARE: Richarichia coli
US-09-989-339-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 NALVAMAIESLGAHARSFTGSQAGVITTGTHGNAK----IIDVTFGRLQTALEEGRVVL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 VAGFOGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADPRIVRNARK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 TQGFIG-SENKGRTTTLGRGGSDYTAALLAEALHASRVDIWTDVPGIYTTDPRVVSAAKR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 IDEIAPAEAATFGAKVLHPATLLPAVRSDIPVFVGSSKDPRAGGTLVCNKTENP--- 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189 LDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGSIKDVPMED 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----APPPRELDMLLTAGERIS 73
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14.2%; Score 310.5; DB 11; Length 449;
Best Local Similarity 30.2%; Pred. No. 4.6e-21;
Matches 102; Conservative 55; Mismatches 118; Indels 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 PILTGVAHDRSEAKVTIVGLPDI--PGYAAKVFRAVAR 284
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Search completed: November 21, 2003, 16:38:11 Job time : 18.537 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 21, 2003, 15:57:31 ; Search time 8.84535 Seconds (without alignments) 4609.825 Million cell updates/sec Run on:

US-09-688-672A-4 2193 1 VQKYGGSSVADAERIRRVAE......SAATRRPRCTRGRDGRWACQ 424 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	. <u>⊊</u>	aspartokinase [imp	kinase	aspartate kinase (	le a	tate k	othetic	tate kin	rtate kinas	rtate	art	artokinase,	rtokinase II	aspartate kinase (	a)	rtokinase II	e II	rtokinase	rtate kinase	rtokinase -	se.	artokinase [	artokinase I	artate		K protein (AF3	rtokinase,	aspartokinase II [	artokinase
SUMMARIES	ΩI	079	719	242	527	538	353	S76764	894	164	226	186	107	403	40	039	224	236	184	931	9	158	S	22	27	F306	ч	8231	97	94
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مان	Query Match	ω.	70.5	۲.	56.1	ά.	7	37.2	'n.	'n.	ď.	4.	4.	4,	'n	ش	ς.	ო	ď	ď.	32.4	'n	ď.	'n.	ä	σ,	29.9	œ	ů.	'n
	Score	615.	545.	œ	229.	14	$^{\circ}$	816.5	ω	77	776.5	o	92	۲.	٠	₹.	₹.		72	•	711	O	0	70	•	ഗ	ഹ	m	œ	φ
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C46665	AB1617	D97845	AD1254	C64371	E71635	D97123	D69337	F75405	AH0056	T48575	AC0502	DEECK	B90629	B85480	70000
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24.3 40														~	
532 24.3 40		23.7							17.9	17.2			16.8	.5 16.8	

## ALIGNMENTS

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Local Similarity 77.00 nes 302; Conservative
A;Residues: 1-421 <CIR>
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N.Alternate names: aspartokinase alpha chain
C;Species: Mycobacterium smegmatis
C;Species: Mycobacterium smegmatis
C;Species: Mycobacterium smegmatis
C;Date: O'May-1998 #sequence_revision 15-May-1998 #text_change 18-Jun-1999
C;Accession: 542422; 31801
R;Cirillo, J.D.; Weisbrod, T.R.; Pascopella, L.; Bloom, B.R.; Jacobs Jr., W.R.
Mol. Microbiol. 11, 629-639, 1994
A;Ritle: Isolation and characterization of the aspartokinase and aspartate semialdehyde
A;Reference number: 542421; MUID:94254720; PMID:7910936
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C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Suppr-2001 #sequence_revision 20-Apr-2001 #text_change 14-Dec-2001
C;Accession: G87199
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R; Davies, R.W.; Devlin, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Ruther, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
A;Authors: Ruther, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
A;Accession: G87199
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: G87199
A;Residues: 1-421 <STO>
A;Residues: 1-421 <STO>
A;Coses-references: GB:AL450380; NID:g13093941; PIDN:CAC31839.1; GSPDB:GN00147
C;Genetias;
A;Gene: ask
C;Superfamily: aspartate kinase; aspartate kinase homology
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  SHPGVTATFCEALAAVGVNIELISTSEDQRSRCCAAT 389
                      SHPGVTATFCEALAAVGVNIELISTSEIRISVLCRDT 392
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80.4%;
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A;Molecule type: DNA
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A; Residues: 1-421 - 6PDS
A; Cross-references: EMBL:X57226; NID:940509; PIDN:CAA40502.1; PID:9580983
A; Experimental source: ATCC 13032
R; Serebrijski, I.; Mojcik, F.; Reyes, O.; Leblon, G.
Submitted to the EMBL Data Library, November 1994
A; Description: Two loci of Corynebacterium glutamicum ATCC17965 that complement B, Reference number: $49977
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A)Cross-references: EMBL:217372; NID:944506; PIDN:CAA78984.1; PID:9581352 A;Note: the authors translated the initiation codon GTG for residue 1 as VG Genetics.

A;Start codon: GTG
C;Superfamily: aspartate kinase, aspartate kinase homology
C;Keywords: alternative initiators; phosphotransferase
F;1-421/Product: aspartate kinase alpha chain #status predicted <ASA>F;3-466/Domain: aspartate kinase homology <a href="https://domain.aspartate">https://domain.aspartate</a> kinase homology <a href="https://domain.aspartate">https://domain.aspartate</a> kinase homology <a href="https://domain.aspartate">https://domain.aspartate</a> kinase beta chain #status predicted <ASA>F;250-421/Product: aspartate kinase beta chain #status predicted <ASB>
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Roman, S.; Yuan, Y.; Brady, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J., Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A; Tritle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Reference number: A82950; MUID:20437337; PMID:10984043
A; References: CB3531
A; Status: preliminary
A; Residues: 1-412 <STO>
A; Cross-references: GB:AE004525; GB:AE004091; NID:g9946805; PIDN:AAG04293.1; GSPDB:GN001: C; Genetics:
A; Experimental source: strain PA01
C; Genetics:
A; Gene: 1ysC; PA0904
C; Superfamily: aspartate kinase; aspartate kinase homology
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      VDEGNVAIVAGFQGVSQDSKDITTLGRGGSDTTAVALAAALDADVCEIYTDVDGVFTADP 184
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                                                                                                                                                                                             241 -IK--DVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRR-----RQHRH
                                                                     RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                        292 GAAERLOGRGRODRHHIHILPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37:5%; Score 823; DB 2; Length 41 Best Local Similarity 42.6%; Pred. No. 1.6e-53; Matches 170; Conservative 80; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGKVSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                            352 RSHPGVTATFCEALAAVGVNIELISTSE 379
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Typesies: Streptomyces coelicolor
C; Species: Streptomyces coelicolor
C; Species: Streptomyces coelicolor
C; Species: Streptomyces coelicolor
C; Species: Streptomyces coelicolor
C; Accession: Typesias
R; Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
R; Murphy, L.; Harris, Data Library, June 1999
A; Reference number: Z21576
A; Accession: T35383
A; Streterence number: Z21576
A; Accession: T35383
A; Streterence number: DNA
A; Residues: L-425 aNUR.>
A; Residues: 1-425 aNUR.>
A; Cross-references: EMBL; AL079348; PIDN: CAB45482.1; GSPDB:GN00070; SCOEDB:SC66T3.26c
C; Genetics:
A; Genetics:
A; Gene: ask; SCOEDB:SC66T3.26c
C; Superfamily: aspartate kinase; aspartate kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTFGRLQTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA------RRRRQHR 290
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                                                                                                                                                                                                                                                                                                                                                                                             5 VQKYGGSSLESAERIRNVAERIVATKKAGNDVVVVVSAMGDTTDELLELAAAVNPVPPAR
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                                                                                                                                                                                                                           Length 421;
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Best Local Similarity 61.6%; Pred. No. 3.9e-77;
Matches. 239; Conservative 54; Mismatches 79; Indels 16
                                                                                                                                                                                                                                                                                      58; Indels
C,Genetics:
A;Gene: lysC-alpha
A;Start codon: GTG
C;Superfamily: aspartate kinase, aspartate kinase homology
C;Keywords: alternative initiators; phosphotransferase
F;3-406/Domain: aspartate kinase homology <DKI>
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                                                                                                                                                                                                                       Query Match
56.1%; Score 1229.5; DE
Best Local Similarity 64.3%; Pred. No. 1e-83;
Matches 252; Conservative 55; Mismatches 5
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                                                                                                                                           C;Species: Synechocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C;Accession: 876764

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

R;Koneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

D; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                   179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 P----PVQNRSLVGLEIAKAVDGVEYDADQAKVALLRVPDRPGVASKLFRDIAQQQVDID 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 LIIQSIHDGNSNDIAFTVVKDLLNTAEAVTSAIAPALRSYPEADGEA---EIIVEKGIAK 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344 VSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSE-----DQR--SRCCAATFN 391
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                                                                                                                                                                                                                                                                                                                                                                      VQKYGGSSVADAERIRRVAERIVATKKOGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
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                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                               Length 600;
                                                                                                                                                                                                                                                                                                                                          Indels
               (strain PCC 6803)
                                                                                                                                                                                                                                                                                                            Score 816.5; DB 2;
Pred. No. 7.6e-53;
83; Mismatches 118;
                 Synechocystis sp.
                                                                                                                                                                                                                                                                                                            37.2%;
                                                                                                                                                                                                                                                                                                                          Best Local Similarity 43.9
Matches 183; Conservative
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hypothetical
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A Note: this material was purified beta chain; the beta chain apparantly was not blocked of Comment: The amino terminal Met of the beta chain is preceded by a strongly predicted of comment: The amino terminal Met of the beta chain is preceded by a strongly predicted; comments of a second of the alpha chain region. This suggests that express constructs.

A Start codon: GTG

C, Superfamily: aspartate kinase, aspartate kinase homology

C, Keywords: alternative initiators; heterotetramer; lysine biosynthesis; phosphotransfers F; 2-245, Product: aspartackinase II alpha chain #status predicted <ALH>
F; 2-46-411/Product: aspartate homology <ALKIN
F; 2-46-411/Product: aspartokinase II beta chain #status predicted <BET>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVVGS
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sequence modified after extraction from NCBI backbone sequence extracted from NCBI backbone (NCBIN:117802)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----HIGKVSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.8%; Score 785; DB 2;
42.1%; Pred. No. 1e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81; Mismatches
                                                                                                                                              purified alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 42.19
Matches 170; Conservative
                                                  A,Accession: B48946
A,Molecule type: protein
A,Residues: 2-9 -SC2>
A,Note: this material was pu
A,Accession: C48946
A,Molecule type: protein
A,Residues: 246-253 -SC3>
A,Note: this material was pu
C,Comment: The amino termina
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aspartate kinase (EC 2.7.2.4) II - Bacillus stearothermophilus
M.Alternate names: aspartickinase II
C;Alternate names: aspartickinase II
C;Species: Bacillus stearothermophilus
C;Date: 10-May-1996 #sequence\_revision 19-Jul-1996 #text\_change 18-Jun-1999
C;Accession: UG440
C;Accession: UG440
C;Accession: UG440
C;Accession: UG440
A;Title: Sequence of the Bacillus stearothermophilus gene encoding aspartokinase
A;Title: Sequence of the Bacillus stearothermophilus gene encoding aspartokinase
A;Accession: UG4640

Ξ

A;Molecule type: DNA
A;Residues: 1-407 <CAN>
A;Residues: 1-407 <CAN>
A;Cross-references: GB:L46351; NID:g928810; PIDN:AAB06216.1; PID:g928811
C;Comment: This enzyme is the first key enzyme in the biosynthetic pathway of the aspart: C;Genetics:
A;Gene: ask

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Applicate kinase (EC 2.7.2.4) II precursor - Bacillus sp. (strain MGA3)
NyAlternate names: lysine-sensitive aspartckinase II
NyAlternate names: lysine-sensitive aspartckinase II
NyChternates: aspartckinase II alpha chain; aspartckinase II beta chain
CySpecies: Bacillus sp.
CyDate: 21-Jan-1994 #sequence revision 24-Feb-1995 #text\_change 18-Jun-1999
CyDate: 21-Jan-1994 #sequence revision 24-Feb-1995 #text\_change 18-Jun-1999
CyDate: 21-Jan-1994 #sequence revision 24-Feb-1995 #text\_change 18-Jun-1999
CyCacession: A48946 #38946 #38946 #38946 #38946 #38946 #38946 #38946 #389486 #389486 #389486 #389486 #389486 #389486 #389486 #389486 #3899899 #399

A,Gene: ask C,Superfamily: aspartate kinase; aspartate kinase homology C,Reywords: aspartic proteinase; phosphotransferase ഗ

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Aspectate kinase (EC 2.7.2.4) NMA1701 [imported] - Neisseria meningitidis (strain 22491 s aspartate kinase (EC 2.7.2.4) NMA1701 [imported] - Neisseria meningitidis
C;Species: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: H8166.
C;Accession: H8166.
A;Parkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A;Pitle: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A;Accession: H81865
A;Actus: preliminary
A;Residues: 1-405 < PAR>
A;Acsidues: 1-405 < PAR>
A;Residues: 1-405 < PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTAGKVVIVAGFQGISSE-GDISTLGRGGSDTSAVALAAALKADECQIYTDVDGVYTTDP 183
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                                                                                                                                                                                                                                                                               304 OSIH-----SHPKSDEAE 349
PRIVPEAQLMGEITCNEMLELASLGAKVLHPRAVEIARNYGMPLVVKSSWTDDPGTWVTT 244
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                                                                                                 ----GSIKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRR-----R
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                                                                                                                                                                                                                                                                                                                                                                                           350 VMVEQNIAKVSIAGAGMIGRPGVAAQMFATLABAGVNIQMISTSE 394
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Best Local Similarity 40.8%; Pred. No. 6.1e-49;
Matches 161; Conservative 82; Mismatches 116; Indels
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C,Superfamily: aspartate kinase
C,Keywords: phosphotransferase
                                                                                                                                                                                                                                    OHRHGAAERLOGRG---
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AE2261
aSpacies: Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. strain PCC 7120
C;Accession: AE2261
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Reference number: AB1807; MUD:21595285; PMID:11759840
A;Accession: AE2261
A;Status: preliminary
A;Residues: 1-606 < kUR>
A;Accession: AE2261
A;Status: preliminary
A;Residues: 1-606 < kUR>
A;Cross-references: GB:BA000019; PIDN:BAB75343.1; PID:g17132777; GSPDB:GN00179
A;Genetics: A;Genetics: Strain PCC 7120
C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Gen
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EMDMLLSTGEQVSIALLAMSLHEKGYKAVSLTGWQAGITTBEMHGNARIMNIDTTRIRRC 124
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                                                                                Length 407;
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                                                                             ; Score 778; DB 2;
; Pred. No. 3.4e-50;
77; Mismatches 98;
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                F;3-397/Domain: aspartate kinase homology <DKI>
                                                                         35.5%;
ilarity 43.2%;
Conservative 7
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Best Local Similarity
Matches 173; Conserv
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aspartokinase, alpha and beta chains NWB1498 [imported] - Neisseria meningitidis (strain cispecies: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Accession: R81076
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B, strain MC59
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A;Cross-references: GB.AP001517; GB:BA000004; NID:g10175500; PIDN:BAB06815.1; GSPDB:GN0d
A;Experimental source: strain C-125
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.7%; Score 760; DB 2; Length 405; 40.8%; Pred. No. 7.3e-49; tive 81; Mismatches 117; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-405 <TET>
A;Cross-references: GB:AE002499; GB:AE002098; NID:g7226737, A;Experimental source: serogroup B, strain MC58 C;Genetics: A;Gene: NMB1498 C;Superfamily: aspartate kinase; aspartate kinase homology
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C;Superfamily: aspartate kinase; aspartate kinase homology
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A;Residues: 1-400 <PAR>
A;Residues: 1-400 <PAR>
A;Cross-references: GB:AL139075; GB:AL111168; NID:g6967817; PIDN:CAB75218.1; PID:g6968045
A;Experimental source: serotype O2, strain NCTC 11168
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                                                                                                                                                                                       EMDMLLATGEQVTIALLAMALHKRGQEATSLTGWQAGMITESHHGNARILEVERARMDEL 124
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                                                                                                                                                                                                                               121 LEEGRYVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
                                                                                                                                                                                                                                                          RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                  241 IKDVPMEDPILT-GVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAERLQG
                                                                          1 VOKYGGSSVADAERIRRVAERIVATKKOGNDVVVVVSAMGDITDDLLDLAQQVCPAPPR
                                                                                                             VQKYGGTSVGSVQRIEHVANRIIATAASGKKVVVVVSAMGKTTDELVGLASEITDEPRKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---QT-SGPPPWKNWTRSETRSASTQLL---
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DMDMLLSSGERVTSALLSIALNEKGCPAISFSGRKAGIITDSVFTKARIHHIDTKAIKSE
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                                     73;
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C;Superfamily: aspartate kinase; aspartate kinase homology
34.5%; Score 757.5; DB 2;
42.0%; Pred. No. 1.1e-48;
ive 64; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.9%; Score 742.5; DB 2;
39.9%; Pred. No. 1.4e-47;
ive 89; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                             - BEGTMEONLLVRGIAFENDVTKVTVHGLP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 RGRODRHHLHLLP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 39.9
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181 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 240

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aspartokinase - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 18-Jun-1999
C;Accession: B70399
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: GB.AE000726; NID:g2983612; PIDN:AAC07182.1, PID:g2983613, GB.AE00066
A,Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: B70399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAERLQGR 300
                                                                                                                                                                ----TRSETRSASTQLLYDDHIGKVSL 346
                                                                                                                                                                                          --NENINVDMIIQNVGVDGATNLGFTVPQNELELAKNAMQKILSSKTTIESDSAVLKVSI 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:|| || |: : || || : || 65 EMDTLLAVGEQKAIALFANTLNKLGYPAVSLCGWQVPIITDNVHTKARIRKIGISRLLSL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 -EDEVMEKVAVRGITVDTKETRFTVVRVPDKPGIAAEIFKAL------GDAHIVVDM 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --ERLÖGRGRQDRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAGMR 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Status: preliminary; nucleic acid sequence not shown; translation not shown A,Molecule type: DNA
A,Residues: 1-415 <AQF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 33.5%; Score 734.5; DB 2; Length 9 Best Local Similarity 42.4%; Pred. No. 5.9e-47; Matches 164; Conservative 76; Mismatches 124; Indels
                                                                                                 241 -KEDGMEQALVSGIALDKNQARVTLRNIEDKPGIAAEIFSVLA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: lysC
C;Superfamily: aspartate kinase; aspartate kinase homology
F;3-400/Domain: aspartate kinase homology <DKI>
                                                                                                                                                                                                                                                       347 IGAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                    341 VGVGMKSHSGVASKAFKALADEGINIGMISTSE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHPGVTATFCEALAAVGVNIELISTSE 379
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2193
1 VQKYGGSSVADAERIRRVAE......SAATRRPRCTRGRDGRWACQ 424
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GenCore version 5.1.6
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Q911a3 streptomyce	Q8rt65 bartonella	Q58656 methanococc	Q8r6g5 fusobacteri	P59295 bifidobacte	Q8ufml agrobacteri					P94989 mycobacteri	P59008 xanthomonas
ARGB_STRCO	PYRH_BARBA	PYRH METUA	PYRH FUSNN	ARGB_BIFLO	PYRH_AGRT5	PYRH ANASP	PYRH ZYMMO	ARGB_STRCL	PYRH XANCP	ARGB MYCTU	PYRH_XANAC
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306	239	226	239	318	241	242	242	302	240	294	240
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75	174.5	151	150	149	146	145.5	145.5	145	143.5	143	141.5
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## ALIGNMENTS

AK_MYCTU ID_AK	MYCTU S
AC DT	P97048; O69676; P97181; 30-MAY-2000 (Rel. 39, Created)
E E	0-MAY-2000 (Rel. 39, Last
E	se (EC 2.7, 2.4) (Aspartate kinase)
e e	Aspartokinase beta subunit R MTV025.057C.
So	400000000000000000000000000000000000000
20	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
XO N	NCBI_TaxID=1773;
Z.	SEQUENCE FROM N.A.
RC S	STRAIN=H37Rv;
R F	Gilker J.M., Jucker M.I.; "Mycobacterium tuberculosis ask-alpha, ask-beta and asd genes.";
RI.	EMBL/GenBank/DDBJ databases.
RN C	[2]
κ r r	SEÇCENCE FROM N.A.
Z X	MEDLINE=98295987; PubMed=9634230;
RA	Brosch R., Parkhill J., Garnier T., Chur
ξ.	, Eiglmeier K., Gas S., Barry C.E. III, Tekaia
χ ρ ξ α	Badcock K., Basham D., Brown D., Chillingworth I., Comfor K., Davies P. Devlin K. Beltwell T. Gentles S. Hamlin N. Holroyd S.
5 Z	I., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA	
Z.	Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
\$ £	Sulfacion (J.E., Idylor K., Millemed S., Battell B.G., "Desimbering the biology of Mycoberterium fulberoulogia from the
Z E	une biology of mycobacceilum cuberculosis from
RL	93:537-544 (1998
Z c	[3]
ቷ p	SEGUDING FICE N.A.
A A	J.A., Carpenter L., White C
RA	Gwinn M.L., Haft D., Hickey E.,
R G	M.D.,
¥ 6	U., MICULI H., GILL U., MINUIA
2 2	"Whole genome comparison of Mycobacterium tuberculosis clinical and
RT	cory strains.";
Z.	Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
ع د	- CAIABILL ACLIVILL ALF + B-ASPALCACE - ABF +
88	-!- ENZYME REGULATION: FEEDBACK INHIBITION BY LYSINE AND THREONINE (BY
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ဗဗ	-!- PATHWAY: FIRST STEP IN THE COMMON BIOSINTHETIC PATHWAY LEADING FROM ASP TO THE CELL WALL PRECURSOR MESO-DIAMINOPIMELATE, TO LYS,
ដូ	TO ILE AND TO THR.
ខ្លួ	-!- SUBUNIT: Tetramer consisting of 2 isoforms Alpha (catalytic) and 2 isoforms beta (function not thoum) (by similarity)
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356 SHPGVTATFCEALAAVGVNIELISTSEIRISVLCRDT 392

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Matches 302; Conservative
                                                                                                                         InterPro; IPPCO; IPPCO
InterPro; IPPCO; IPPCO; IPPCO; IPPCO; IPPCO; IPPCO; IPPCOOSE6,

InterPro; IPPCOOSE6,

InterPro; IPPCOOSE6, askinase; 1.

DR Pfam; PFOOSE6; asp_kinases; 1.

DR TIGRFAMS; TIGROOGE5; asp_kinases; 1.

DR TIGRFAMS; TIGROOGE5; asp_kinases; 1.

KW Transferase; Kinase; Diaminopimelate biosynthesis; KW Lysine biosynthesis; Alternative initiation; Complete proteome.

FT CHAIN 1250 421 ASPARTOKINASE, ISOFORM BETA.

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FT TINIT WET 250 421 ASPARTOKINASE, IN REF
                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEEGRIVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 IKDVPMEDPILITGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAE,---- 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 RLQGRGRQDRHHLHLLLPQTS---GPPPWKWWTRSETRSASTQLLYDDHIGKVSLIGAGMR 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 VLÓNVSKVEDGKTDITFTCSRDVGPAAVEKLDSLRNEIGFSQLLYDDHIGKVSLIGAGMR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCELYTDVDGIFSADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIVENARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIVRNARKLDTVIFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                     Comment=2 isoforms, Alpha/Aspartokinase alpha subunit (shown here) and Beta/Aspartokinase beta subunit, may be produced by
                                                         alternative initiation; SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      353 SHPGVTATFCEALAAVGVNIELISTSEDQRSRCCAAT 389
                                                                                                                                                                                                                                                                                                                                                                                             Tuberculist; Rv3709c; -.
Tuberculist; Rv3709c; -.
InterPro; IPR001048; Aa kinase.
InterPro; IPR002912; ACT.
InterPro; IPR003260; Asp kin monofn.
InterPro; IPR001341; Aspartate_kinase.
  Event=Alternative initiation;
                                                                                                                                                                                                                                                                                                                      EMBL; AL022121; CAA18031.1; -. EMBL; AE007178; AAK48180.1; -. PIR; F70794; F70794.
                                                                                                                                                                                                                                                                              EMBL; U90239; AAB49995.1; -. EMBL; U90239; AAB49994.1; -.
                                                                                                                                                                                                                                                                                                                                                                              TIGR; MT3812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185
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                                                                                                                                                                                                                                  [Contains: Aspartokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- ENZYME REGULATION: FEEDBACK INHIBITION BY LYSINE AND THREONINE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PATHWAY: FIRST STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING FROM ASP TO THE CELL WALL PRECURSOR MESO-DIAMINOPIMELATE, TO LYS, TO MET, TO ILE AND TO THR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO MET, TO ILE AND TO THR.
--- SUBUMT: Tetramer consisting of 2 isoforms Alpha (catalytic) and isoforms Beta (function not known) (By similarity).
--- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative initiation;
Comment=2 isoforms, Alpha/Aspartokinase alpha subunit (shown
here) and Beta/Aspartokinase beta subunit, may be produced by
alternative initiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Citillo J.D., Weisbrod T.R., Pascopella L., Bloom B.R., Jacobs W.R. Jr., "Isolation and characterization of the aspartokinase and aspartate
                                                                                                                                                               01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Aspartokinase (EC 272.4) (Aspartatk kinase) [Contains: Asparto)
alpha subunit (ASK-alpha); Aspartokinase beta subunit (ASK-beta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   semialdehyde dehydrogenase operon from mycobacteria.";
Mol. Microbiol. 11:629-639(1994).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.4%; Score 1478.5; DB 1; Length 421; 77.6%; Pred. No. 1.2e-96; ative 31; Mismatches 35; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase; Kinase; Diaminopimelate biosynthesis;
Lysine biosynthesis; Alternative initiation.
CHAIN 421 ASPRIOKINASE, ISOFORM ALPHA.
CHAIN 250 421 ASPARTOKINASE, ISOFORM BETA.
INIT MET 250 250
SEQUENCE 421 AA, 44458 MW; 926B9FC8625E20CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                   421 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, 217372; CAA78984.1; --
EMBL, 217372; CAA78985.1; ALT_INIT.
EMBL, 24722; GA422.
Inte.Pro; IPR001048; Aa kinase.
InterPro; IPR002912; ACT.
InterPro; IPR0012912; ACT.
InterPro; IPR001341; Aspartate_kinase.
Pfam; PF00896; aakinase; 1.
Pfam; PF01842; ACT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMS; TIGRO0656; asp kin monofn; 1.
TIGRFAMS; TIGRO0657; asp kinases; 1.
PROSITE; PS00324; ASPARTOKINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
15-SEP-2003 (Rel. 42, Last ann
                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                     Mycobacterium smegmatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=ATCC 607 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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SEQUENCE
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the European Bioinformatics Institute. There are no restrictions on its
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most fied and this statement is not removed. Usage by and for commercial
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or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERLOGRGRODRHHLHLLPQTSGPPPWKWWTRSETRSASTQLLYDDHIGKVSLIGAGMRSH 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRR-----RQHRHGAA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AK_CORGL STANDARD; PRT; 421 AA.
P25512; Q59286;
01-AUG-1992 (Rel. 23, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Aspartokinase (EC 2.7.2.4) (Aspartate kinase) (Contains: Aspartokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ELDMLLTAGERISNALVAMAIESLGAHARSFIGSQAGVITTGIHGNAKIIDVTPGRLQTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCELYTDVDGIFSADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 VOKYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLDLAAAVNPVPPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferace; Kinase; Diaminopimelate biosynthesis;
Lysine biosynthesis; Alternative initiation; Complete proteome.
CHAIN ASPRATOKINASE; ISOFORM ALPHA.
CHAIN ASPARTOKINASE; ISOFORM BETA.
INIT MET 250 250 FOR ISOFORM BETA.
SEQUENCE 421 AA; 44793 MW; FOD638306983CB5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBL_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.9%; Score 1248.5; DB 1; Length
65.2%; Pred. No. 1.7e-80;
iive 58; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha subunit; Aspartokinase beta subuniti
LYSC OR CGL0251.
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR005260; Asp kin monofn.
InterPro; IPR001341; Aspartate_kinase.
Pram; PP00696; aakinase; 1.
Pfam; PP01842; ACT; 2.
TIGRFAMS; TIGR00656; asp kin monofn; IIGRFAMS; TIGR00657; asp_kinases; 1.
PROSITE; PS03324; ASPARTOKINASE; 1.
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                                                                                                                                                                                                                                   EMBL; AB063129; BAB88820.1; -
EMBL; AP062214; BAC17030.1; ALT_INIT.
InterPro; IPR001048; As Kinase.
InterPro; IPR002912; ACT.
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BYZYME REGULATION: FEEDBACK INHIBITION BY LYSINE AND THREONINE.

PATHWAY: FIRST SIEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING
FROM ASP TO THE CELL WALL PRECURSOR MESO-DIAMINOPIMELATE, TO LYS,
TO MET, TO ILE AND TO THR.

TO MET, TO LIE AND TO THR.

SUBDINIT: Tetramer consisting of 2 isoforms Alpha (catalytic) and
isoforms Beta (function not known).

ALTERNATIVE PRODUCTS:

EVENT. STATE ALLERNATIVE PRODUCTS:
                                                                        VOKYGGSSVADAERIRRVAERIVETKKAGNDVVVVVSAMGDTTDDLLDLARQVSPAPPPR
                                                                                                                                                ELDMLLTAGERISNALVAMAIESLGAHARSFIGSQAGVITTGTHGNAKIIDVTPGRLQTA
                        VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
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SIRALN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
Tkeo K., Suzuki M., Mshima J., Itoh T., Yamagishi A., Nishio Y.,
Usuda Y., Sugimoto S.;
The entire genomic sequence of Corynebacterium efficiens YS-314.";
The entire Genomic sequence of Corynebacterium efficiens YS-314.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
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Itaya H., Kimura E., Kawahara Y., Sugimoto S.;
"JysC of Corynebacterium efficiens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Aspartokinase (EC 2.7.2.4) (Aspartate kinase)
alpha subunit; Aspartokinase beta subunit].
LYSC OR ASK OR CE0220.
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                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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-!- ENZYME REGULATION: FEEDBACK INHIBITION BY LYSINE AND THREONINE.
-!- PATHWAY: FIRST STEP IN ALL COMMON BIOSYNTHETIC PATHWAY LEADING.
FROM ASP TO THE CELL WALL PRECURSOR MESO-DIAMINOPIMELATE, TO LYS,
TO MET, TO ILE AND TO THR.
-!- SUBBUNIT: Terramer consisting of two isoforms Alpha (catalytic) and
two isoforms Beta (function not known).
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SECURNCE OF 158-421 FROW N.A.
STRAIN-ATCC 1303 / DSM 20300 / NCIB 10025;
STRAIN-ATCC 1303 / DsM 20300 / NCIB 10025;
Kalinowski J., Bachmann B., Thierbach G., Puehler A.;
Kalinowski J., Bachmann B., Thierbach G., Puehler A.;
Aspartokinase genes lysc alpha and lysc beta overlap and are
adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in
Corynebacterium glutamicum.";
Mol. Gen. Genet. 224:317-324 (1990).
-! CATALYIIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-51 FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
MEDLINE=94161495; PubMed=8117072;
Patek M., Krumbach K., Eggeling L., Sahm H.;
"Leucine synthesis in Corynabacterium glutamicum: enzyme activities, structure of leuk, and effect of leuk inactivation on lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (shown
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Comment=2 isoforms, Alpha/Aspartokinase alpha subunit (show here) and Beta/Aspartokinase beta subunit, are produced by alternative initiation;
SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
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TIGREAMS; TIGRO0657; asp kinases; 1.

PROSITE; PS00324; ASPARTOKINASE; 1.

Transferase; Kinase; Diaminopimelate biosynthesis;
Lysine biosynthesis; Alternative initiation; Complete proteome. CHAIN

421 ASPARTOKINASE, ISOFORM ALPHA.
SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
MEDLINE=22065816; PubMed=1956296;
Kalinowski J., Cremer J., Bachmann B., Eggeling L., Sahm H.,
                                                                                                                                                                                 the aspartokinase from
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
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InterPro; IPR002912; ACT.
InterPro; IPR005260; Asp kin monofn.
InterPro; IPR001341; Aspartate_kinase.
Pfam; PF00896; aakinase; 1.
                                                                                                                                  Puehler A.; "Genetic and biochemical analysis of "Genetic and biochemical", Corynebacterium glutamicum."; Mol. Microbiol. 5:1197-1204(1991).
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EMBL; X57226; CAA40503.1; -.
EMBL; AR005274; BAB97644.1; -.
EMBL; X70959; CAA50296.1; ALT_SEQ.PIR; S15276; S15276;
                                                                                                                                                                                                                                                                                                                                                                                 Nakaqawa S.;
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                                                                                                                                                                                                                                                      BLDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
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-!- PATHWAY: FIRST STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING FROM ASP TO THE CELL WALL PRECURSOR MESO-DIAMINOPIMELATE, TO LYS, TO NET, TO ILE AND TO THR.
-!- SUBUNIT: Tetramer consisting of 2 isoforms Alpha (catalytic) and isoforms Beta (function not known) (By similarity).
                                                                                                                                                         Gaps
                 250 FOR ISOFORM BETA.
301. S--Y: FEEDBACK-RESISTANT AND ENHANCED EXPRESSION OF THE ASD GENE.
40 C --> V (IN REF. 1 AND 3).
44754 MM, E3684D0681DE0827 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Follettie M.T., Peoples O.P., Agoropoulou C., Sinskey A.J., "Gene structure and expression of the Corynebacterium flavum N13 ask-asd operon.";
                                                                                                                                                     27;
                                                                                                                      DB 1; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 175:4096-4103(1993).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterinea, Corynebacterinea, Corynebacterinea, NCBI_TaxID=28028,
                                                                                                                                                       59; Indels
       ASPARTOKINASE, ISOFORM BETA
                                                                                                                    55.8%; Score 1224.5; DB 364.0%; Pred. No. 8.1e-79; iive 55; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
115-SED-2003 (Rel. 42, Last annotation update)
Aspartokinase (EC 2.7.2.4) (Aspartate kinase)
115-SED subunit; Aspartokinase beta subunit].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
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                                                                                                                                                       Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                    421 AA;
                                                                                                                                       Similarity
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CHAIN
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                                                                    CONFLICT
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P41398;
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STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
STRAIN=20437337; PubMed=10984043;
STRAIN=20437337; PubMed=10984043;
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino B., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folker K.R., Kas A., Larbig K.R., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aspartate.
--- PATHYAY: EIRST STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING FROM ASP TO DIAMINOPIMELATE, TO MET, TO ILE AND TO THR.
---- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 198-412 FROM N.A.
STRAIN=ATCC 15692 / PAO1;
Hindle Z., Throup J.P., Francis K.P., Bycroft B.W., Williams P.,
Stewart G.S.A.B.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
16-OCT-2001 (Rel. 40, Last annotation update)
Aspartokinase (EC 2.7.2.4) (Aspartate kinase)
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                                                                                                                                            Pseudomonadaceae; Pseudomonas
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Best Local Similarity 42.6'
Matches 170; Conservative
                                                                                     Pseudomonas aeruginosa
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SEQUENCE 412 AA; 4
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                                                             OR PA0904.
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                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                              Comment=2 isoforms, Alpha/Aspartokinase alpha subunit (shown here) and Beta/Aspartokinase beta subunit, are produced by alternative initiation;
                                                                                                                    SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
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44388 MW; A06ACAA5E914F337 CRC64;
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InterPro; IPR002912; ACT.
InterPro; IPR002912; ACT.
InterPro; IPR001341; Aspartate_kinase.
Pfam; PF00696; aakinase; 1.
Pfam; PF01842; ACT; 2.
TIGRPAMs; TIGR00656; asp_kin_monofn; 1.
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303
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STRAIN=ATCC 33923 / DSM 674 / AT-62;
MEDLINE=95291465; PubMed=7773416;
Mishiyama M., Kukimoto M., Beppu T., Horiouchi S.;
"An operon encoding aspartokinase and purine phosphoribosyltransferase in Thermus flavus.";
                                                                                                                                                                                                                     244 DEEESMEOPIISGIAFNRDEAKLTIRGVPDTPGVAFKILGPISAANVEVDMIVQNVAHDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- PATHWAY: FIRST STEP IN THE COMMON BIOSYNTHEFIC PATHWAY LEADING FROM ASP TO DIAVINOPIMELATE, TO MET, TO ILE AND TO THR.
-1- SUBUNIT: Tetramer consisting of 2 isoforms Alpha (catalytic) and isoforms Beta (function not known) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kobashi N., Nishiyama M., Tanokura M., Tanokura M., "Aspartate kinase-independent lysine synthesis in an extremely thermophilic bacterium, Thermus thermophilus: lysine is synthesized V. a alpha-aminoadipic acid not via diaminopimelic acid."; J. Bacteriol. 181:1713-1718(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Comment=2 isoforms, Alpha/Aspartokinase alpha subunit (shown here) and Beta/Aspartokinase beta subunit, may be produced by alternative initiation; alternative initiation; SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microbiology 141:12i1-1219(1995).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                      241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 IGKVSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341 IAKVSIVGVGMRSHAGVASRMFEALAKESINIQMISTSE 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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InterPro; IPR001048; Aa\_kinase.

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MEDI-TRE-9907380; PubMed=1444390;
Schendel F.J., Flickinger M.C.;
"Cloning and nucleotide sequence of the gene coding for aspartokinase
II from a thermophilic methylotrophic Bacillus sp.";
Appl. Environ. Microbiol. 58.2806-2814(1992).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 IKDVPME-DPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARR------
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last unotation update)
Aspartokinase 2 (EC 2.7.2.4) (Aspartokinase II) (Aspartate kinase 2)
[Contains: Aspartokinase II alpha subunit; Aspartokinase II beta
R InterPro; IPR002912; ACT.

JR InterPro; IPR005260; Asp kin monofn.

DR Plan; PF00696; aakinase; 1.

DR TIGRPAMS; TIGR00656; asp kin_monofn; 1.

DR TIGRPAMS; TIGR00657; asp kin_monofn; 1.

DR TIGRPAMS; TIGR00657; asp kin_monofn; 1.

DR TIGRPAMS; TIGR00657; asp kin_monofn; 1.

DR TIGRPAMS; TIGR00657; asp kin_monofn; 1.

DR TIGRPAMS; TIGR00657; asp kin_ses; 1.

DR TIGRPAMS; TIGR00657; asp kin_ses; 1.

TATANSTEASE; Kinase; Diaminopimelate biosynthesis; KW Lysine biosynthesis; Alternative intiation.

FT CHAIN 1405 ASPARTOKINASE, ISOFORM BETA.

FT CHAIN 245 ASPARTOKINASE, ISOFORM BETA.

TINIT_MET 245 L45 FOR ISOFORM BETA.

126 126 B -> D (IN STRAIN AT-62).

127 Inength 405;
                                                                                                                                                                                                                                                                                                                                                                                                      58;
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Bacillus sp. (strain MGA3),
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1409;
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                                                                                                                                                                                                                                                                                                                                                              37.3%; Score 819; DB 1;
43.2%; Pred. No. 2.2e-50;
ive 78; Mismatches 94
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-!- ENZYME REGULATION: LYSINE-SENSITIVE.
                                                                                                                                                                                                                                                                                                                                                                                                   Matches 175; Conservative
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Q59229;
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AK2_BACSP
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SEQUENCE FROM N.A.
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                                                                                                                      subunit]
    PPPEEEE SOOS BEEEE FFF SOOS COOLOUS CONTRACTOR SOOS COOLOUS CONTRACTOR SOOS COOLOUS CONTRACTOR SOOS CONTRACTOR SOOS COOLOUS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CONTRACTOR SOOS CO
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                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 240
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---QNRINVDIIIQSA------TDAETTNLSFSIKSDDLEETMAVLENNKNLLNYQGI 333
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                                                                                                                                       Comment=2 isoforms, Alpha/Aspartokinase II alpha subunit (shown bere) and Beta/Aspartokinase II beta subunit, are produced by alternative initiation; simiLaRITY: BELONGS TO THE ASPARTOKINASE FAMILY:
PATHWAY: FIRST STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING FROM ASP TO DIAMINOPIMELATE AND LYS, TO MET, TO ILE AND TO THR. SUBUNIT: Tetramer consisting of 2 isoforms Alpha (catalytic) and isoforms Beta (function not known).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASPARTOKINASE 2, ISOFORM ALPHA. ASPARTOKINASE 2, ISOFORM BETA. FOR ISOFORM RETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.8%; Score 785; DB 1; Length 411; 42.1%; Pred. No. 5.5e-48; tive 81; Mismatches 97; Indels
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InterPro; IPR001048; Aa kinase.
InterPro; IPR002912; ACT.
InterPro; IPR001341; Aspartate kinase.
InterPro; IPR001341; Aspartate kinase.
Pf00896; aakinase; 1.
Pfam; PF008942; ACT; 2.
TIGREAMS; TIGR00656; asp kin monofn; 1.
PROSTITE; PS00324; ASPARTOKINASE; 1.
PROSTITE; PS00324; ASPARTOKINASE; 1.
Iransferase; Kinase; Diaminopimelate biosynthesis; lysine biosynthesis; Alternative initiation.
                                                                                             ALTERNATIVE PRODUCTS:
Event=Alternative initiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411 AA; 44342 MW;
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Best Local Simi:
Matches 170; (
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SEQUENCE
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AK2\_BACST P53553;

AK2\_BACST ID AK2\_B AC P5355 RESULT 9

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EMDMLLSTGEQVSIALLAMSLHEKGYKAVSLTGWQAGITTEEMHGNARIWNIDTTRIRRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VOXYGGSSVADAERIRRVAERIVATKKOGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- ALTERNATIVE PRODUCTS:

Event=Alternative initiation;

Comment=2 isoforms, Alpha/Aspartokinase II alpha subunit (shown here) and Beta-Aspartokinase II beta subunit, may be produced by alternative initiation;

-!- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aspartate.
-!- ENZYME REGULATION: LYSINE-SENSITIVE (BY SIMILARITY).
-!- PATHWAY: FIRST STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING
-!- STEPM ASP TO DIAMINOPIMELATE AND LYS, TO MET, TO ILE AND TO THR.
-!- SUBDNIT: Tetramer consisting of 2 isoforms Alpha (catalytic) ar isoforms Beta (function not known).
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-SBP-2003 (Rel. 42, Last annotation update)
Aspartokinase Z (EC 2-7.2.4) (Aspartokinase II) (Aspartokinase [Contains: Aspartokinase II alpha subunit; Aspartokinase II beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL: L46351; AABO6216.1; -

R InterPro: IPR0010148; Aa kinase.

R InterPro: IPR002912; AZT.

R InterPro: IPR003912; AZT.

R InterPro: IPR003914; Aspartate kinase.

R InterPro: IPR001341; Aspartate kinase.

R InterPro: IPR00596; aakinase; 1.

R IGRPAMS; IGR00656; asp kin monofn; 1.

R IGRPAMS; IGR00656; asp kin monofn; 1.

R TIGRPAMS; IGR00657; asp kinases; 1.

R TIGRPAMS; IGR00657; asp kinases; 1.

R TIGRPAMS; IGR00657; asp kinases; 1.

R TOATTE; PS00324; ASPARTOKINASE; 1.

R TANS Frase; Kinase; Diaminopimelate biosynthesis;

W Transferase; Kinase; Diaminopimelate biosynthesis;

CHAIN 246 407 ASPARTOKINASE 2, ISOFORM ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aspartokinase II.";
Gene 169:135-136(1996).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 407;
                                                                                                                                                                                                                                       Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
NCBI_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cantoni R., Labo M., de Rossi E., Riccardi G., "Sequence of the Bacillus stearothermophilus gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98; Indels
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43.2%; Pred. No. 1.7e-47;
tive 77; Mismatches 98;
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Matches 173; Conservative
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AK HELPJ Q9\overline{Z}JZ7;
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                                                                                                                                                            299
                                                                                                                                                                                                                                                                  339
LDEGAIVIVAGFQGVT-ETGEITTLGRGGSDTTAVALAAALKAEKCDIYTDVTGVFTTDP 183
                                                                                                           241
                                                                                                                                                                                                                                                                                                           287 ----GINVDIIIO-----NATNSETASVSFSIRTEDLPETLOVLOALEGADVHYES 333
                                                                                  241 IKDVPMEDP-ILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAERLQG
                                                                                                                                                                                                                                                          300 RGRQDRHHLHLLPQTSGPPPWKWTRSETRSAS------TQLL----YDD
                                                    RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98196666; PubMed=9537320; Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead W.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: FIRST SIEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING FROM ASP TO DIAMINOPIMELATE, TO MET, TO ILE AND TO THR. -!- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 392:353-358(1998).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
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PER, B70399; B70399; B70399; B70399; B70399; B70399; B70399; B70399; B70399; B70399; B70399; B703902912; Aa kinase.

InterPro; IPR002912; AaCT.
InterPro; IPR002912; AaCT.
Ffam; PF00696; aakinase; Lagran, PF00896; aakinase; Lagran, PF00896; aakinase; Lagran, FF00892; ACT; 2...

TICRFAMS; TIGR00656; asp. kinases; 1...
FFOSTE; PS00324; ASPARTOKINASE; 1...
FFOSTE; PS00324; ASPARTOKINASE; 1...
FFOSTE; PS00324; ASPARTOKINASE; 1...
FFOSTE; PS00324; ASPARTOKINASE; 1...
FFOSTE; PS00324; ASPARTOKINASE; 1...
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FFOSTE; PS00324; ASPARTOKINASE; 1...
FFOSTE; PS00324; ASPARTOKINASE
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Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
                                                                                                                                                                                           340 HIGKVSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                 334 GLAKVSIVGSGMISNPGVAARVFEVLADQGIEIKMVSISE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
2.4) (Aspartate kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Creat 30-MAY-2000 (Rel. 39, Last 16-OCT-2001 (Rel. 40, Last Aspartokinase (EC 2.7.2.4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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067221;
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Gaps

23;

Length 415;

Query Match 33.5%; Score 734.5; DB 1; Length Best Local Similarity 42.4%; Pred. No. 1.9e-44; Matches 164; Conservative 76; Mismatches 124; Indels

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                                                                                                                                                                                                                                                                    240
                                                                                     ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
                                                                                                                                  EMDTLLAVGEQKAIALFAMTLNKLGYPAVSLCGWQVPIITDNVHTKARIRKIGISRLLSL 124
                                                                                                                                                                                                                                                                                                                                                           294
                                                                                                                                                                                                                                                                                                                                                                                                        291
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                                            64
                                                                                                                                                                                                                                                                                                                                                                                          VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
                              121 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
                                                                                                                                                                                                                    125 IEEGYIPVVAGFOGVTEDW-EITTLGRGGSDTTAVALAAALKAD-CEINTDVPGVFTADP
                                                                                                                                                                                                                                                                    RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                           --BRLQGRGRQDRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAGMR
                                                                                                                                                                                                                                                                                                                                                           241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-99120557; PibMed-9921882;
ALD LING B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Tibbson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
Trust T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
LYSC OR JHP1150.
LYSC OR JHP1150
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PATHWAY: FIRST STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING FROM ASP TO DIAMINOPIMELATE, TO MET, TO ILE AND TO THR. -!- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 405 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350 SAYGVAGRMFDILARNGINIKAISTSE 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 SHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
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PIR, H71843, H71843.
INTERPRO; IPR001048, Aa kinase.
InterPro; IPR002912, AGT.
InterPro; IPR005260; ASP_kin_monofn.
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Microbiology 142:3067-3078(1996).
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Sanders J., Emmerson P.T., Harwood C.R.;
"The dnaB-phah (256 degrees-240 degrees) region of the Bacillus
subtilis chromosome containing genes responsible for strees responses,
the utilization of plant cell walls and primary metabolism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SIKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRQHRHGAABRLQ
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                                                                                                                                                                                                                                                                       Gaps
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Chen N.-Y., Hu F.M., Paulus H.;
"Nucleotide sequence of the overlapping genes for the subunits of
Bacillus subtilis aspartokinase II and their control regions.";
J. Biol. Chem. 262:8787-8798(1987).
                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                            Length 405;
                                                                                                                                                                                                                     32.9%; Score 721; DB 1; Length 405, 41.4%; Pred. No. 1.7e-43; ive 84; Mismatches 120; Indels
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                                                                                                                                                           Lysine biosynthesis, Complete proteome.
SEQUENCE 405 AA, 44219 MW; E43AOD62E890A8EF CRC64;
                         Pfam; PF00696; aakinase; 1.
Pfam; PF01842; ACT; 2.
TIGRFAMS; TIGR00657; asp kin monofn; 1.
TIGRPAMS; TIGR00657; asp kinases; 1.
PROSITE, PS00324; ASPARTÖKINASE; 1.
Transferase; Kinase; Diaminopimelate biosynthesis;
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       InterPro; IPR001341; Aspartate_kinase.
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nes 161; Conservative
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                                                                                                         MEDLINE-98044033; PubMed=9384377;

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Raderothi M., Tamakoshi A., Tanaka T., Targerra P., Tognoni A.,

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Radelis R., Yashikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

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Comment=2 isoforms, Alpha/Aspartokinase II alpha subunit (shown here) and Beta/Aspartokinase II beta subunit, are produced by alternative initiation;
-:- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aspartate.
-!- BNZYME REGULATION: LYSINE-SENSITIVE.
-!- PATHWAY: FIRST STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING
FROM ASP TO DIAMYNOPPHRELATE AND LYS, TO MET, TO ILE AND TO THR.
-!- SUBUNIT: Tetramer consisting of 2 isoforms Alpha (catalytic) and isoforms Bete (function not known).
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-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
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Chen N.-Y., Paulus H.;
"Mechanism of expression of the overlapping genes of Bacillus
                                                                                         MEDLINE=98044033; PubMed=9384377;
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SubtiList; BG10350; lysC.
InterPro; IPR001048; Aa kinase.
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SEQUENCE FROM N.A.
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Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.
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004795; 031759;
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Pfam; PF01842; ACT; 2.
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TIGR; HP1229;
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Cotton M.D., Weidman J.M., Fujil C., Bowman C., Watthey L., Wallin E.,
                                                                                                                                                                                                                                                                                            1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
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                                                                                                                                                                                                                                                   39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
          InterPro; IRRO0266; Asp kin monofn.
InterPro; IRRO0266; Asp kin monofn.
InterPro; IRRO0341; Aspartate_kinase.
Pfam; PF01695; aakinase; 1.
TIGRPAMS; TIGR00656; asp_kinases; 1.
TIGRPAMS; TIGR00657; asp_kinases; 1.
TROOSTED; PS00324; ASPARTOKINASE; 1.
Transferase; Kinase; DiaminopimeLate biosynthesis;
Chain aspartokinase; JaminopimeLate biosynthesis;
CHAIN 246 ASPARTOKINASE 2, ISOFORM BETA.
CHAIN 246 ASPARTOKINASE 2, ISOFORM BETA.
INIT MET 246 FOR ISOFORM BETA.
                                                                                                                                                                                                                      ; Score 712.5; DB 1; Length
; Pred. No. 6.6e-43;
82; Mismatches 116; Indels
                                                                                                                                                                               166 V -> A (IN REF. 2).
43836 MW; BE718FCDAAB05B96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGRQDRHHLHLLPQTSGPP----PWKNWTRSETRSASTQLLYDD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |::|:||| | 342 SIVGSGMVSNPGVAAEMFAVLAQKNILLIKAVSTSE 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLIGAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Aspartoxinase (EC 2.7.2.4) (Aspartate kinase)
LYSC OR HP1229.
                                                                                                                                                                                                                    32.5%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1] SEQUENCE FROM N.A.
STRAIN=26695 / ATCC 700392;
                                                                                                                                                                                                                                                  Matches 158; Conservative
InterPro; IPR002912; ACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                   246
246
246
166
198 AA;
                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=210;
                                                                                                                                                              INIT MET
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            65
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                                                                                                                                                                                                                                                                                                                                                                                      121
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                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
AK HELLY
AK HELLY
AC 202582
DT 30-MA
DT 30-MA
DT 16-OC
DE LASPAT
GN Helic
OC Helic
OC Helic
OC Helic
OC Helic
OC Helic
COX NCBI
RN NCBI
RN SEQUE
RR SEQUE
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RR SEQUE
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RR SEQUE
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RR SEGUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |-| ::: || :|: || :| | :| | | | | :| :| || EMDRIVSVGELVSSAALSWALERYGHRAISLSGKEAGILTSSHFQNAVIQSIDTKRITEL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 KDFKGERMETPIVSGIALDKNQARVSMEGVEDRPGIAAEIFGALA----EYRINVDMIVQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 TIGRDGKTDLDFTIVKTQ-----IESTKQALKPFLAQMDSIDYDENIAKVSIVGVG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 -SIKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAERLQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VOXYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 GRGRQDRHHLHL-LPQTSGPPPWKNWTRSETRSASTQLL-----YDDHIGKVSLIGAG
                                                                                                                                                                                      COMMON BIOSYNTHETIC PATHWAY LEADING
complete genome sequence of the gastric pathogen Helicobacter
                                      pylori.";
Nature 388:539-547(1997).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                               -!- PATHWAY: FIRST STEP IN THE COMMON BIOSYNTHETIC PATHWAY FROM ASP TO DIAMINOPIMELATE, TO MET, TO ILE AND TO THR. -!- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 405;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lysine biosynthesis; Complete proteome. SEQUENCE 405 AA; 44133 MW; 74723D671FF49395 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase, Kinase, Diaminopimelate biosynthesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.4%; Score 711; DB 1; L. 40.6%; Pred. No. 8.4e-43; iive 85; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 MRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 MKSHSGVASIAFKALAKDNINIMMISTSE 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMS; TIGRO0656; asp_kin_monofn; 1.
TIGRFAMS; TIGRO0657; asp_kinases; 1.
PROSITE; PS00324; ASPARTÖXINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001048; Aa kinase.
InterPro; IPR002912; ACT.
InterPro; IPR005260; Asp_kin_monofn.
InterPro; IPR001341; Aspartate_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000628; AAD08274.1; -. PIR; E64673; E64673.
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404 AA

PRT;

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Subtilist; BG10784; dapG.
InterPro; IPR01048; Aa kinase.
InterPro; IPR005260; Asp kin monofn.
InterPro; IPR001341; Aspatrate_kinase.
Pfam; PF00696; aakinase; 1.
TIGRPAMS; TIGR00656; asp kin monofn; 1.
PROSITE: PS00324; ASPATTOKNASE; 1.
PROSITE: PS00324; ASPATTOKNASE; 1.
Transferase; Kinase; Diaminopimelate biosynthesis;
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               엄
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDINE-Seguates N. S. Pubmac-21843/7;

Kunst R., Ogasawara N. Moszar I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Barsiser L., Brans A., Braun M., Brigals S.C., Bron S.,
Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Brouillet S., Brischi C.V., Caldwell B., Capuano V., Daniel R.A.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Brian S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Brian S.Y., Claser P., Offeteu A., Gollghtly B.J., Grands G.,
Britz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
R.A Entis C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
R.A Hilbert H., Holsapel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Hilbert H., Holsapel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
A Cobayashi Y., Koetter P., Koffeau A., Gallend M., Kroph S., Kumano M.,
Kobayashi Y., Levine A., Liu H., Masuda S., Mauel C., Medgue C.,
R. Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Kumano M.,
R. Noone D., O'Reilly M., Cgawa K., Ogiwara A., Oudega B., Park S.H.,
R. Prescan E., Pujic P., Purnelle B., Ropeport G., Redgue F.,
A Reger M., Rivolta C., Roche B., Rose M., Sadaie Y.,
A Reger M., Rivolta C., Roche B., Rose M., Sadaie Y.,
A Scallan B., Schleich S., Schroeter R., Scoffone F.,
A Schleich J., Serror P., Shin B.S.,
A Toscohi A., Tanaka T., Tarakanshi H., Takemaru K.,
A Takeuchi M., Tamakoshi A., Tanaka T., Tarkensger T.,
A Takeuchi M., Tamakoshi A., Tanaka T., Tarkensger T.,
A Takeuchi M., Tamakoshi A., Tanaka T., Takensger T.,
A Takeuchi M., Tamakoshi A., Tanaka T., Takensen P., Wassarotti A.,
A Vaari A., Wambut R., Wadler B., Wedler H., Wansance Y., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto K.,
A Wani R., Walla K., Yoshikawa H.F., Soroti K., Yoshikaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- BNZYME REGGLATION: DIAMINOPIMELATE-SENSITIVE.
-!- PATHWAY: FIRST STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING FROM ASP TO DIAMINOPIMELATE AND LYS, TO MET, TO ILE AND TO THR.
-!- SUBUNIT: TETRAMER CONSISTING OF TWO ALPHA (CATALYTIC) AND TWO BETA (FUNCTION NOT KNOWN) CHAINS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
                                                  28-FEB-2003 (Rel. 41, Last annotation update)
Aspartokinase 1 (EC 2.7.2.4) (Aspartokinase I) (Aspartate kinase 1)
[Contains: Aspartokinase I alpha subunit; Aspartokinase I beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93252813; PubMed=8098035; Chen N.-Y., Jiang S.-Q., Klein D.A., Paulus H.; Chen N.-Y., Jiang S.-Q., Klein D.A., Paulus H.; Chen and nucleotide sequence of the Bacillus subtilis diaminopimelate operon, a cluster of genes encoding the first threenzymes of diaminopimelate synthesis and dipicolinate synthase."; J. Blol. Chem. 268:9448-9465(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                                                                          Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus, NCBI_TaxID=1423;
               30-MAY-2000 (Rel. 39, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, L08471; AAA22384.1; -. EMBL, Z99112; CAB13549.1; -. PIR, C46665; C46665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                     65 AISPREQDLILSCGETISSVVFTSMLDNGVKAAALTGAQAGFLTNDQHTNAKIIBMKPE 124
                                                                                                                                                                                                                     1 VOKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGD-----TTDDLLDLAQQVCP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 VV------VGSIKDVPMEDPILIGVAH--DRSEAKVTI-VGLPDIPGYAAKVFRAVARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=JALI / DSM 2661 / ATCC 43067;
STRAIN=JALI / DSM 2661 / ATCC 43067;
BULC C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Bake O.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.L.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidem J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSADPRIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 MTADPRVVENAKPLPVVTYTEICNLAYQGAKVISPRAVEIAMQAKVPIRVRSTYSNDKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286 RRQHRHGAAERLQGRGRQDRHHLHLLPQTSGPPPWKNWTRSE-----TRSASTQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -------NAGISVDFFNITPSEIVYTVAGNKTETAQRILM
                                                                                                                                                                                                                                          5 VQKFGGTSVKDDKGRKLALGHIKEAISEGYKVVVVVSAMGRKGDPYATDSLLGLLYGDQS
                                                                                                                                                                                                                                                                                                                                                                                  116 RLQTALEEGRVVLVAGFOGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGI
                                                                                                                                                                                 Gaps
                                                                                                                                                                               68;
                                                                                                                                       24.3%; Score 532; DB 1; Length 404; 36.5%; Pred. No. 3e-30;
Complete proteome.
04 ASPARTOKINASE I ALPHA SUBUNIT.
04 ASPARTOKINASE I BETA SUBUNIT
                                                                                                                                                                               62; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable aspartokinase (EC 2.7.2.4) (Aspartate kinase)
                                                                              -> V (IN REF. 1).
49A6DA70D70047C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---YDDHI----GKVSLIGAGMRSHPGVTATFCEALA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DMGYDPWVTRNCAKVSAVGAGIMGVPGVTSKIVSALS 364
                                                           (BY SIMILARITY)
                                                                                  ы
                                                                                                   42978 MW;
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                            404
                       404
                                                                                                                                                              Similarity
    Lysine biosynthesis;
                                                                                399 3
404 AA;
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Q57991,
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                                                                                                   SEQUENCE
                                                                                                                                           Query Match
Best Local (
                                                                                CONFLICT
                                            CHAIN
                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 IVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYS-DRPGTVVVGS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 KVGDFIKFIREKHYKAIBEAIKSBEIKEBVKKIIDSRIEBLEKVLIGVAYLGBLTPKSRD 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 IKDVPMEDPILTGVAHDRSEAKVTI---VGLPDIPGYAAKVFRAVARRRRQHRHGAAERLQ 298
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Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 MLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKI--IDVTPGRLQTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
22.4%; Score 492; DB 1; Length 473;
Best Local Similarity 27.2%; Pred. No. 2.3e-27;
Matches 129; Conservative 92; Mismatches 126; Indels 128; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -STOLLYDDHIGK----VSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSEDQ 381
                                                                                                                   -!- PATHWAY: FTRST STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING FROM ASP TO DIAMINOPIMELATE AND LYS, TO MET, TO ILE AND TO THR -!- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGREAMS; TIGRO0656; asp kin monofn; 1.
TIGREAMS; TIGRO0657; asp kinases; 1.
PROSITE; PSO0324; ASPARTOKINASE; 1.
Transferase; Kinase; Threonine biosynthesis; Complete proteome.
SEQUENCE 473 AA; 51392 MW; 811C6E0F4B66EC5F CRC64;
                                                               Science 273:1058-1073(1996).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR001048; Aa kinase.
InterPro; IPR002912; ACT.
InterPro; IPR005260; Asp kin monofn.
InterPro; IPR001341; Aspartate kinase.
Pfam; PF00696; aaknase; 1.
                                                                                                                                                                                                                                                                                                                                             EMBL; U67506; AAB98565.1; -. PIR; C64371; C64371.
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Search completed: November 21, 2003, 16:04:16 Job time : 5.99955 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                          OM protein - protein search, using sw model
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November 21, 2003, 15:56:56; Search time 20.8635 Seconds (without alignments) 5244.295 Million cell updates/sec US-09-688-672A-4 2193 1 VQXYGGSSVADAERIRRVAE......SAATRRPRCTRGRDGRWACQ 424 Title: Perfect score: Run on:

Sequence:

Scoring table:

830525 segs, 258052604 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

830525

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database :

SPTREMBL 23:\*

1: Sp\_bacteria:\*

2: Sp\_bacteria:\*

3: Sp\_inng:\*

5: Sp\_invertebrate:\*

6: Sp\_mammal:\*

7: Sp\_morranel:\*

8: Sp\_plant:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Q8kq29 sireptomoce Q9rq25 amycolatops Q9rq25 amycolatops Q9rq25 corvebacte Q9ac55 corvebacte Q9xa17 streptomyce Q9xa17 streptomyce Q93x4 stigmatella P74569 synechocyst Q6fq65 leptospira Q8ru02 methylobaci Q8ru02 methylobaci Q8ru02 methylobaci Q8dhw0 synechococc Q94yr14 amabaana sp Q96yr6 bifidobacte Q9fyf bifidobacte Q9cb77 mycobacteri Description SUMMARIES Q9CB77 Q8KQ29 Q9RQ25 Q93C57 Q93C55 Q93C55 Q93C55 Q93C125 P74569 Q8F865 Q8RU02 Q8DHW0 Q8YR14 Q8G6Y6 Query Match Length DB Score 1545.5 1272.5 1267.5 1232.5 1228.5 1224.5 1127 816.5 803 798.5 786.5 776.5 773.5 Result No.

Q9jyn6 neisseria m Q9k8b0 bacillus ha Q9pht4 campylobact Q9x1k6 thermotoga Q9wz17 thermotoga Q8y073 ralstonia s	0920h4 listeria in Q9a9w8 caulobacter Q8y7n9 listeria mo Q8y197 brucella me Q8fykl brucella su Q9ev19 bradyrhizob	06450001	Q9ev36 staphylococ Q8nws7 staphylococ Q8csws staphylococ Q9ka90 bacillus ha Q8cqt0 oceanobacil Q92br9 listeria in Q92qf9 rickettsia Q8y765 listeria mo Q8xj86 clostridium
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Q9JYN6 Q9K8B0 Q9PHT4 Q9X1K6 Q9WZ17	Q92CH4 Q9A9W8 Q8Y7N9 Q8YJ97 Q8FYK1 Q9EV19	Q808C0 Q92MK3 Q98KUH4 Q8EBS2 Q8RA48 Q8DC48	Q9EV36 Q8NWS7 Q8CSMB Q9KA90 Q9EQT0 Q92ER9 Q92GF9 Q8Y765
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## ALIGNMENTS

9 64 120

124

180

184

240

244 295

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61 ELDMLITAGERISNALVAMAIESLGAHARSFIGSQAGVITTGTHGNAKIIDVTPGRLQTA
                                                                                                                                                                                          185 RIVPDARKLDSVPYBEMLELAASGSKILHIRSVEYARRYGVPIRVRSSYSDKPGTTVTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                            296 RLO-----GRGRODRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VQKYGGSSVADAËRIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
                                                                                                                                                                                                                                                 121 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
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                                                                                                                                                                                                                                                                                                                                                                                                                    241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAE----
                                              Gaps
                                           21;
  Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
                                           60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9RQ25
Q9RQ25,
Q1-MAY-2000 (TrENBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Aspartchinase subunit A (EC 2.7.2.4) (Aspartate kinase)
ASKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44393 MW; 633D9C2D023145E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Nocardia mediterranei).
    DB 2;
  Score 1272.5; DB
Pred. No. 7.5e-78;
                                           51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354 MRSHPGVTATFCEALSKVGVNIEIINTSE 382
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TIGREPAMS; TIGRO0657; asp kinases; 1.
TIGREPAMS; TIGRO0656; asp kin monofn; 1.
PROSITE; PSO0324; ASPARTOKINĀSE; 1.
58.0%;
66.1%;
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Pfam; PF01842; ACT; 2.
                        al Similarity 66.13
257; Conservative
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SEQUENCE 421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 AA;
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                                                                                                                                                                                                                                                                                                                                  181
  Query Match
Best Local S
                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 VLQNVSKVEDGKTDITFTCSRDSGPIAVAKLGSLRDEIGFTQLLYDDHIGKVSLIGAGMR 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                   241 IKDVPMEDPILIGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAE---- 295
                                                                                                       9
                                                                                                                                            64
                                                                                                                        VQKYGGSSVADADRIRRVAERIVQTKKQGNDIVVVVSAMGDTTDDLLDLAQQVCPEPPAR
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                                                                                                                                                                                 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
                                                                                                                                                                                                                                                                                             1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ankara,
                                                             17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tunca S.,

"Isolation and characterization of the aspartokinase and aspartate
"Isolation dehydrogenase genes from cephamycin C-producer
Streptomyces clavuligerus.";
Thesis (2002), University of Middle East Technical University, Ank
                     Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                = ADP + 4-PHOSPHO-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces,
NCBI_TaxID=1901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Aspartate kinase alpha subunit (EC 2.7.2.4) (Aspartokinase)
               ; Score 1545.5; DB 16; Lengt; Pred. No. 3e-96; 18; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44399 MW; 08262D81045735C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: ATP + L-ASPARTATE = ADP + 4-ASPARTATE.
-!- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY:
EMBL; AY112728; AAMS4736 1; -
InterPro; IPR001048; Aa kinase.
InterPro; IPR02912; ACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHPGVTATFCEALAAVGVNIELISTSEDQRSRCCAAT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHPGVTATFCEALAAVGVNIELISTSEIRISVLCRDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0474; GLUSKINASE.
TIGRFAMS; TIGR00657; asp_kinases; 1.
TIGRPAMS; TIGR00656; asp_kin monofn; 1.
PROSITE; PSO0124; ASPARTOKINASE; 1.
Kinase; Transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPRO01341; Aspartate kinase.; IPR005260; Asp kin monofn.; IPR001057; Glu_Skinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBKQ29;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last seq
01-MAR-2003 (TrEMBLrel. 22, Last ann
                 70.5%;
80.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00696; aakinase; 1.
Pfam; PF01842; ACT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces clavuligerus.
             Query Match 70.5
Best Local Similarity 80.4
Matches 319; Conservative
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61 ELDMLLTAGERISNALVAWAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
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                                                                                    65 EMDMLLITAGERISNALVAMAIESLGAEAQSFTGSQAGVLTTERHGNARIVDVTPGRVREA 124
                                                                                                                                  121 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                                                                                  241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA------RRRRQHR 290
                                                               ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
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Thesis (2000), Department of Area of Microbiology, University of Leon,
                                                                                                                                                                 125 LDEGKICIVAGFQGVNKETRDVTTLGRGGSDTTAVALAAALNADVCEIYSDVDGVYTADP
                                                                                                                                                                                                 RIVRNARKLIDTVTFFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                  291 HGAAERLQGRGRQD-RHHLHLL--PQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI
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                   5 VQKYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLELAAAVNPVPPAR
 1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVSAMGDTTDDLLDLAQQVCPAPPPR
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Leon, Spain.

- I. CARLYTIC ACTIVITY: ATP + L-ASPARTATE = ADP + 4-PHOSPHO-L-ASPARTATE: AJ298904; CAC37034.1; - SMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.

R InterPro: IPRO01949; Ad. Kinase.

R InterPro: IPRO01941; Aspartate kinase.

R InterPro: IPRO01941; Aspartate kinase.

R InterPro: IPRO01957; Glu Skinase.

R Ffam; PFO0696; aakinase; 1.

R Ffam; PFO0842; ACT; 2.

R Pfam; PFO0843; ASPARTOKINASE.

R PIGREMA; TIGRO057; asp kinases; 1.

R PROSITE; PS0034; ASPARTOKINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
NCBI_TaxID=1913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
Aspartokinase alpha subunit (BC 2.7.2.4) (Aspartate kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.0%; Score 1228.5; DB 2; Length
64.3%; Pred. No. 7e-75;
cive 52; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 AA; 44141 MW; 802FBE02D01B7F95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
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                                    Gaps
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
Feedback-resistant aspartokinase Lysc alpha subunit (EC 2.7.2.4)
                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.2%; Score 1232.5; DB 2; Length 421; llarity 64.3%; Pred. No. 3.7e-75; Conservative 55; Mismatches 58; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium crenatum.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-ASPARTATE = ADP + 4-PHOSPHO-L-
 Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu Y., Ding J., Wang J.; "Cloning and sequence analysis of aspartokinase genes from
                                 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 AA; 44738 MW; 473A19409C0215E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASPARTATE.
-1- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
EMEL; AF4140684; AALONGO T.1; -.
INTERPRO: IPR001248; Aa Kinase.
INTERPRO: IPR001341; ASPARTATE Kinase.
INTERPRO: IPR001341; ASPARTATE Kinase.
PERM: PF00596; aakinase; 1.
PF00896; aakinase; 1.
   7
57.8%; Score 1267.5; DB 65.3%; Pred. No. 1.6e-77; iive 53; Mismatches 61
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TIGRFAMS; TIGRO0656; asp_kin_monofn; 1.
PROSITE: PSO0324; ASPARTÖKINĀSE; 1.
Kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Query Match
Best Local Similarity 65.3
Matches 254; Conservative
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01-DEC-2001 (
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Matches 252;
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240
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   125 LDEGKICIVAGFQGVNKETRDVTTLGRGGSDTTAVALAAALNADVCEIYSDVDGVYTADP 184
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                                                                                                                291 HGAAERLOGRGROD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                   RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
Bentley S.D. Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Hopwood D.A.;
Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of the model actinomycete Streptomyces coelicolor {\rm A3}\,(2)\,.\,,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=A31(2);
James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                               241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA
                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative aspartokinase.
ASK OR SCO3615 OR SC6613.26C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomycineae, Streptomycetaceae, Streptomyces NOBI_TaxID=1902;
                                                                                                                                                                                                                            348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
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EMBL, AL939117, CAB4548.1; -.
InterPro; PR001049; Aa kinase.
InterPro; IPR001212, ACT.
InterPro; IPR001341; Aspartate kinase.
InterPro; IPR00560; Asp_kin_monofn.
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MEDLINE=97000351; PubMed=8843436;
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                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Submitted (JUN-1999) t
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                                                                                                              241 IXDVPMEDPILIGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAE---- 295
                                                                                                                                                                           296 VLQNVSNTSSGRTD--ITFTLSKANGPKAVASLEKIKEELGFSSVLYDDHVGKVSLVGAG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                               184
                                                                                                                                                                                                                       296 RLQ-----GRGRQDRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAG 350
EMDMLLTAGDGISNALVAMAISAQGAQAWSFTGSQAGVVTTAVHGNARIIDVTPSRVSER 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124
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                               LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
                                                125 LEQGYVALVAGFQGVAQDTKDITTLGRGGSDTTAVALAAALNADVCEIYSDVDGVYSADP
                                                                                            RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQKYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLELAAAVNPVPPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.8%; Score 1224.5; DB 2; Length 421; 64.0%; Pred. No. 1.3e-74; ive 55; Mismatches 59; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu Y., Ding J., Wang J.;
"Cloning and sequence analysis of aspartokinase genes from
                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 13, Last annotation update)
01-MAR-2003 (TrEMBLrel Last annotation update)
Aspartokinase LysC alpha subunit (BC 2.7.2.4) (Aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
EMBL; AF414085; AAL07809_1; -
INTECPTO; IPRO01048; Aa kinase.
INTECPTO; IPRO02912; AGT.
INTECPTO; IPRO02912; AGT.
INTECPTO; IPRO05260; ASP, Kin_monofn.
Pfam; PF00665; aakinase; 1.
Pfam; PF00665; aakinase; 1.
TIGREAMS; TIGR00657; asp, kinases; 1.
TIGREAMS; TIGR00656; asp_kin_monofn; 1.
PROSITE; PS00334; ASPARTOKINĀSE; 1.
Kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44754 MW; E36B4D0081DE0827 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    Ź
                                                                                                                                                                                                                                                                                                       354 MRSHPGVTATFCEALCKVGVNIEIINTSE 382
                                                                                                                                                                                                                                                                                       MRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                  421
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium crenatum."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium crenatum.
                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI TaxID=168810;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=1542;
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ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
                                                                                                                                                                                                                                                   STGLTDIS-----FTLPKAEGRKAIDALERAKGSIGFESLRYDDQIAKISLVGAGMKT 357
ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
                  21 VQXYGGTSVGDTERIKOVAKRCIAAQKAGHDVVVVVSAMSGETNRLLKLVSQITERPNER
                                                                                                                 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                   241 IK-DVPMEDPILIGVAHDRSEAKVIIVGLPDIPGYAAKVFRAVARRR-----RQHRHGA
                                                                                                                                                                                           245 PQGDQKVEHAIISGVAHDVSEAKVTVVGVPDKPGEAAAIFRAIANAEVNIDMVVQNVSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VOKYGGSSVADAERIRRVAERIVATKKOGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                         LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
                                                                                                                                                                                                                                  294 AERLOGRGRODRHHLHLILPQTSGPPPWKWWTRSETRSASTQLLYDDHIGKVSLIGAGMRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Deltaproteobacteria, Myxococcales,
Cystobacterineae, Cystobacteraceae, Stigmatella.
NCBI_TaxID=41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative aspartokinase (EC 2.7.2.4) (Aspartate kinase).
Stigmațella aurantiaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46023 MW; D400C1992D888B56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
EMBL, AF319998, AAK57182.1; -
INTERPO; IPR001048; AA kinase.
INTERPO; IPR00213, ACT.
INTERPO; IPR001341; ASPARTATE kinase.
INTERPO; IPR001341; ASPARTATE.
INTERPO; IPR001057; Glu_Skinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.4%; Score 821; DB 2;
Local Similarity 44.3%; Pred. No. 2.2e-47;
les 178; Conservative 79; Mismatches 119.
                                                                                                                                                                                                                                                                                                                                                                                                  434 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMS; TIGRO0657; asp kinases; 1.
TIGRFAMS; TIGRO0656; asp kin monofn; 1.
PROSITE; PSO0324; ASPARTOKINĀSE; 1.
                                                                                                                                                                                                                                                                                                                   358 NPGVTAGFFEALSDAGVNIELISTSE 383
                                                                                                                                                                                                                                                                                               354 HPGVTATFCEALAAVGVNIELISTSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF00696; aakinase, 1.
Pfam, PF01842; ACT; 2.
PRINTS; PR00474; GLUSKINASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Matches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                   245 PIKOGEKHVEQALISGVAHDTSEAKVTVVGVPDKPGEAAAIFRAIADAQVNIDMVVQNVS 304
                                                                                                                                                                                                                     ELDMELTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
                                                                                                                                                                                                                                        ELDMLLTAGERISMALLAMAIKNIGHEAQSFTGSQAGVITDSVHNKARIIDVTPGRIRTS 124
                                                                                                                                                                                                                                                                                  LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                                                                                                                291
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAERLQGRGRQDRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAGM 351
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                                                                                                                                                                                                                                                                                                                                                                                                  -IK--DVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRR-----RQHRH
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                                                                                                                                                                              5 VQKYGGSSVADAEGIKRVAKRIVEAKKNGNQVVAVVSAMGDTTDELIDLAEQVSPIPAGR
                                                                                                                                                               1 VOKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Amplification of the ask-asd operon in aminoethoxyvinylglycine-
producing Streptomyces sp. NRRL 531 results in stimulation of
aminoethoxyvinylglycine production.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                 16;
                                                                                                     425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces sp. NRRL 5331.
Bacteria, Actinobacteridae, Actinomycetales;
Streptomycineae, Streptomycetaceae; Streptomyces.
NCBL_TaxID=159599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81; Indels
                                                                                                   Query Match 52.0%; Score 1141; DB 16; Length Best Local Similarity 61.6%; Pred. No. 5.6e-69; Matches 239; Conservative 54; Mismatches 79; Indels
                                                           Complete protecme.
E 425 AA; 44779 MW; 4A61177D9D12BD15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423 AA; 44581 MW; 6DA2938627D9366A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.4%; Score 1127; DB 2; 60.4%; Pred, No. 4.9e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423
 Pfam, PF01842; ACT; 2. TIGRPAMS; TIGRO0657; asp. kinases; 1. TIGRPAMS; TIGRO0656; asp. kin monofn; 1. PROSITE; PS00324; ASPARTOKINĀSE; 1.
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity
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Cuadrado Y.;
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SEQUENCE
                                                            Kinase, Co
SEQUENCE
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244
                                                                                                                                                                                                                                                                                                                                   245 P----PVQNRSLVGLEIAKAVDGVEYDADQAKVALLRVPDRPGVASKLFRDIAQQQVDID 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                     200 NWVPAARKLERIAYEEMLELASVGAKVLQIRSVEFAMKYKVPLWVKSSFTDDPGTLVCE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura E
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSHPGVTATFCEALAAVGVNIELISTSEDQRSRCCAATPNWT 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
SEQUENCE 600 AA; 63533 MW; B30B7101E9FC4D46 CRC64;
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Bacteria, Cyanobacteria, Chroococcales, Synechocystis.
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Last annotation update)
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TIGRFAMS; TIGR00656; asp_kin_monofn; 1.
PROSITE; PS00324; ASPARTÖKINÄSE; 1.
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InterPro; IPR001048; Aa kinase.
InterPro; IPR002912; ACT
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Pfam; PF01842; ACT; 4.
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SEQUENCE FROM N.A.
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Tabata S.;
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                                                                                                                                                                                               Motoyama H., Anazawa H.; "Analysis of the nucleotide sequence of lysC of Methylobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                         43;
                                                                                                    LYSC.
Methylobacillus glycogenes.
Bacteria; Proteobacteria; Becaproteobacteria; Methylophilales;
Methylophilaceae; Methylobacillus.
NCBI_TaXID=406;
                                                                                                                                                                                                                                 nitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CATALYTIC ACTIVITY: ATP + L-ASPARTATE = ADP + 4-PHOSPHO-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 36.4%; Score 798.5; DB 2; Length Best Local Similarity 41.7%; Pred. No. 6.5e-46; Matches 168; Conservative 78; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 IGKVSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSEDQRS 383
                                                                                                                                                                                                                                                                                                                                                                                                            44328 MW; 3894F2315A6EBD75 CRC64;
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-!-SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
EMBL; AB038354; BAB84686.1; -.
InterPro; IPR001048; Aa Kinase.
InterPro; IPR002912; ACT.
                                                                01-JUN-2002 (TrEMBLrel. 21, Last sequence update) . 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Aspartate kinase (EC 2.7.2.4) (Aspartokinase).
                                 408 AA
                                                                                                                                                                                                                                                                                                              InterPro; IPR001341; Aspartate kinase.
InterPro; IPR005260; Asp_kin_monofn.
Pfam; PF00696; aakinase; 1.
TIGRFAMs; TIGR00657; asp_kinases; 1.
TIGRFAMs; TIGR00656; asp_kinases; 1.
KINSTEMS; TIGR00656; asp_kin monofn; 1.
Kinase; Transferase.
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Submitted (FE)
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RESULT 13 Q8DHW0 ID Q8

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EMBL, AP005375, BAC09385.1; -. Kinase; Complete protecome.
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35.9%; Score 786.5; DB 16; Length
Best Local Similarity 45.7%; Pred. No. 7e-45;
Matches 184; Conservative 67; Mismatches 129; Indels
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                                                                                                Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
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Kaneko T., Nakamura Y., Wolk C.P.,
                                                                                                                                                                                                              STRAIN=BP-1;
MEDLINE=22225144; PubMed=12240834;
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completed: November 21, ie : 22.8635 secs
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RA Kishida Y., Kohara M., Ishikawa A., Kawashima K., Kimura T., RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yamada M., Tabata S.;
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing Cyanobacterium Anabaena sp. strain PCC 7120.";
RD DNA Res. 8:206-213 (2001).
R InterPro: IPR0019912; ACT.
R InterPro: IPR0019912; ACT.
R InterPro: IPR001966; Askinase.
R InterPro: IPR001966; Askinase.
R Pfam; PF00696; aakinase; I.
R TIGRFAMS: "TOTA A T.
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MEDLINE=22294977; PubMed=12381787;
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B., Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M., Pridmore R., R., Arigoni F.;
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Bacteria, Actinobacteria, Actinobacteridae, Bifidobacteriales,
Bifidobacteriaceae; Bifidobacterium.
NCBI_TaxID=216816;
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Last annotation update)
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TIGRFAMS; TIGR00657; asp kinases; 1.
TIGRFAMS; TIGR00656; asp_kin_monofn; 1.
PROSITE; PS00324; ASPARTOKINĀSE; 1.
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les 175; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence of Bifidobacterium longum reflects its adaptation
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                                                                                                                                                                                    DB 16; Length 254;
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                   to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002).
EMBL. AE014669; AAN24333.1;
SKinase; Complete proteome.
SEQUENCE 254 AA; 27041 MW; 28D9F48C68822225 CRC64;
                                                                                                                                                                                                                                          46;
                                                                                                                                                                                 35.3%; Score 773.5; DB 1
64.3%; Pred. No. 1.7e-44;
ive 38; Mismatches 46
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                                                                                                                                                                                                                Best Local Similarity 64.38
Matches 153; Conservative
     genome
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                                                                                                                                                                                          Query Match
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27463, A 31388, A 2, Appli 6, Appli 6, Appli 2, Appli

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Sequence 20601. A Sequence 1953, A Sequence 3979, Appli Sequence 30698, A Sequence 2, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli Sequence 5687, Appli S
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APPLICANT: Skeiky; Yasir A.W.
APPLICANT: Skeiky; Yasir A.W.
APPLICANT: Davin C.
APPLICANT: Campos-Netc, Antonio
APPLICANT: Campos-Netc, Antonio
APPLICANT: Campos-Netc, Daniel
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Daniel
TITLE OF INVENTION: COMPOINDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COMPTRY: Washington
COMPTRY: Washington
COMPUTER: READABLE FORM:
MEDIJM TYPE: Floppy disk
COMPUTER: READABLE FORM:
MEDIJM TYPE: Bloppy disk
COMPUTER: Batentin Release #1.0, Version #1.30
COMPTRY: US/98
SOFTWARE: 13-MAR-1997
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
REGISTRATION NUMBER: 21021.411C6
TELECOMMUNICATION NUMBER: 21022.4900
TELEBRAY. CORE, CARCE NUMBER: 21026.603.
      Sequence
                                                             Sequence
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                US-09-046-086-2
US-09-524-643-2
US-09-525-991A-31388
US-09-252-991A-31388
US-08-336-4088-2
US-08-364-088-2
US-08-9115-6
US-08-925-991A-19533
US-09-252-991A-19533
US-09-132-991A-19533
US-09-132-991A-19533
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US-09-132-991A-30698
US-09-057-351-2
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US-09-252-991A-32329
                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 77, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (200, 22-6031)
TELEPHONE: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 66; Conserv
  STRANDEDNESS
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Sequence 77, Appl
Sequence 78, Appl
Sequence 78, Appl
Sequence 214, App
Sequence 219, App
Sequence 21917, A
Sequence 16, Appl
Sequence 16, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 176, Appli
Sequence 176, Appli
Sequence 176, Appli
Sequence 176, Appli
Sequence 26229, A
Sequence 27169, Appli
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324
1 VIDIIGTSPTSWEQAAAEAV......KITYRIKLEVSFKMRPAQPR 66
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-072-596-74

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US-09-072-596-78

US-09-072-591A-21917

US-09-072-591A-21917

US-09-031-392-7

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US-09-252-991A-16702
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                                                                                                                                                                                                                                                                                                                                                     328717 seqs, 42310858 residues
                                                                                           protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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61 RPAQPR 66
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US-09-072-596-78
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VIDIIGTSPISWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 60
                                         1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 60
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 78, Application US/08818111
| Patent No. 6338852
| GENERAL INFORMATION:
| APPLICANT: Reed, Steven G. |
| APPLICANT: Skeiky, Yasir A.W. |
| APPLICANT: Dillon, Davin C. |
| APPLICANT: Houghton, Raymond |
| APPLICANT: Houghton, Raymond |
| APPLICANT: Wadvick, Thomas S. |
| APPLICANT: Twardzik, Daniel R. |
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| APPLICANT: Twardzik, Daniel R. |
| APPLICANT: Tward
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APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INPORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-056-556-77
US-09-056-556-77
Sequence 77, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 78:
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Best Local Similarity 100.0
Matches 66; Conservative
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STATE: Washington
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US-08-818-111-78
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TUBERCULOSIS
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APPLICANT: Skeiky, Yasir A.W.

PEPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Genter, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INCORNATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael G.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
ATITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                        COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELD PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/POCKET NUMBER: 31,392
REFERENCE/POCKET NUMBER: 210121.457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 324; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.3e-37;
Matches 66; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 78, Application US/09072596 Patent No. 6458366
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CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 amino acids
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ADDRESSEE: SEED and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Shilon, Davin C.
APPLICANT: Campos-Weto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Lodes, Michael R.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                   100.0%; Score 324; DB 4; Length 802; 100.0%; Pred. No. 5.9e-36; ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 5.9e-36;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMFUTER: Floppy disk
COMFUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                            09, Application US/09072596
6458366
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NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 3.392
REFERENCE/DOCKET NUMBER: 21012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6931
INFORMATION FOR SEQ ID NO: 209:
SEQUIENCE CHRARACTERISTICS:
LENGTH: 802 amino acids
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Best Local Similarity 100...
...hes 66; Conservative
                                                                                           Best Local Similarity 100.
Matches 66; Conservative
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    ; TOPOLOGY: linear
US-09-056-556-214
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STREET: 63
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US-09-072-596-209
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                                                                          Query Match
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Patent No. 6350456
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 324; DB 4; Length 66; Best Local Similarity 100.0%; Pred. No. 2.3e-37; Matches 66; Conservative 0; Mismatches 0; Indels
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CITY: SC.

STATE: Washing.

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURSENT APPLICATION NUMBER: US/09/056,556

FILING DATE: 07-APR-1998

CLASSIFICATION: NUMBER: 31,392

ATTONEY/AGENT INFORMATION:

MAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REBERNEN/EDOCKET NUMBER: 31,392

REJECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

"TIEPHONE: (206) 622-4900

"TIEPHONE: (206) 622-4900

"TIEPHONE: (206) 622-4900

"TIEPHONE: (206) 622-4900

"TIEPHONE: (206) 622-4900

"TIEPHONE: (206) 622-4900

"TIEPHONE: (206) 622-4900

"TIEPHONE: (206) 622-4900

"TIEPHONE: (206) 622-4900
                               CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/072,596

FILING DATE: 05-MAY-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: MAKI, DAYLd J.

REGISTRATION NUMBER: 210121.417C9

REGISTRATION NUMBER: 210121.417C9

TELEPRONE: (206) 682-4900

TELEPRONE: (206) 682-6031

INFORMATION FOR SEQ ID NO: 78: SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

TYPE: AMINO acid

TYPE: AMINO acid

STRANDEDNESS: single
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STREET: 6300 Columbia Center, 701 Fifth Avenue
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 21.
SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abun...
STREET: 6300.
CITY: Seattle
...mr: Washington
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US-09-056-556-214
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US-09-072-596-78
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Sequence 2518, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VIDIIGTSPTSWEQA---AAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVS 57
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US-09-16
US-09-16
15 Application US/09300909
15 Sequence 16, Application US/09300909
16 Tatent No. 6306580
17 GENERAL INFORMATION:
17 TITLE OF INVENTION: PREPARATION OF HUMAN PAPILLOMAVIRUS E1 HAVING
17 TITLE OF INVENTION: HELICASE ACTIVITY AND METHOD THEREFOR
17 TITLE OF SEQUENCES: 27
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 MEDIUM TYPE: Floppy disk
10 COMPUTER: PLOPPY disk
10 COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOPPY MS. NO. COMPUTER: PLOP
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COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy DEACHIDE
COMPUTER: Floppy DEACHIDE
COMPUTER: PETENTIA SETENT: PC-DOS/MS-DOS
SOFTWARE: PATENTIA NOTA:
APPLICATION NUMBER: US/09/300,909
FLING DATE:
PRIOR APPLICATION NUMBER: US 60/083,942
FILING DATE: 01-MAY-1998
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              21.3%; Score 69; DB 4; 25.4%; Pred. No. 0.038;
; CURRENT APPLICATION NUMBER: US/09/252,991A; CURRENT FILING DATE: 1999-02-18; PRIOR APPLICATION NUMBER: US 60/074,788; PRIOR FILING DATE: 1998-02-18; PRIOR APPLICATION NUMBER: US 60/094,190; PRIOR FILING DATE: 1998-07-27; NUMBER OF SEQ ID NOS: 33142; SEQ ID NO 21917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 61.5; D
Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21917
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Best Local Similarity 25.4%
Marches 15, Conservative
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Best Local Similarity 29.24
Matches 19; Conservative
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107 TELSP 111
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US-09-252-991A-25318
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Ratent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 VIDIIGTSPISWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 68
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                                                                                                                                                                                                                                                        APPLICANT: Reed, Steven G.
APPLICANT: Reed, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vadvick, Thomas S.
APPLICANT: Vadvick, Thomas S.
APPLICANT: Lodes, Michael R.
APPLICANT: Lodes, Michael J.
APPLICANT: Michael J.
APPLICANT: Michael J.
APPLICANT: Michael J.
APPLICANT: Michael J.
APPLICANT: Michael J.
APPLICANT: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 324; DB 4; Length 8
100.0%; Pred. No. 5.9e-36;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLESSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/ACENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                    Sequence 346, Application US/09072596
Patent No. 6458366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 346:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 802 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                 RPAQPR 74
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US-09-252-991A-21917
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                                                                                                                                                      US-09-072-596-346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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227 EAAAKKALQTLRGWDSVDR-EVAEIRQEDEAEKAAGFISV-LKL---FRMR 272
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CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                 RESULT 12
US-09-299-549-7
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                                                                                                                                                                                                                                                                                                         17.9%; Score 58; DB 4; Length 446; nlarity 24.7%; Pred. No. 9.7; Conservative 14; Mismatches 31; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, Xu.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING GLUTEX AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
CCUNTRY: USA
ZIP: 02110-2804
ZIP: 02110-2804
CCMPUTER: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: TEM COMPATIBLE
COMPUTER: TEM COMPATIBLE
COMPUTER: TEM COMPATIBLE
COMPUTER: TEM COMPATIBLE
COMPUTER: TEM COMPATIBLE
COMPATING SYSTEM: Windows Version 2.0
CURRENT AMPLICATION NAMER: US/09/031,392
FILING DATE: 26-FEB-1998
ATTORNEY/AGRNI INFORMATION:
NAME: Mekklejohn, Ph.D. Amita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/072001
TELECOMONIOATION INFORMATION:
TELECHONE: 617/542-5070
TELECHONE: 617/542-5070
TELEPAX: 617/542-8906
CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR PRILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25318

LENGTH: 446

TYPE: PRT

CREANISM: Pseudomonas aeruginosa

US-09-252-991A-25318
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Patent No. 5942398
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// MOLECULE TYPE: protein
US-09-031-392-7
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Matches 18; Conserv
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US-09-031-392-7
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STATE:
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Gaps
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APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
GLUTEX AND USES THEREOF
Sequence 7, Application US/09299549
Patent No. 6136547
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, Xun
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: GLUTEX AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: Mindows95
SOFTWARE: FastSEG for Windows Version 2.0
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,549
FILING DATE: 26-APR-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/031,392
FILING DATE: 26-FEB-1998
ATTORNEY/AGGNT INFORMATION:
NAME: Melklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
17.7%; Score 57.5; D
Best Local Similarity 43.1%; Pred. No. 13;
Matches 22; Conservative 9; Mismatches
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RADRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07334/072002
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Patent No. 6346374
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        500 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                              ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-09-328-352-8072
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PAPLICATION NUMBER: US,60/052,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US,60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-7
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26229
LENGTH: 633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 17.7%; Score 57.5; DB 4; Length 500; Best Local Similarity 43.1%; Pred. No. 13; Matches 22; Conservative 9; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 633;
                CORPUTER FACTORIES FORT:

COMPUTER: IBM Comparible

COMPUTER: IBM Comparible

OPERATING SYSTEM: Windows95

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/610,417

FRIDK APPLICATION DATA:

APPLICATION NUMBER: 09/299,549

FRIDK APPLICATION NUMBER: 09/299,549

ATTORNEY/AGENT INFORMATION:

NAME: Weiklelphn, Ph.D., Anita L.

REFERENCE/DOCKET NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 35,283

TELECHMUNICATION INFORMATION:

TELECHMUNICATION INFORMATION:

TELERAX: 617/542-5000

TELERAX: 2001542-5000

TELERAX: 2001542-5000

TELERY: 2001542-5000

TELERY: 20015484CFRESTICS:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 17.7%; Score 57.5; DB Similarity 31.7%; Pred. No. 18; 20; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) MOLECULE TYPE: protein SEQ ID NO: 7: US-09-610-417-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-09-252-991A-26229
; Sequence 26229, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 500 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 GAV 319
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RESULT 15

Sequence 80.2, Application US/09328352
; Sequence 80.2, Application US/09328352
; Patent No. 6562058
; GENERAL INFORMATION:
 APPLICANT GAIY L. Breton et al.
 ITILE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
 TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC99-03P4
; CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
LENGTH: 900
; TYPE: PRT

 ORGANISM: Acinetobacter baumannii

 ORGANISM: Acinetobacter baumannii

 CORANISM: Acinetobacter baumannii

 OSCOBILIA ACINETORIA

M. tuberculosis fu M. tuberculosis fu M. tuberculosis fus M. tuberculosis fus Antigenic fusion p M. tuberculosis TD P.denitrificans CO Drosophila melanog Human papillomavir Human papillomavir

Mycobacterium Mycobacterium

Drosophila melanog Salmonella typhi c Human ORF313 prote Cotton (+)-delta-c M. tuberculosis an Streptomyces virid Sucrose-specific p

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Drosophila melanog Fruit fly E93 prog Gene 2 human secre

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Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis.
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AAR21516
AAY40501
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ABU05888
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AAB39229
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95US-0523436.
95US-0533634.
96US-0620874.
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 Campos-neto A, Dillon DC,
Twardzik DR, Vedvick TH;
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(CORI-) CORIXA
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Copyright (c) 1993 - 2003 Compugen Ltd.
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AAW81668
AAW64305
AAX39107
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AAE29718
AAE17582
AAW81746
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Gapop 10.0 , Gapext 0.5
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1 VIDIIGTSPTSWEQAAABAV.
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AAW81668 standard; Protein; 66 AA.
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96US-0730510.
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Best Local Similarity 100.
Matches 66; Conservative
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                                                                                     A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TDRa3. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins BSAT-6, are useful in vaccines, preferably when formulated with a mon-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or prevention).
                                                                                                                                                                                                                              0; Gaps
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                             New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also
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100.0%; Score 324; DB 18; Length 66;
Best Local Similarity 100.0%; Pred. No. 1e-35;
Matches 66; Conservative 0; Mismatches 0; Indels 0
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                                                                    Example 3; Page 113; 168pp; English.
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95US-0523435.
95US-0532136.
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Twardzik DR, Vedvick TH,
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N-PSDB; AAT91412.
WPI; 1997-192903/17.
N-PSDB; AAT91475.
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22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
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                                                     (or
A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or modifications). The present sequence represents a M.tuberculosis antigen, passa; The immunogenic polypeptide can be used to diagnose antibodies in flection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
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100.0%; Pred. No. 1e-35;
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    4. tuberculosis immunogenic polypeptide TbRa3.

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61 RPAOPR
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18-FEB-1998;
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                                                              1 VIDIIGTSPTSWEQAAABAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 60
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                                                1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
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  DB 19; Length 66;
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100.0%; Score 324; DB 19;
100.0%; Pred. No. 1e-35;
ive 0; Mismatches 0;
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96US-0729622
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             Similarity 100.
66; Conservative
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Reed SG, Skeiky YAW,
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Best Local Similarity
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N-PSDB; AAV44353.
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                                     1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 60
1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antigens from Mycobacterium tuberculosis useful in diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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100.0%; Score 324; DB 20; Length 66;
Best Local Similarity 100.0%; Pred. No. 1e-35;
Matches 66; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M. tuberculosis antigen TbRa3 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campos-Neto A, Dillon DC, Hendrickson RC, Ho
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 107; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                   AAY39107 standard; Protein; 66 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US03268.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-527409/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ19263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPAOPR
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AAY38970;

vaccine;

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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. tuberculosis TbRa3 antigenic protein.
                                                                                                                                                                                                                                                                                                                               New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polymucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 324; DB 23;
100.0%; Pred. No. 1e-35;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 107-108; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium species TbRa3 protein.
                                                                                                                                                                                                                                 Guderian J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE17582 standard; Protein; 66
                                                                                                    13-MAR-2002; 2002WO-US08223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUN-2001; 2001WO-US19959.
                                                                                                                                            13-MAR-2001; 2001US-275837P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66; Conservative
                                                                                                                                                                                                                               Skeiky Y, Brannon M,
                                                                                                                                                                                                                                                                       WPI; 2002-759844/82.
N-PSDB; AAD47095.
                                                                                                                                                                                       (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RPAQPR 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium sp.
                    WO200272792-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200198460-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-APR-2002
                                                          19-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel recombinant antigens and their encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                               Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine; immunity; diagnostic agent; gene therapy; TbRa3 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20; Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Houghton R;
k, Vedvick TS;
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100.0%; Pred. No. 1e-35;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis TbRa3 antigenic protein.

    M. tuberculosis recombinant antigen protein TbRa3.

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Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
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                                                          AAY38970 standard; Protein; 66 AA.
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98US-0024753.
                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US03265
                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-527416/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP.
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Best Local Similarity
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18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                     WO9942118-A2
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AAE29718

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RESULT 7 AAE29718

Matches

8 g à

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Gaps

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Indels

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97WO-US18214.
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96US-0729622.
                                   .97US-0818112.
96US-0730510.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66; Conservative
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Reed SG, Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
                                                                                        (CORI-) CORIXA CORP.
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N-PSDB; AAV55801.
                                                                                                                                                                               WPI; 1998-261042/23.
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Best Local Similarity
Matches 66; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    802 AA;
                                                                                                                                                                                                N-PSDB; AAV64567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RPAQPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPAOPR
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                                   13-MAR-1997;
11-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-OCT-1997;
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11-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW64379;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              엄
                                                                                                                                                                                                                                                                           The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and prevention of Mycobacterium infection. The fusion proteins and the prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnosis, treatment and prevention of Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis to generate or monitoring of disease progression, as immunogens to generate or alicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human immal. Sequences of the invention are also used as vaccines. MTB32A fusion proteins of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tuberculosis, immunogenic; soluble, antigen, protective immunity, TB; vaccine, pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                              Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 324; DB 23; Length 66; 100.0%; Pred. No. 1e-35; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                   Claim 9; Page 123-124; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M. tuberculosis fusion protein TbF-2.
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                                                                                        Alderson M;
20-JUN-2000; 2000US-0597796.
01-FEB-2001; 2001US-265737P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 66, Conservative
                                                                                                                        WPI; 2002-147798/19.
N-PSDB; AAD28353.
                                                  (CORI-) CORIXA CORP
                                                                                        Reed S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPAQPR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPAQPR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TbRa3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9816646-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JAN-1999
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                                                                                        Skeiky Y,
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1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
                                                                                                                                                                                                                                            Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the fusion protein TbF-2 which is composed cimmunogenic polypeptides from Mycobacterium tuberculosis (MT). This protein is used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 324; DB 19; Length 802; 100.0%; Pred. No. 2.4e-34; ive 0; Mismatches 0; Indels 0
Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;
Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dillon DC, Houghton R, Lodes Mi
y YAW, Twardzik DR, Vedvick TS;
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                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 208-211; 230pp; English.
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This polypeptide comprises a fusion protein, designated TbF-2, composed of Mycobacterium tuberculosis antigens TbRa3 (see AAW64255), 38 kDa antigen (see AAW64364), Tb38-1 (see AAW64321) and DBEP (see AAW64322). It was produced by PCR amplification (see AAW44450-57) of the appropriate antigen DNA sequences, cloning into an expression vector, and expression in E. coli. TbF-2 can be used for serodiagnosis of tuberculosis. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising antigens or limmunogenic portions of M. tuberculosis antigens, or fusion proteins, DNA sequences encoding such polypeptides, recombinant expression vectors and host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VIDIIGTSPISWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis -
               New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tuberculosis, antigen, fusion protein, TbF-2, TbRa3, 38kD; Tb38-1, DPEP, diagnosis, therapy, vaccine, immunogen.
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                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 324; DB 19; Length 802; 100.0%; Pred. No. 2.4e-34; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis antigen fusion protein TbF-2.
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                                                                              Example 7; Page 223-226; 250pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY32063 standard; Protein; 802 AA.
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98US-0223040.
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                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
hes 66; Conservative
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                                                                                                                                                                                                                                                                                                                                           802 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypebtides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to
                                                                                                                                                                                                                                                                                                          0; Gaps
The start antigen fusion protein, termed TbF-2, composed of the antiger TbRa3, 39kD, Tb38-1 and DPBP. The fusion protein is expressed in the color carrying a polynucleotide (see AAZ20198) comprising the 4 coding sequences. The invention provides fusion proteins (see AAY32059-71) containing at least 2 M tuberculosis antigens. The new fusion proteins and polynucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed), detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
                                                                                                                                                                                                                                                                         Length 802;
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i, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M. tuberculosis fusion protein TbF-6 amino acid sequence.
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                                                                                                                                                                                                                                                                       100.0%; Score 324; DB 20;
100.0%; Pred. No. 2.4e-34;
ive 0; Mismatches 0;
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Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 37; Page 271-273; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY39224 standard; Protein; 802 AA.
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98US-0025197.
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Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                          66; Conservative
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N-PSDB; AAZ19457.
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Best Local Similarity
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                                                                                                                                                                                                                                     802 AA;
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                                                                                                                                                                                                      components.
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Gaps

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Indels

Length 802;

Sequence

Query Match Matches.

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9 VIDIIGTSPTSWEQAAABAVQRARDSVDDIRVARVIBQDMAVDSAGKIIYRIKLEVSFRM 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M tuberculosis infection in biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigen; diagnosis; detection; infection; antibody; immunisation; vaccine; immunity.
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100.0%; Pred. No. 2.4e-34;
ive 0; Mismatches 0;
                 100.0%; Score 324; DB 20; 100.0%; Pred. No. 2.4e-34;
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YAW, Twardzik DR,
                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  M tuberculosis fusion protein TbF-6.
                                                                                                                                                                                                                                                                                                                          AAY39081 standard; Protein; 802 AA
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98US-0024753.
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Lodes MJ, Reed SG, Skeiky
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                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                      Similarity
66; Conserv
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Best Local S
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Matches
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M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion tuberculosis-immune subjects. AAZ19245 to AAZ19460 and AAX39083 to AAX39225 are used in the exemplification of the present invention.
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                                                                                                                                                                                                        Gaps
M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ1949 to AAZ19460 and AAX39083 to AAX39225 are used in the exemplification of the present invention.
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skin tests and protective or therapeutic vaccines or compositions
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                                                                                                                                                                 Length 802;

 M. tuberculosis fusion protein TbF-2 amino acid sequence.

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                                                                                                                                                               100.0%; Score 324; DB 20; 100.0%; Pred. No. 2.4e-34;
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YAW, Twardzik DR,
                                                                                                                                                                                                        0; Mismatches
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Lodes MJ, Reed SG, Skeiky
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98US-0025197.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                        66; Conservative
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RPAQPR 74
                                                                                                                                                                                  Local Similarity
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                                                                                                                          802 AA;
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18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-NOV-1999
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Synthetic

AAY39176;

69

g ò 0

Gaps

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Indels

Sequence

Length 802;

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RESULT 15

us-09-688-672a-6.rag

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This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                       Antigen; diagnosis; detection; infection; antibody; immunisation; vaccine; immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                            Houghton R;
R, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                            Campos-Neto A, Dillon DC, Hendrickson RC, Ho
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 10; Page 251-253; 323pp; English.
                                                                                           M. tuberculosis fusion protein TbF-2.
             AAY39033 standard; Protein; 802 AA.
                                                                                                                                                                                                                                                                        98US-0072596.
98US-0024753.
                                                                                                                                                                                                                                               99WO-US03265
                                                                                                                                                               Mycobacterium tuberculosis
                                                               05-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-527416/44.
N-PSDB; AAZ19156.
                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          802 AA;
                                                                                                                                                                                        WO9942118-A2
                                                                                                                                                                                                                                              17-FEB-1999;
                                                                                                                                                                                                                                                                        05-MAY-1998;
18-FEB-1998;
                                                                                                                                                                                                                   26-AUG-1999.
                                       AAY39033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
AAY39033
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ó Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
Matches 66; Conservative 0; Mismatches 0; Indels 0. g à

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61 RPAQPR 66

RPAQPR 74

Search completed: November 21, 2003, 16:03:12 Job time : 4.99592 secs

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Sequence 37, Appl Sequence 10, Appl Sequence 10, Appl Sequence 314, App Sequence 329, App Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appli Sequence 239, Appli Sequence 239, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 77, Appl
Seguence 78, Appl
                                                                                                 November 21, 2003, 16:08:22 ; Search time 2.57415 Seconds (without alignments) 4680.740 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                      US-09-688-672A-6
324
1 VIDIIGTSPTSWEQAAAEAV.......KITYRIKLEVSFKMRPAQPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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2 US-10-133-002-78
2 US-10-133-012-78
2 US-10-20-84-843-214
2 US-10-084-843-214
2 US-10-193-002-346
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2 US-10-193-002-346
2 US-10-193-002-346
3 US-10-16-225A-63
5 US-10-16-225A-63
6 US-10-115-20
6 US-10-115-20
7 US-10-115-20
7 US-10-115-20
7 US-10-115-20
7 US-10-0815-213952
7 US-10-0815-213952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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Maximum DB seq
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
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                                                                                                        Run
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Sequence 1264, Ap. Sequence 97, Appl Sequence 97, Appl Sequence 106, Appl Sequence 106, Appl Sequence 108, Appl Sequence 172, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1855, Appl Sequence 1857, Appl Sequence 1855, Appl Sequence 1857, Appl Sequence 1855, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Ap
                                                                                                                                                                                                                                                                                                                                                             Sequence 44, Appl
Sequence 12054, A
Sequence 4, Appli
Sequence 6, Appli
Sequence 8, Appli
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6,
Sequence 8,
                                      5 US-10-198-070-98

5 US-10-198-070-97

2 US-10-198-070-97

2 US-10-198-070-108

5 US-10-198-070-108

5 US-10-198-070-108

5 US-10-198-070-63

5 US-10-198-070-63

5 US-10-198-070-108

6 US-10-188-071-1

7 US-10-188-070-108

10 US-09-981-947A-7

5 US-10-188-070-108

6 US-10-188-070-12

10 US-10-188-070-12

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10 US-10-188-070-12

10 US-10-188-070-16

10 US-10-185-081-6

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10 US-10-185-081-6

10 US-10-185-081-6

10 US-10-185-081-6

10 US-10-183-219-4
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## ALIGNMENTS

```
APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos.Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardick, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
CONTRY: USA
CONTRY: USA
CONTRY: USA
CONTRY: USA
CONTRY: USA
CONTRY: USA
CONTRY: USA
CONTRY: USA
CONTRY: USA
CONTRY: USA
CONTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
COMPUTER: PEN PC compatible
COMPUTER: PEN PC compatible
COMPUTER: PEN PC compatible
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FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                      Sequence 77, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
RESULT 1
US-10-084-843-77
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
TILLE REFERENCE: 014058-009020US
                                                                                                                                                                                                                                          1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 60
                                                                                                                                                                                                                                                                           1 VIDIIGTSPISWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Graderian, Jeffrey
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-0120100S
CURRENT APPLICATION NUMBER: 105/10/098,732A
CURRENT FILING DATE: 2003-04-29
                                                                                                                                                                                                  Gaps
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                                                                                                                                                Query Match
100.0%; Score 324; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.7e-35;
Matches 66; Conservative 0; Mismatches 0;
                                                    TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 78:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/287,849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 37
LENGTH: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37, Application US/10098732A
Publication No. US20030175294A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/09287849
Patent No. US20020009459A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                  STRANDEDNESS: single
         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
COTHER INFORMATION: TDRa3
US-10-098-732A-37
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US-09-287-849-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
US-10-193-002-78
US-10-193-002-78
Sequence 78, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos Neto, Autonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Rohald C.
Hendrickson, Rohald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                      ·
0
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FLING DATE: 10-Jul-2002
CLASSIFICATION NUMBER: US/09/072,596
FILING DATE: CASSIFICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6200 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 324; DB 12; Best Local Similarity 100.0%; Pred. No. 1.7e-35; Matches 66; Conservative 0; Mismatches 0;
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOWAUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                 ; TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 77: US-10-084-843-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               682-6031
                                                                                                                                                                    LENGTH: 66 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 66 amino acids
                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Washington
COUNTRY: USA
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1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
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Lodes, Michael J.
Hendrickson, Ronald C.
HITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
                                                                                                                                                                                                                                                                                                                                  Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPES: FLOPPY disk

MEDIUM TYPES: FLOPPY disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

PILING DATE: 25-Feb-2002

CLASSIFICATION: vUNNER: US/10/084,843

FILING DATE: 25-Feb-2002

CLASSIFICATION NUMBER: US/09/072,967

FILING DATE: 05-MAY-1998

ATPORNEY/AGENT INFORMATION:

NAME: MAKI, David J.

RECISTRATION NUMBER: 31,392

REFERENCE/DOCKET WUMBER: 210121.411C9

TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 324; DB 12; Best Local Similarity 100.0%; Pred. No. 3.8e-34; Matches 66; Conservative 0; Mismatches 0,
               210121.41109
                                                                                                                                                         LENGTH: 802 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 351, Application US/10084843 Publication No. US20030143243A1 GENERAL INFORMATION:
                               TELECOMMUNICATION INFORMATION TELEPHONE: (206) 622-4901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 351:
SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
TYPE: amino acid
                                                                             TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 214: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
STATE: Washington
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence:tetra-fusion US-09-287-849-10
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Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
HITLE OF INVENTION: COMPOUNDS FOR IMMUNO'
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-34; Matches 66; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
CURRENT FILING DATE: 1999-04-07

PRIOR APPLICATION NUMBER: US 08/818,112

PRIOR FILING DATE: 1997-03-13

PRIOR FILING DATE: 1997-0-01

PRIOR PILING DATE: 1997-10-01

PRIOR PILING DATE: 1997-0-01

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-04-07

PRIOR FILING DATE: 1998-04-07

PRIOR FILING DATE: 1998-04-07

PRIOR FILING DATE: 1998-04-07

PRIOR FILING DATE: 1998-12-30

NUMBER OF SEQ ID NOS: 46

SEQ ID NO 10

LENGTHARE: PATCHTIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 214, Application US/10084843; Publication No. US20030143243A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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JS-10-193-002-346
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Matches
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Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Romald C.
TILLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 324; DB 12; Length 802; 100.0%; Pred. No. 3.8e-34;
                                                                                                               Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIF: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORM:
MEDIUM TYPE: FLORM:
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC COMPAINS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                 Score 324; DB 12;
Pred. No. 3.8e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 351:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 209: US-10-193-002-209
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 209, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skeiky, Yasir A.W. Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
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NAME: Maki, David J.
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STRANDEDNESS: single
                                                                                                               100.0%;
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Seattle
STATE: Washington
                                                                                                                                                      66; Conservative
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                                                                                                               Query Match
Best Local Similarity
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Best Logal Similarity
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                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
US-10-193-002-209
                                                                        US-10-084-843-351
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Matches
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                                                                                      9 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 68
                                            1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDWAVDSAGKITYRIKLEVSFKM
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                           Skeiky, Yasir A.W.

Skeiky, Yasir A.W.

Dillon, Davin C.

Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.

Twardzik, Daniel R.

Lodes, Michael J.

Hendrickson, Romald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATIÓN NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION UNBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO: 346:
US-10-193-002-346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                    Sequence 346, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 802 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                            Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Maki, David J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206) 68
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPOLOGY: linear
Conservative
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Reed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                        61 RPAQPR 66
                                                                                                                                                                                     69 RPAQPR 74
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; LENGTH: 342
; TYPE: PRT
ORGANISM: Rickettsia prowazekii
US-10-166-225A-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Microsoft Office 97
SEQ ID NO 154
LENGTH: 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRGANISM: Zea mays
US-10-078-770-154
                                                                                                                                                                                    :|
272 SG 273
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                                             1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: Description of Artificial Sequence:tetra-fusion
US-10-359-460-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

100.0%; Score 324; DB 12; Length 802;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
Matches 66; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-166-228A-63

Sequence 63, Application US/10166225A

Publication No. UG20030148416A1

GENERAL INFORMATION:
APPLICANT: BERRY, Alan
APPLICANT: HUBBELL, Werner
APPLICANT: HUBBELL, Warner
APPLICANT: HUBBELL, Warner
APPLICANT: HOPEZ-ULIBERRI, Rual
APPLICANT: YELISEW, Alexei A.
TILE OF INVENTION: INPROVED ISOPRENOID PRODUCTION
FILE REFERENCE: C38435/121966
CURRENT APPLICATION NUMBER: US/10/166,225A

CURRENT FILING ADTE: 2002-06-05
NUMBER OF SEQ ID NOS: 197

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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RPAQPR 74
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(+)-Delta-Cadinene-8-Hydroxylase Gene from Cotton
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US-10-080-170-539

US-10-080-170-539

SEQUENCE 539, Application US/10080170

Publication No. US20030129601A1

SEGNERAL INFORMATION:
THILE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR

TITLE OF INVENTION: IDEMTIFYING TRAGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR

TITLE OF INVENTION: USBWIFFING TRAGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR

TITLE OF INVENTION: 120495.018

FILE REFERENCE: 03495.0218

CURRENT FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: 60/270,123

PRIOR FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 652

SOFTWARE: PATCHIN Ver. 2.1
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                                Gaps
                                                                                8 SPISWEQAAAEAVQRARDSVDDIRVARVIEQDMA-VDSAGKITYRIKLEVSFKMRP 62
                                                                                                                25 SPMSW-----IERIKSNITPTRKASIPEGVWTKCDSCGOVLYRAELERNLEVCP 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
18.5%; Score 60; DB 14; Length 535;
Best Local Similarity 28.2%; Pred. No. 23;
Matches 22; Conservative 15; Mismatches 23; Indels
                                20; Indels
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                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chen, Xiao-ya APPLICANT: Chen, Xiao-ya APPLICANT: Luo, Ping APPLICANT: Luo, Ping APPLICANT: Luo, Ping TITLE OF INVENTION: CDNA Clone of (+)-Delta FILE REFERENCE: 006602-113
CURRENT APPLICATION NUMBER: US/10/067,534
CURRENT FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: US 60/267,160
PRIOR PILICANTON NUMBER: US 60/267,160
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 WEQAAAEAVQRARDSVDDIRVARVIEQDMA 41
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ilarity 43.3%; Pred. No.
Conservative 7; Mismato
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ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                Sequence 2, Application US/10067534
Publication No. US20020187538A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 RYLDAAVKETFRLHPPMP 397
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Essenberg, Margaret K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 TY-RIKLEVSFKMRPAQP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Gossypium arboreum
                                16; Conservative
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Best Local Similarity
Matches 13; Conserv
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LENGTH: 535
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APPLICANT: Gusyatiner, Mikhail M
APPLICANT: Rostova, Yulia G
APPLICANT: Yampolskaya, Tatyana A
APPLICANT: Yampolskaya, Tatyana A
APPLICANT: Yampolskaya, Tatyana A
TITLE OF INVENTION: New Mutant Carbamoylphosphate
TITLE OF INVENTION: Compounds Derived from Carbamoylphosphate
TITLE APPLICANTON NUMBER: US/10/210,115
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: RU 2001-121697
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 IDIIGTSPTSWEQAAAEAVQRARDSVDDIRV----ARVIEQDMAVDSAGKITYRIKLEV 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Xu H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
19.0%; Score 61.5; D:
Best Local Similarity 29.0%; Pred. No. 35;
Matches 18; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE KEPEAGACHE ELITARA ULIA
CURRENT PEDELICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PELLING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/205
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-12-2
PRIOR FILING DATE: 2000-12-2
PRIOR FILING DATE: 2000-12-2
PRIOR FILING DATE: 2001-12-2
PRIOR FILING DATE: 2001-12-2
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASLESEQ for Windows Version 4.0
SEGITARE: 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13952, Application US/09815242
Patent No. US20020061569A1
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28.6%;
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APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT;
CRGANISM: Escherichia coli
US-10-210-115-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Salmonella typhi
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Best Local Similarity
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Search completed: November 21, 2003, 16:38:11 Job time : 2.57415 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                        Run on:
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November 21, 2003, 15:57:31 ; Search time 1.37687 Seconds (without alignments) 4609.825 Million cell updates/sec 324 1 VIDIIGTSPTSWEQAAAEAV......KITYRIKLEVSFKWRPAQPR 283308 segs, 96168682 residues Gapop 10.0 , Gapext 0.5 US-09-688-672A-6 **BLOSUM62** Scoring table: Perfect score: Sequence: Searched: Title:

283308 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

LES	Description	probable protein	tical	ica	hypothetical prot	carbamoy1-phospha	carbamoy1-phosphat	transcription regu	hypothetical prot	carotenoid biosynt	flagellin [import	protein kinase -	cobM protein - Pse	El protein - huma	beta-glucosidase (	carbamoy1-phosphe	tumor supressor I	hypothetical prote	myosin-RhoGAP pro	carbamoy1-phosphe	hypothetical prote	cell division pro	hypothetical prote	ransport	probable Helix-tur	desmin - African	ABC transporter,	probable leucyl-t	acetyl-CoA acetylt	, ,
SUMMAKIES	Ω	F70833	E84298	B83641	D95850	D90633	C85484	AE1822	C71704	H97792	AD3528	849313	H36145	W1WL18	S08243	SYECCP	T13797	H84227	T31099	AE0510	\$23604	AF2652	C97434	H69803	C70867	355	H69382	269	AH2916	
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A39127	S15193	T13283	D86468	H70785	T08523	832177	T03461	F84225	A23662	T46858	F86185	G02864	A36629	F84946	D87564
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505	202	1221	121	361	559	559	881	395	1576	394	441	481	501	1079	423
18.2	18.2	18.2	18.1	18.1	18.1	18.1	18.1	17.9	17.9	17.7	17.7	17.7	17.7	17.7	17.6
5 6	50	50	58.5	58.5	58.5	58.5	58.5	28	28	57.5	57.5	57.5	57.5	57.5	57
30	31	32	33	34	35	36	37	38	90	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

F70833
probable protein tansport protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C,Accesion: F70833
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A, Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome :
A; Reference number: A70500; MUID: 98295987; PMID: 9634230
A; Accession: F70833
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A, Molecule type: DNA
A; Residues: 1-71 < COL>
A; Cross-references: GB: AL021931; GB: AL123456; NID: 93261526; PIDN: CAA17385.1; PID: e1252494
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: sec

0; Gaps Query Match 100.0%; Score 324; DB 2; Length 71; Best Local Similarity 100.0%; Pred. No. 5e-30; Matches 66; Conservative 0; Mismatches 0; Indels

.. 0

9 65 6 VIDIIGTSPTSWEQAAABAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 61 RPAQPR 66 ઠ

RESULT 2

66 RPAQPR 71

DP.

E84298

Lower Paralyse Halobacterium Sp. NRC-1
C;Species: Halobacterium Sp. NRC-1
C;Species: Halobacterium Sp. NRC-1
C;Species: Halobacterium Sp. NRC-1
C;Species: Halobacterium Sp. NRC-1
C;Species: Halobacterium Sp. NRC-1
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001
C;Accession: E84298
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T.2176-12181, 2000
A;Nuthors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lianthors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lianthors: Draininary
A;Reference number: A84160; MuID:20504483; PMID:11016950
A;Accession: E84298
A;Ketatus: preliminary
A;Nelecule type: DNA
A;Residues: 1-77 <STO>

us-09-688-672a-6.rpr

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Page

4

Gaps

18;

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Carbamoyl-phosphate synthase large subunit [imported] - Escherichia coli (strain O157:H7, Cipecies: Escherichia coli (strain O157:H7, Cipecies: Escherichia coli (strain O157:H7, Cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia cipecies: Escherichia coli (cipecies: Escherichia coli (cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Escherichia cipecies: Esch
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A;Molecule type: DNA
A;Residues: 1-1073 <HAY>
A;Cress_references: GB:BA000007; PIDN:BAB33459.1; PID:g13359492; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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Pred. No. 27;
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Pred. No.
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Best Local Similarity 30.6%;
Matches 19; Conservative 1
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Best Local Similarity
Matches 19; Conserv
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C85484
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R,Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathon, A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: B83641

A;Accession: D83641

A;Residues: 1-71 <STO
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           GB:AE004437; NID:g10580943; PIDN:AAG19753.1; GSPDB:GN00138
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31.2%; Score 101; DB 2; L
Best Local Similarity 31.1%; Pred. No. 0.00013;
Matches 19; Conservative 22; Mismatches 20;
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Best Local Similarity
Matches 15; Conserv
A,Cross-references:
C,Genetics:
A,Gene: VNG1446H
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Carbamoyl-phosphate synthase large subunit (imported) - Escherichia coli (strain O157:H7, C) Species: Escherichia coli (c) Species: Escherichia coli (c) Species: Escherichia coli (c) Species: Escherichia coli (c) Species: Escherichia coli (d) Species: Escherichia coli (d) Species: Escherichia coli (d) Species: Escherichia coli (d) Species: Escherichia (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d) Species: (d
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A;Cross-references: GB:AE005174; NID:g12512719; PIDN:AAG54335.1; GSPDB:GN00145; UWGP:2003
A;Experimental source: strain 0157:H7, substrain EDL933
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A;Gene: carB
A;Gene: carB
C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; biotin
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        Gaps
        7
19; Indels
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Mismatches

17;

19; Conservative

Matches

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Hagelin [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AD3528
C;Accession: AD3528
E; Selkov, E.; Elzer, P.H.; Hagius, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc Proc. Natl. Acad. Sci. US.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens: A;Reference number: AD3252; PMID:11756688
A;Accession: AD3528
A;Accession: AD3528
A;Accession: AD3282
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C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Bacession: S52076; S49313
R;Wetterauer, B.W.; Hamker, U.; von Haeseler, A.; MacWilliams, H.K.; Simon, M.N.; Veron, Biochim. Biophys. Acta 1265, 97-101, 1995
A;Title: A protein kinase from Dictyostelium discoideum with an unusual acidic repeat don A;Reference number: S52076; MUID:95161460; PMID:7857991
                                                                                                                                                                                  (strain Malish
                                                                                                                                                         Carotenoid biosynthesis proteins homolog [imported] - Rickettsia conorii (strain Maracarotenoid biosynthesis proteins homolog [imported] - Rickettsia conorii (strain Maracarotesia s10-sep-2001 #sequence_revision 30-sep-2001 #text_change 22-Oct-2001 C;Accession: H97792 R;Ogata, H; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, IS-Cience 233, 209-2038, 2001 Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;Accession: H97792 A;A
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Pred. No. 15;
6; Mismatches 18; Indels
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25.8%; Pred. No. 13;
ive 13; Mismatches
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Best Local Similarity 36.8%;
Matches 14; Conservative
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SG 273
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A; Map position: II
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C.Special Secondary PCC 7120
A;Note: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AEIB82
R;Kaneko, T.; Nakamura, Y.; Nolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: ABIB07; MUDD:21595285, PMID:11759840
A;Actuale type: DNA
A;Residues: 1-96 <KUR>
A;Residues: 1-96 <KUR>
A;Cross references: GB:BA000019; PIDN:BAB77649.1; PID:g17135103; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Genetics:
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A;Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14909.1; PID:g38610G
C;Genetics:
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Cyspecias: Rickettsia prowazekii
Cyspecias: Rickettsia prowazekii
Cybate: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
CyAccession: C71704
RyAndersson, S.G.B.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A; Andersson, S.G.B.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A; Reference number: A71630; MUID:99039499; PMID:9823893
A; Reference number: A71630; MUID:99039499; PMID:9823893
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-342 < AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A; AND-A
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                                                                                                                     2 IDIIGTSPTSWEQAAAEAVQRARDSVDDIRV----ARVIEQDWAVDSAGKITYRIKLEV 56
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            Gaps
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19.6%; Score 63.5; DB 2; Length 342;
Best Local Similarity 25.8%; Pred. No. 13;
Matches 16; Conservative 14; Mismatches 13; Indels 13
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19; Indels
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Best Local Similarity 26.7%
Matches 16; Conservative
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SY 718
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107 TELSP 111
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                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                           A)Introns: 35/3; 104/1; 166/2
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homold
C;Reywords: ATP
F;20-281/Domain: protein kinase homology «KIN»
F;28-36/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cispedies: Pseudomonas sp.

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C'Species: human papillomavirus type 18
C'Date: 30-89-1987 #sequence_revision 30-8ep-1987 #text_change 16-Jul-1999
C'Accession: C26465, C26251
S'Seedorf, K.; Oltersdorf, T.; Kraemmer, G.; Roewekamp, W.
BMBO J. 6, 139-144, 1987
A;Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16
A;Reference number: A91068; MUID:87218459; PMID:3034571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Accession: C26165
A,Molecule type: DNA
A,Residues: 1-274 <SEE>
A,Residues: 1-274 <SEE>
A,Cross-references: GB:X04773; NID:g60876; PIDN:CAA28468.1; PID:g60879
A,Cross-references: GB:X04773; NID:g60876; PIDN:CAA28468.1; PID:g60879
B,Cole, S.T.; Danos, O.
A, Molle Biol. 193, 599-608, 1987
A,Title: Nucleotide sequence and comparative analysis of the human papillomavirus type
A,Reference number: A92937; MUID:87283862; PMID:3039146
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A,Accession: S52076
A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-1094 <ME2>
A,Cross-references: EMBL:Z37991; NID:g551445; PIDN:CAA86053.1; PID:g551446
C,Genetics:
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68;
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Best Local Similarity 30.0%
Matches 15; Conservative
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A;Residues: 1-657 <COL>
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A;Molecule type: DNA
A;Residues: 1-1073 <YUR>
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A;Residues: 1-1073 <YUR>
A;Residues: 1-1073 <YUR>
A;Residues: 1-1073 <YUR

A;Residues: EMBL: Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collanter, F.; Rose, D.U.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Reference number: A64724
A;Retus: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5) large chain (validated) NyAlternate names: carbamoyl-phosphate synthetase (glutamine-hydrolyzing) ammonia chain (species: Bscherichia coli cipate synthetase (glutamine-hydrolyzing) ammonia chain cipate: 19-Feb-1984 #sequence revision 31-Dec-1991 #text_change 01-Mar-2002 (species: A01198; S40556; A64724) Proc. Natl. Acad. S40556; A64724 (species: A01198; S40556; A64724) Accession: A01198; S40556; A64724 (species: A01198; A11047) Acad. Sci. U.S.A. 80, 4629-4633, 1983 Applicated gene coding for the large subunity Application: A01198 MUID:83273669; PMID:6308632 Applicated type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Residues: 1-1073 cNVU>
A.Rossidues: 1-1073 cNVU>
A.Rossidues: 1-1073 cNVU>
A.Roross-references: GB:001597; NID:g145461; PIDN:AAA23539.1; PID:g145464

R.YUNE, T.; Nori, H.; Nagai, H.; Nagais, T.; Ishihama, A.; Fujita, N.; Isono, K.; Mizobuc submitted to the EMBL Data Library, December 1992
A.Resforton: Systematic sequencing of the Escherichia coli genome: analysis of the 0-2.
A.Reference number: 840531
A.Accession: 840556
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                                                                                                                                                                                                                                                                                                                                57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Ruminococcus albus
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 15-Oct-1999
C;Accession: S08243
                                                                                                                                                                                                                                                                                                                                1 VIDIIGTSPISWEQA---AAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVS
                                                                                                                                                                                                                                                   Gaps
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Nucleic Acids Res. 18, 671, 1990
A;Title: DNA sequence of a beta-glucosidase from Ruminococcus albus.
A;Reference number: S08243; MUID:90175009; PMID:2106673
A;Accession: S08243
A;Accession: DNA
A;Molecule type: DNA
A;Residues: 1-947 < CHM>A;Residues: 1-947 < CHM>A;CNS-references: EMBL:XIS415; NID:g45967; PIDN:CAA33461.1; PID:g45968
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
A,Cross-references: GB:X05015, NID:g60975; PIDN:CAA28666.1, PID:g60978 C,Superfamily: papillomavirus El protein C,Keywords: early protein
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m
                                                                                                                                                              Length 657;
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                                                                                                                                                                                                                                               29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            beta-glucosidase (EC 3.2.1.21) - Ruminococcus albus
                                                                                                                                                              19.0%; Score 61.5; D 29.2%; Pred. No. 44; ive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.0%; Score 61.5; D
llarity 33.3%; Pred. No. 66;
Conservative 11; Mismatches
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A;Residues: 1-1073 <br/>
A;Cross-references: GB:AE000113; GB:U00096; NID:92367095; PIDN:AAC73144.1; PID:91786216;<br/>
A;Experimental source: strain K-12, substrain MG1655<br/>
C;Genetics:<br/>
A;Gene: carB<br/>
A;Gene: carB<br/>
A;Gene: carB<br/>
A;Gene: carB<br/>
A;Gene: carB<br/>
A;Gene: carB<br/>
A;Gene: carB<br/>
A;Gene: carbonovl-posphate by the large chain (PIR:SYECCP) and small chain (PIR:SYECCS) [validated C;Function:<br/>
C;Function:<br/>
A;Description: EC 6.3.5.5 [validated, MUID:83273669]; catalyzes formation of carbamcyl-prosphate by the large chain encleotide biosynthesis<br/>
C;Function:<br/>
A;Peathway: glutamate metabolism; pyrimidine nucleotide biosynthesis<br/>
C;Superfamily: carbamcyl-phosphate synthase (glutamine-hydrolyzing) large chain, biotin<br/>
C;Keywords: arginine biosynthesis; ATP; duplication, heterodimer; ligase; nucleotide bir<br/>
F;2-1073/Pomain: carbamcyl-phosphate synthase (glutamine-hydrolyzing) large chain homold<br/>
F;9-1053/Domain: biotin carboxylase homology AGC1><br/>
F;66-992/Domain: biotin carboxylase homology AC1><br/>
F;66-992/Domain: biotin carboxylase homology APC1><br/>
F;66-992/Domain: biotin carboxylase homology APC1><br/>
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19.0%; Score 61.5; DB 1; Length 10
Best Local Similarity 29.0%; Pred. No. 76;
Matches 18; Conservative 18; Mismatches 19; Indels
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Search completed: November 21, 2003, 16:09:52 Job time: 2.37687 secs |: SY 718 57 SF 58 717 ð d

Db

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

November 21, 2003, 15:51:11; Search time 0.778231 Seconds (without alignments) 3988.226 Million cell updates/sec Run on:

US-09-688-672A-6

324 1 VIDIIGTSPTSWEQAAAEAV.......XITYRIKLEVSFKMRPAQPR 66 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 Total number of hits satisfying chosen parameters: 127863 seqs, 47026705 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	escherichi	rickettsi			psend		P15885 ruminococcu	P00968 escherichia	Q9xh45 brassica ol	Q98915 rhizobium 1	Q8z9l7 salmonella	P14846 salmonella	Q9cph2 pasteurella	P23239 xenopus lae	Q9yd97 aeropyrum p	O70318 mus musculu	P22340 salmonella									homo sap		mycobact			Q8pvq1 methanosarc		ĕ
SUMMARIES		ΩI	CARB_ECO57	IDI2 RICCN	IDI2_RICPR	HUTU CAEEL	COBM_PSEDE	VE1 HPV18	BGLS RUMAL	CARB ECOLI	RS7 BRACL	IDIZ RHILO	CARB SALTI	CARB SALTY	K6PF_PASMU	DESM_XENLA	SYL AERPE	E412 MOUSE	SCRY SALTY	COBT MYCTU	E4L2 HUMAN	TRP4 MOUSE	TRP4 HUMAN	TRP4 RAT	TRP4_BOVIN	MYSH_ACACA	PANB RHILO	GTRS HUMAN	CARB_BUCAI	DP3A_MYCTU	VPI HAEIN	YSY1 CAEEL	SYC METMA	LEUI HAEIN	ASPH_BOVIN
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		Score	5.	63.5	щ	63		61.5	•	•	φ	٥.	60.5	o.	9	φ.	59.5	6	59	œ.	58.5	58	58	28	58	28	۲.	57.5	۲.	57	56.5	Ġ	56	56	56
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                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate. Tetramer of heterodimers (alpha, beta) 4 (By similarity). SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
18opentenyl-diphosphate delta-isomerase (EC 5.3.3.2) (IPP isomerase)
(Isopentenyl pyrophosphate isomerase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS, PRODOS, CORAGE.

TIGRAMS, TIGRO1369; CPSAGE.

TIGROTHE; PSO0866; CPSASE.1; 2.

PROSITE; PSO0867; CPSASE.2; 2.

Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; Argining Manganese; Complete proceome.

INIT MET 1 402 CARROXYPHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
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17; Mismatches 19; Indels
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EMBL; AE015640; AAM41696.1; --
EMBL; AE015640; AAM41696.1; --
EMBL; AE015640; AAM41696.1; --
EMBL; AE015040; AAM41696.1; --
EMBL; D90633; D90633.
HAMAP; MF 01210; --
InterPro; IPR006475; CarA_L glu.
InterPro; IPR005481; CPase_L D2.
InterPro; IPR005481; CPase_L D3.
InterPro; IPR005480; CPase_L D3.
InterPro; IPR00481; CPase_L D3.
InterPro; IPR00481; CPase_L D3.
InterPro; IPR00481; CPase_L D3.
InterPro; IPR00481; CPase_L D3.
InterPro; IPR00481; CPase_L D3.
InterPro; IPR00481; CPase_L D3.
InterPro; IPR00481; CPase_L D3.
IPEam; PF02789; CPSase_L D3; 1.
Pfam; PF02789; CPSase_L D3; 1.
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1072 AA; 117724 MW;
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AC Q92HM7;
DT 28-FEB-2003
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DT (1sopentenyl-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Indels 19; Gaps
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last amontation update)
18-PEB-2003 (Rel. 41, Last amontation update)
18opentenyl-diphosphate delta-isomerase (EC 5.3.3.2) (IPP isomerase)
(Isopentenyl pyrophosphate isomerase).
Rickettsia prowazekii.
                                                                                                                                                                                                                                                                                                                                                                                          "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                        Science 293:2093-2098(2001).

-!- FUNCTION: Catalyzes the 1.3-allylic rearrangement of the homoallylic substrate isopentenyl (IPP) to its allylic isomer, dimethylallyl diphosphate (DMAPP) (By similarity).

-!- CATALYTIC ACTIVITY: Isopentenyl diphosphate = dimethylallyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=Madrid E;
MEDLINE=99039499; PubMed=9823893;
Anderson S.G.E., Zomorodipour A., Anderson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
                                                                                                                                                                                                            STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
Rickettsia conorii.
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
NCBI_TaxID=781,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.6%; Score 63.5; DB 1; Length 342; 25.8%; Pred. No. 11; ive 13; Mismatches 14; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR, H97792, H97792.
HAMAP, WF 00354; -, 1.
INTENTY: IPROJ3009, FAN enzyme.
ISOMERASE, ISOPTENE bioSynthesis; Flavoprotein, FMN; NADP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 AA; 37336 MW; D346003CCD99B7A3 CRC64;
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Les 16; Conservative
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SEQUENCE 342 AA.
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                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VIDIIGTSPTSWEQAAAEAVQRARDS------VDDIRVARVIEQDMAVDS 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                      Nature 396:133-140(1998).

-!- FUNCTION: CATALYZES THE 1.3-ALLYLIC REARRANGEMENT OF THE HOMOALLYLIC SUBSTRATE ISOPENTENYL (IPP) TO ITS ALLYLIC ISOMER, DIMBERHYLALLYL DIFFUSCHATE (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: Isopentenyl diphosphate = dimethylallyl
genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                               / Match 19.6%; Score 63.5; DB 1; Length 342; Local Similarity 25.8%; Pred. No. 11; Nes 16; Conservative 14; Mismatches 13; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sulston J.E.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-! CATALYTIC ACTIVITY: 3 - (5 - oxo - 4, 5 - dihydro-3 - H-imidazol-4-
Yl)popanoate = urocanate + H(2)O.
-! COPACTOR: NAD (By similarity).
-! PATHWAY: Histidine degradation, second step.
-! SIMILARITY: BELONGS TO THE UROCANASE FAMILY.
                                                                                                       COFACTOR: FWN AND NADPH (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the IPP isomerase type 2 family.
                                                                                                                                                                                                                                                                                                HAWAP, MF 00354; -; 1.
InterPro; IPR003009; FMN enzyme.
Isomerase; Isoprene biosynthesis; Flavoprotein; FMN; NADP;
                                                                                                                                                                                                                                                                                                                                                      342 AA; 37363 MW; FE452A843CA1B950 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable urccannate hydratase (EC 4.2.1.49) (Urccanase)
(Imidazolonepropionate hydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        731 AA.
                                                                                                                                                                                                                                                                     EMBL; AJ235271; CAA14909.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                    C71704; C71704
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SG 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CBIF/COBM
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Crouzet J., Cameron B., Cauchois L., Rigault S., Rouyez M.-C., Blanche F., Thibaut D., Debussche L., "Genetic and sequence analysis of an 8.7-kilobase Pseudomonas dentrificans fragment carrying eight genes involved in transformation of precorrin-2 to cobyrinic acid."; J. Bacteriol. 172:5980-5990(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Precorrin-4 Cll-methyltransferase (EC 2.1.1.133) (Precorrin-3 methylase)
                                                                                                                                                                                                                                              Length 731;
                                                                         Pfam; PF01175; Urocanase; 1.
ProDom; PD025423; Urocanase; 1.
PROSITE; PS01233; UROCANASE; 1.
PROSITE; PS01233; UROCANASE; 1.
SEQUENCE 731 AA; 81523 MW; 891E1F61C9A604E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       687 GVTRRSWSGNAKAQEAIQRAEKQVDGLRVTLPVEAD 722
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                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                              Score 63;
Pred. No.
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InterPro; IPR000878; Cor/por Metransf.
InterPro; IPR003043; Uropor Metransf.
Pfam; PF00590; TP methylase; 1.
TIGRPAMs; TIGR01465; cobM cbiF; 1.
PROSITE; PS00839; SUMT_1; 1.
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MEDLINE=91008976; PubMed=2211521;
                                                   InterPro; IPR000193; Urocanase.
EMBL; AL132952; CAB61139.1; -. WormPep; Y51H4A.7; CE22333.
                                                                                                                                                                                                                                              19.4%;
41.7%;
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nes 15; Conservative
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Pfam; PF00519; E1; 1.
Pfam; PF00524; E1 N; 1.
Brarly protein; DNĀ replication; Helicase; ATP-binding; DNA-binding; Nuclear protein.
NP BIND 484 491 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruminococcus
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P15885;
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SEQÜENCE
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س
                                                                                                                                                                                                                                   4 IIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLE---VSFKM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schneider-Gaedicke A., Schwarz E.,
"Different human cervical carcinoma cell lines show similar
transcription patterns of human papillomavirus type 18 early genes.";
EMBO J. 5:2285-2292(1986).
-!- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
CONTAINS BINDING SITES FOR BOTH PROTEINS.
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequence and comparative analysis of the human papillomavirus type 18 genome. Phylogeny of papillomaviruses and repeated structure of the E6 and E7 gene products.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Terada M., Sugimura T.;
"Nuclectide sequences of cDNAs for human papillomavirus type 18
                                                                                                                                                              7;
PROSITE; PS00840; SUMT 2; 1.
Cobalamin biosynthesis; Porphyrin biosynthesis; Transferase;
Methyltransferase.
                                                                                                                   Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S.,
Terada M., Sugimura T.;
                                                                                                                ; Score 61.5; DB 1; Length 2
; Pred. No. 13;
14; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus type 18.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                   253 AA; 26862 MW; 50F5E6F5F67FF733 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           657 AA
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MEDLINE=88188247, PubMed=2833614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=87283882; PubMed=3039146;
Cole S.T., Danos O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-30 FROM N.A.
MEDLINE=87053870; Pubmed=3023067;
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EMBL, M20325; AAA99516.1; -.
EMBL, M26798; AAA46948.1; -.
PIR, C26165; WIWLL8.
InterPro, IPR001177; Papillom_E1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virol. 62:1640-1646(1988).
                                                                                                              19.0%;
                                                                                                    Query Match
Best Local Similarity 32.3%
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Replication protein El
                                                                                                                                                                                                                                                                                                                                             107 TPGVP 111
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P06789;
                                                                   SEQUENCE
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101 HP918
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                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Beta-glucosidase (EC 3.2.1.21) (Gentiobiase) (Cellobiase) (Beta-D-glucosida glucohydrolase).
Ruminococcus albus.
Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 EQAAABAVQRARDSVDDIRVARV--IEQDMAVDSAGKITYRIKLEVSFKMRPAQ
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"DNA sequence of a beta-glucosidase from Ruminococcus albus.";
Nucleic Acids Res. 18.671-671(1990).
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing be glucose residues with release of beta-D-glucose.
-!- PATHWAY: Cellulose degradation.
-!- SATHWAY: Celluloss TO FAMILY 3 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ω,
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                                                                                                                                        29; Indels
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94 94 T -> K (IN REF. 2).
657 AA; 73736 MW; B18E68BCEIDB330A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X15415; CAA33461.1; -.
PIR; S08243; S08243.
InterPro; IPR002772; Glyco hydro 3C.
InterPro; IPR001764; Glyco hydro 3N.
Pfam; PF01913; Glyco hydro 3; 1.
Pfam; PF01913; Glyco hydro 3; 1.
PRINTS; PR00133; GLHYDRLASE3 -.
PROSITE; PS00775; GLHYDRAL F3; 1.
                                                                                    DB 1;
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                                                                                                                                        14; Mismatches
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; Pred. No. 47;
11; Mismatches
                                                                                 19.0%; Score 61.5; I
29.2%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=F-40;
MEDLINE=90175009; PubMed=2106673;
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                                                                                                                                        19; Conservative
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                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                     107 TELSP 111
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MEDINE-84248072; PubMed-6330744;
Plette J., Wyunoya H., Lusty C.J., Cunin R., Weyens G., Crabeel M., Charlier D.R.M., Glansdorff N., Pierard A.;
"DNA sequence of the carA gene and the control region of carAB: tandem promoters, respectively controlled by arginine and the pyrimidines, regulate the synthesis of carbamoyl-phosphate synthetase in Bscherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                 MEDLINE=84248073; PubMed=6377309;
Bouvier J., Patte J.-C., Stragier P.;
"Multiple regulatory signals in the control region of the Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
MEDLINE=97317071; PubMed=9174345;
Thoden J.B., Holden H.M., Wesenberg G., Raushel F.M., Rayment I.;
"Structure of carbamoyl phosphate synthetase: a journey of 96 A from Substrate to product.";
Biochemistry 36:6305-6316(1997).
                                                                                                                                                                                                                                           Nyunoya H., Iusty C.J.;
"The carB gene of Escherichia coli: a duplicated gene coding for the
large subunit of carbamcyl-phosphate synthetase.";
Proc. Natl. Acad. Sci. U.S.A. 80:4629-4633(1983)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
STRAIDSALZ / MG165A.
STRAIDSALZ / MG167; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92334977; PubMed=1630901;

Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,

Yura T., Mizobuchi K., Nakata A.;

"Systematic sequencing of the Escherichia coli genome: analysis of
the 0-2.4 min region.";

Nucleic Acids Res. 20:3305-3308 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98301363; PubMed=9636022; Moden J. B., Miran S.G., Phillips J.C., Howard A.J., Raushel F.M., Holden H.M.; Carbamoyl phosphate synthetase: caught in the act of glutamine
                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Carbamcyl-phosphare synthase large chain (EC 6.3.5.5) (Carbamcyl-phosphate synthetase ammonia chain)
                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                     coli carAB operon.";
Proc. Natl. Acad. Sci. U.S.A. 81:4139-4143(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 81:4134-4138(1984).
                                              PRT; 1072 AA.
                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 1-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
                                                                                                                                                                                                                               MEDLINE=83273669; PubMed=6308632;
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                                              STANDARD;
                                                                                                                                  CARB OR PYRA OR B0033.
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                             Escherichia coli
                                                                                                                                                                                NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphate synthetese.";
J. Biol. Chem. 274:22502-22507(1999).

-! CATALYITY: ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.
-! CATALYITY: Arginine biosynthesis.
-! PATHWAY: Arginine biosynthesis.
-! PATHWAY: Pyrimidine biosynthesis; first step.
-! PATHWAY: Pyrimidine biosynthesis; elso glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by promotes the hydrolysis of glutamine to ammonia, which is used by Tetramer of heterodimers (alpha, beta)4.
-! SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE=20056035; PubMed=10597438;
Thoden J.B., Huang X., Raushel F.M., Holden H.M.;
"The small subunit of carbamoyl phosphate synthetase: snapshots along
                           X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
MEDLINE=99190825; PubMed=10089390;
Thoden J.B., Raushel F.M., Benning M.M., Rayment I., Holden H.M.;
"The structure of carbamoyl phosphate synthetase determined to 2.1-A resolution.";
                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
MEDLINE=99155207; PubMed=10029528;
Thoden J.B., Wesenberg G., Raushel F.M., Holden H.M.;
"Carbamoyl phosphate synthetase: closure of the B-domain as a result of nucleotide binding.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
The Span J. B., bubmed=10428826,
Thoden J.B., Raushel F.M., Wesenberg G., Holden H.M.;
"The binding of inosine monophosphate to Escherichia coli carbamoyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=20056035; Pubmed=10587438;
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ECOGENE; E010135; carB.
HAMAP, MF. 01210; -; 1.
InterPro; IPR006475; CarA_L_glu.
InterPro; IPR005479; CPase_L.
InterPro; IPR005483; CPase_L.D2.
InterPro; IPR005481; CPase_L.D3.
InterPro; IPR005481; CPase_L.D3.
InterPro; IPR005481; CPase_L.D3.
InterPro; IPR005481; CPase_L.D3.
InterPro; IPR005481; CPase_L.D3.
InterPro; IPR005481; CPase_L.D3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the reaction pathway.";
Biochemistry 38:16158-16166(1999).
                                                                                                                                                                                                                                                       Acta Crystallogr. D 55:8-24(1999).
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Biochemistry 37:8825-8831(1998).
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PDB; 14DB; 17-07UN-98.
PDB; 14DR; 21-0-07-98.
PDB; 1ERR; 26-40L-99.
PDB; 1CRB; 26-40L-99.
PDB; 1CRB; 20-40C-99.
PDB; 1CRB; 20-40C-99.
PDB; 1CRS; 21-DEC-99.
PDB; 1CRS; 21-DEC-99.
PDB; 1CRS; 21-DEC-99.
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                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                  CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
    Pfam; PF02142; MGS; 1.

PRINTS; PR00099; CPSASE.

TIGRPAMS; TIGKO1169; CPSASE.

PROSITE; PS00866; CPSASE.1; 2.

PROSITE; PS00867; CPSASE.2; 2.

Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; Arginine biosynthesis; Digase; Repeat; Arginine biosynthesis; Digase; Repeat; NIT MET 0 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
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MANGANESE 1.
MANGANESE 2.
MANGANESE 3.
MANGANESE 3.
                                                                                      (POTENTIAL).
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29.0%; Pred. No. 53;
:ive 18; Mismatches
PF02787; CPSase L D3; 1.
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Best Local Similarity
Matches 18; Conserv
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Brassica.
NCBI_TaxID=3712;
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SEQUENCE FROM N.A.

MEDLINE=21082930; PubMed=11214968;

Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,

Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,

Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,

Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                    οĘ
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Gossen K.K., Katavic V., Taylor D.C.;
Gossen K.K., Katavic V. a cDNA from microspore derived embryos o
"Nucleotide sequence of a cDNA from microspore derived embryos o
Brassica oleracea is homologous to 40S ribosomal protein S7.",
(In) Plant Gene Register PGR99-096.
-! SIMILARITY: BELONGS TO THE S7E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23; Indels 12;
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FNI OR WIR6371.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobianes,
Phyllobacteriaceae, Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
18.8%; Score 61; DB 1; Length 191;
Best Local Similarity 23.1%; Pred. No. 11;
Matches 15; Conservative 15; Mismatches 23; Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annocation update)
Isopentenyl-diphosphate delta-isomerase (EC 5
                                                                         Last sequence update)
Last annotation update)
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191 AA
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InterPro; IPR000554; Ribosomal S7E.
Pfam; PF01251; Ribosomal S7e; 1.
ProDom; PD006276; Ribosomal S7E; 1.
PROSITE; PS00948; RIBOSOMAL_S7E; FALSE_NEG.
                                                                                                                                                                        Brassica oleracea (Cauliflower).
                                                Created)
                                           28-FEB-2003 (Rel. 41, Crea
28-FEB-2003 (Rel. 41, Last
28-FEB-2003 (Rel. 41, Last
40S ribosomal protein S7.
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STANDARD;
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SEQUENCE 191 AA;
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68 RLRKA 72
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SEQUENCE
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                                                                                                                                                                               -!- COFACTOR: FWN and NADPH (By similarity).
-!- SUBCELLULAR LOCATION: Cycoplasmic (By similarity).
-!- SIMILARITY: Belongs to the IPP isomerase type 2 family.

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STRANIE-TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Hque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leacher S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                        DNA Res. 7:331-338 (2000).
-!- FUNCTION: Catalyzes the 1,3-allylic rearrangement of the homoallylic substrate isopentenyl (IPP) to its allylic isomer, dimethylallyl diphosphate (DMAPP) (By similarity).
-!- CATALYTIC ACTIVITY: Isopentenyl diphosphate = dimethylallyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Carbamoyl-phosphate synthase large chain (BC 6.3.5.5) (Carbamoyl-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.7%; Score 60.5; DB 1; Length 351; 53.6%; Pred. No. 23; cive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF_00354; -; 1.
InterPro; IPR003009; FMN_enzyme.
Isomerase; Isoprene biosynthesis; Flavoprotein; FMN; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 AA; 36531 MW; 680D504F53E588A3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphate synthetase ammonia chain)
CARB OR STY0077 OR T0068.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP003009; BAB52681.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     llarity 53.6%;
Conservative
                    Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
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les 15; Conserv
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658 VPVIGTSPDAIDR--AEDRERFQHAVDRLKLKQPANATVTAIEQAVEKAKEIGYPLVVRP 715
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J. Bacteriol. 185:2330-2337(2003).

-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + possible to the phosphate + L-glutamate + carbamoyl phosphate.

-!- COFACTOR: Binds 3 manganese ions per subunit (By similarity).
-!- PATHWAY: Arginine biosynthesis.
-!- PATHWAY: Pyrimidine biosynthesis, first step.
-!- PATHWAY: Pyrimidine biosynthesis, the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 IDIIGTSPTSWEQAAAEAVQRARDSVDDIRV----ARVIEQDMAVDSAGKITYRIKLEV
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BY SIMILARITY.
CARBOXPHOSPHATE SYNTHETIC DOMAIN.
OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; ATP-binding; Manganese; Complete proteome.

INIT MET 0 0 BY SIMILARITY.

DOMAIN 403 1 402 CARBANDYL PHOSPHATE SYNTHETIC DOMAIN.

DOMAIN 553 935 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
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ATP (POTENTIAL).

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ATP (POTENTIAL).

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MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

118009 MW; F69DE79502C4CD15 CRC64;
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                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE CARB FAMILY.
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29.0%; Pred. No. 68;
tive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AL627265, CAD01221.1;

EMML, AE016814, AAO67801.1;

HAMAP, MF_012010.1;

INCEPPO, IPR005495, CRAP, Glu.

INCEPPO, IPR005495, CRSE_L

INCEPPO, IPR005485, CRSE_L

INCEPPO, IPR005481, CRSE_L

INCEPPO, IPR005481, CRSE_L

INCEPPO, IPR005481, CRSE_L

Fam, PF00289, CPSSSE_L

PEam, PF02786, CPSSSE_L

PEam, PF02786, CPSSSE_L

PEAM, PF02786, CPSSSE_L

PEAM, PF02786, CPSSSE_L

PEAM, PF02786, CPSSSE_L

PEAM, PF02786, CPSSSE_L

PEAM, PF02786, CPSSSE_L

PEAM, PF02786, CPSSSE_L

PEAM, PF02786, CPSSSE_L

PROSITE, PS00866, CPSSSE_I

PROSITE, PS00866, CPSSSE_I, 2

PROSITE, PS00866, CPSSSE_I, 2

PROSITE, PS00866, CPSSSE_I, 2

PROSITE, PS00866, CPSSSE_I, 2
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P14846; P96067,
01-APR-1990 (Rel. 14, Created)
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Matches 18; Conserv
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us-09-688-672a-6.rsp

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Q9CPH2;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE=88329100; PubMed=2843375;

A Kilstrup M., Lu C.D., Abdelal A., Neuhard J.;

Invalentide sequence of the carA gene and regulation of the carAB
operon in Salmonella typhimurium.";

Eur. J. Biochem. 176:421-429(1988).

-! CATALITIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +
Dhosphate + L-glutamate + carbamoyl phosphate.

-! COFACTOR: Binds 3 manganese ions per subunit (By similarity).

-! CATALITIC ACTIVITY: CATABLASIS.

-! PATHWAY: Pyrimidine biosynthesis.

-! ATHWAY: Pyrimidine biosynthesis.

-! SUBUNIT: Composed of two chains; the small (or glutamine) chain
promotes the hydrolysis of glutamine to ammonia, which is used by
the large (or ammonia) chain to synthesize carbamoyl phosphate.
                                                                                                                                                                                                                                                                                                                               STRAIN=LTZ / SGSC1412 / ATCC 700720;
MEDLINE=11534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
"Complete genome sequence of Salmonella enterica serovar Typhimurium
               28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-
phosphate synthetase ammonia chain).
                                                                                                                       Bacteria; Próteobacteria; Gammaproteobacteria; Enterobacteriales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0098; CPSASE.
TIGREAMS; TIGRO1369; CPSASEII_lrg; 1.
PROSITE; PSO0866; CPSASE_1; 2.
PROSITE; PSO0867; CPSASE_2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
                                                                                                                                                                                                                                                 Lu C.D., Walthall D.A., Abdelal A.T.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
(Rel. 41, Last sequence update) (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, U81260; AAB39256.1; ---
EMBL, AE008696; AAL19031.1; ---
HSSP; P00968; 1A9X.
StyGene; SG10033; carB.
HAMAP; MF 01210; ---
InterPro; IPR006479; CarA Lglu.
InterPro; IPR006479; CarA Lglu.
InterPro; IPR006479; CPase_L.
InterPro; IPR006483; CPase_L.
InterPro; IPR006483; CPase_L.
InterPro; IPR006480; CPase_L.
InterPro; IPR006480; CPase_L.
InterPro; IPR006480; CPase_L.
InterPro; IPR006480; CPase_L.
InterPro; IPR006480; CPase_L.
InterPro; IPR004362; MGS_1%Re.
InterPro; IPR004362; MGS_1%Re.
InterPro; IPR004362; MGS_1%Re.
InterPro; IPR004362; MGS_1%Re.
InterPro; IPR004362; MGS_1%Re.
InterPro; IPR004362; MGS_1%Re.
InterPro; IPR004362; MGS_1%Re.
IPR0M; PP007786; CPSSSE_L.
IPR0M; PP007786; CPSSSE_L.
IPR0M; PP007786; CPSSSE_L.
IPR0M; PP007786; CPSSSE_L.
IPR0M; PP007786; CPSSSE_L.
IPR0M; PP007786; CPSSSE_L.
IPR0M; PP007786; CPSSSE_L.
IPR0M; PP007786; CPSSSE_L.
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IPR0M; PP007786; CPSSSE_L.
IPR0M; PP007786; CPSSSE_L.
IPR0M; PP007786; CPSSSE_L.
IPR0M; PP007786; CPSSSE_L.
IPR0M; PP007786; CPSSSE_L.
IPR0M; PP007786; CPSSSE_L.
IPR0M; PP007786; CPSSSE_L.
IPR0M; PP007786; CPSSSE_L.
IPR0M; PP007786; CPSSSE_L.
IPR0M; PP007786; CPSSSE_L.
IPR0M; PP007786; CPSS
                                                                                                                                                Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-7 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 413:852-856(2001)
                                                                                                      Salmonella typhimurium.
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                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=LT2;
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                                                                                                                                                                    NCBI_TaxID=602;
                                                                                    STM0067
                                                                                  CARB OR
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                                                                                                                                                                                                                                                                                                                                                                                                                                       658 VPVIGTSPDAIDR--AEDRERFQHAVDRLKLKQPANATVTAIEQAVEKAKEIGYPLVVRP 715
                                                                                                                                                                                                                                                                                                                                                                                                                   26
                                                                                                                                                                                                                                                                                                                                                                                                                   2 IDIIGTSPTSWEQAAAEAVQRARDSVDDIRV----ARVIEQDMAVDSAGKITYRIKLEV
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                       OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding; Manganese; Complete proteome.

INIT_MET 0 0 BY SIMILARITY.

DOMAĪN 1 402 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                          2 (BY SIMILARITY)
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
                                                                                                                                                                                                                                                                  SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                              20; Indels
                                                                                                                                                                                                                                                                                                      19243FECE2C8D5C7 CRC64;
                                                                                                                                                                                          SIMILARITY)
                                                                                                                                                                                                                                                  SIMILARITY)
                                                                                                                                                   321 AA
                                                                                                                                                                                                                                                                                                                                                                              17; Mismatches
                                                                                                                                                                                                                                                                                                                                                              68;
                                                                                                                                                                                                                                                                                                                                          Score 60.5;
Pred. No. 68
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HAWAP; MF 00339; -; 1.
Hardrop, IPR000023; Ppfruckinase.
Pfam; PF00365; PFK; 1.
PRINTS; PR00476; PHPRCTKINASE.
ProDom; PD000707; Ppfruckinase; 1.
                                                                                                                                                                                                                                                                                                        118007 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE006042; AAK02153.1; -.
                                                                                                                                                                                                                                                                                                                                            18.7%;
                                                                                                                                                                                                                                                                                                                                                              29.0%;
                                                                                                                                                                                                                                                                                                                                                                                18, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Phosphohexokinase).
PFKA OR PM0069.
                                                                                                                                                                                                                                                                                                    1074 AA;
                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                       403
553
936
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302
284
298
300
828
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SITE
SEQUENCE
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BINDING
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FI OS
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                                                                                                               20
                                                                                              3 DIIGTSPT----SWEQAAABAVQRARDSVDDIRVARVIE-----QDMAVDS--AGKITY
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=90032404; PubMed=2806128;
Herrmann H., Fouquet B., Franke W.W.;
"Expression of intermediate filament proteins during development of
"Expression of intermediate filament proteins during development of
desmin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Development 105:299-307(1989).

-!- FUNCTION: DESMIN ARE CLASS-III INTERMEDIATE FILAMENTS FOUND IN MUSCLE CELLS.

NUSCLE CELLS. IN ADULT STRIATED MUSCLE THEY FORM A FIEROUS NETWORK CONNECTING WYOFIBRILS TO EACH OTHER AND TO THE PLASMA MEMBRANE FROM THE PERIPHERY OF THE Z-LINE STRUCTURES.

-!- SUBJUIL: Homopolymer.

-!- SUBJUILS LOCATION: Cytoplasmic.

-!- SUMILARITY: BELONGS TO THE INTERNEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                             ch 18.5%; Score 60; DB 1; Length 321; Similarity 29.4%; Pred. No. 23; 20; Conservative 11; Mismatches 25; Indels 12;
PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.
Kinase; Transferase; Glycolysis; Complete proteome.
SEQUENCE 321 AA; 35025 MW; 4871609FECCAC91D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00038; filament; 1.
Pfam; PF00038; filament_head; 1.
PROSITE; PS00226; IF; 1.
Intermediate filament; Colled coil; Muscle protein.
DOMAIN 1 96 HEAD.
                                                                                                                                                                                                                                                      01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                 458
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TAIL.
COIL 1A.
LINKER 1.
COIL 1B.
LINKER 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COIL 2A.
LINKER 2.
COIL 2B.
                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A43554; A43554.
InterPro; IPR006821; Filament_head.
InterPro; IPR001664; IF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X16842; CAA34740.1; -.
                                                                                                                                                                    191 IVASEVEF 198
                                                                                                                                                                                                                                                                                                                                                      Xenopodinae; Xenopus.
NCBL_TaxID=8355;
                                                                                                                                              51 RIKLEVSF 58
                                                           Local Similarity
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P23239;
                                               Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                   PIR; H72699; H72699.

HAMMP; MF 00049; -; 1.
InterPro; IPR004493; Leu-tRNA-syntla.
InterPro; IPR004412; LRNA-synt_la.
InterPro; IPR001412; LRNA-synt_la.
InterPro; IPR00131; LRNA-synt_la.
IGRPAMS; TIGR00313; LRNA-synt_la.
IGRPAMS; TIGR003183; Leus Antra II.
Aminoacyl-tRNA synthétase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                  6 GTSPTSWEQAAAEAVQRARDSVDDI--RVARV-IEQDMAVDSAGKITYRIKLEVSFK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahasin M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagagi Y., Nishijima K., Nakazawa H., Yamazaki J., Xushida N., Oguci T., Tanaka T., Kudoh Y., Yamazaki J., Xushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura N., Nomura N., Sako Y., Kikuchi H.; Complete genome sequence of an aerobic hyper-thermophilic cranarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999)
--- CATALYITY: ATP + L-leuine + tRNA(Leu) = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diphosphate + L-leucyl-tRNA(Leu).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                    SYL AERPE STANDARD; PRT; 959 AA.

99YD91;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeurS).
LEUS OR APE1015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
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                                                                                  18.4%; Score 59.5; DB 1; Length 458; ilarity 31.6%; Pred. No. 38; Conservative 11; Mismatches 25; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
18.4%; Score 59.5; DB 1; Length 959;
Best Local Similarity 27.9%; Pred. No. 78;
Matches 17; Conservative 9; Mismatches 12; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aeropyrum pernix.
Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales,
Desulfurococcaceae, Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "KMSKS" REGION.
ATP (BY SIMILARITY).
1, 985CB5168728F7AB CRC64;
                             E96167E1D8FDEB74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---SWEQAABAVORAR---
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342 S
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641
640
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640 6
959 AA;
                          458 AA;
                                                                                        Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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833 VLSLIGGADTLVVTVAAEWKYRAVEAVRARERGASMKEALREAFKVEGVDKREAARLVQ 892

38 0 38

\$ 6

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893 Q 893

Search completed: November 21, 2003, 16:04:17 Job time : 1.77823 secs

Perfect score:

Seguence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

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Q8ydms brucella me
Q8tdms brucella su
Q8rpt1 legionella
Q239193 thizobium m
Q2362 thizobium m
Q9ac6 thizobium l
Q8t391 drosophila
Q8t391 drosophila
Q8t391 drosophila
Q8t10 escherichia
Q8t10 escherichia
Q8t10 escherichia
Q9vb52 drosophila
Q9vb52 drosophila
Q9vb52 drosophila
Q9vb52 drosophila
Q9vb54 kraceri
Q9vb54 kraceri
Q9v554 kraceri
Q9ag66 thizobium e
Q9z1n3 rattus norv
Q8x16 klebisiella
Q9x54 klebisiella
Q9x54 klebisiella
Q8j0z4 cryptococcu
Q8j122 cryptococcu
Q9rcz5 streptomyce
O39829 faba bean n
                                                                                       Q8x0k0 neurospora
Q8kpt8 synechococc
Q8jl22 virus phich
O52068 brucella ab
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STRIN=H97RV;

MEDLINE=982987; PubMed=9634230;

A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

A Badcock K., Perlwell T., Gantles S., Hamlin N., Holroyd S.,

A Hornsby, T., Jagels K., Krogh A., Mchean J., Moule S., Murphy L.,

A Hornsby, T., Jagels K., Krogh A., Mchean J., Moule S., Murphy L.,

A Nutter S., Seeger K., Skalton S., Squares R., Squares R.,

Suleton J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the

I complete genome sequence.",

I Nature 333:537-544(1998).

R Tuberculist; RV0379; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harris D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VIDIIGTSPTSWEQAAABAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Possible protein TANSPORT protein.
SEC OR RV0379 OR MTV036.14.
Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteriah, Actinobacteriah, Actinobacteriah, Actinobacteriah, Actinobacteriahes, Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 324; DB 16; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.5e-29;
Matches 66; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 AA; 7966 MW; 49526FDBCA9C3826 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 AA
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                       QBJ122
QBCZ5
QBXCX0
QBXDX0
QBXDT8
QBI122
OS2068
QBYDM5
QBFUS2
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Q8INJ2
Q8FQL4
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Q8FLB0
Q9VB52
Q76931
Q9HRH0
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Q9X754
Q9G064
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  Complete proteome. SEQUENCE 71 AA;
                                                                                                                                                 NCBI_TaxID=1773;
  053714
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Q75741 human immun
Q9ne33 leishmania
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                                                                                                                                                                                                                                                         324
1 VIDIIGTSPTSWEQAAAEAV.......KITYRIKLEVSFKORFPAQPR
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     - protein search, using sw model
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Result 8

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Q9HPW4;
01-MAR-2001 (TrEMBLrel: 16, Created)
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102
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Best Local Similarity
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61 PAQP 64
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Q9HPW4
ID Q9HP'
AC Q9HP'
DT 01-M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VIDIIGTSPISWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 60
  6 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 65
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 04, Last annotation update)
Hypothetical 7.2 kDa protein (Fragment).
Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
Corynebacteria, Actinobacteria, Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.5%; Score 319; DB 2; Length 116; 98.5%; Pred. No. 1e-28; tive 0; Mismatches 1; Indels
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STRAIN=TB patient sputum #NTI64719;
STRAIN=TB patient sputum #NTI64719;
Sao A.N., Vijaya S.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U85465; AAB58552.1; -
Hypothetical protein.
NOW TER
SEQÜENCE 65 AA; 7240 MW; 9939C19E2306FAIB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.
STRAIN-TB patient sputum #NTI64719;
Rao A.R., Vijaya S.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, U85467; AABS8554.1; -.
Hypothetical protein.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 AA; 12673 MW; DF56D2FF0B479896 CRC64;
                                                                                                                                                                                                                                                            01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 04, Last annotation update)
Hypothetical 12.7 kDa protein (Fragment).
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 AA
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Matches 65; Conservative
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                                                    RPAOPR
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                                                                                                                                                                 Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
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Pred, No. 2e_08;
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Satchidanandam V., Rama Rao A., Hegde S.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF001301; AAB54027.1; -.
Hypothetical protein.
NON_TER 110 110
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Satchiddanandam V., Rama Rao A., Hegde S.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF001302; AABS4028.1; -.
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110 AA; 11903 MW; A21AB7D99A7B4F54 CRC64;
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                                                                    04, Last sequence update)
04, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 04, Last annotation update)
Hypothetical 10.3 kDa protein (Fragment).
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVI 36
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Pred. No. 4.8e-14;
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1; Mismatches
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  110 AA
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                      006124;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence
01-JUL-1997 (TrEMBLrel. 04, Last annotat.
Hypothetical 11.9 kDa protein (Fragment)
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           006125;
01-JUL-1997 (TrEMBLrel. 04, Created)
PRT;
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86.1%;
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  PRELIMINARY;
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Local Similarity 30.0 tes 18; Conservative
                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1097;
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                                                                                          Q8KAD4;
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                                                           Q8KAD4
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Q8KAD4
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                                                                                                                                                                                                                                MEDLINE-20504483; PubMed=11016950;

MEDLINE-20504483; PubMed=11016950;

Ng W.V. Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla'H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
"Genome sequence of Halobacterium species NRC-1.",
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN=MB4 / JCM 11007;

MEDLINE-21992816; PubMed=11997336;

Bao O., = 71an Y. Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,

Tan H., Chen R., Wang J., Yu J., Yang H.;

"A complete sequence of T. tengcongensis genome.";

Genome Res. 12:689-700(2002).

EMBL; ABD11992; AAM24542.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 31.2%; Score 101; DB 17; Length 77; Local Similarity 31.1%; Pred. No. 0.00044; hes 19; Conservative 22; Mismatches 20; Indels
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28.4%; Score 92; DB 16; Length 110;
Best Local Similarity 28.8%; Pred. No. 0.0071;
Matches 17; Conservative 17; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermoanaerobacter tengcongensis.
Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
Thermoanaerobacteriaceae, Thermoanaerobacter.
                                                                                                      Halobacterium sp. (strain NRC-1).
Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
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SEQUENCE 110 AA; 11862 MW; 43C0606A4B05F6DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 AA; 8378 MW; C3C359B65E8A8306 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBRAA6;
01-JUN-2002 (TrEWBLrel. 21, Created)
01-JUN-2002 (TrEWBLrel. 21, Last sequence update)
01-OCT-2002 (TrEWBLrel. 22, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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2 IDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITY-RIKLEVSFKM 60
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN-TLS / ATCC 49652 / DSM 12025;

MEDLINE-22103685; Pubmed=1203901;

A Bisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,

A Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,

A Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

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Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.,

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Photocosynthetic, anaerobic, green-sulfur bacterium.",

Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
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STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PADMEd=10984043;
STRAIN-ATCC CK., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Golter D.T., Folger R.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
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Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                          Chlorobium tepidum.''
Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Indels
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SEQUENCE 70 AA; 7922 MW; 8C662B18D044F153 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein CT2229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical protein PA0038.
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Pred. No. 1.8;
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30.0%; Pred. No. 0.28;
iive 19; Mismatches
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EMBL; AE004443; AAG03428.1;
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Best Local Similarity
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Gaps

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23; Indels

Mismatches

20;

Score 65; DB 16; Length 83; Pred. No. 6.1;

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1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIE-QDMAVDSAGKIT-YRIKLEVSF
                                                                                                                                                                                                                                                                                                                               EMBL, AL646083; CAD18326.1; -. Plasmid, Hypothetical protein; Complete proteome. SEQUENCE 83 AA; 9140 MW; 1EAAD51D4FA4871A CRC64;
                                                                                                                                                               20.1%;
28.8%;
                                                                                                                                                                                                                                     19; Conservative
Nature 415:497-502(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Q962B3
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                                                                                                           10 IELVGSSKTSIEDAINNALAEAAKSIQHLEWFEVVDTRGHIENGAVGHYQVTLKVGFRI 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Finan T.M., Weicher S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puehler A.,
Golding B., Puehler A.,
"The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti.";
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).
BMBL; ALG03642; CAC49468.1; ...
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 69 AA; 7792 MW; F53FBF80AE62C07D CRC64;
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                                                                     2 IDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
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                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical procein RB0068.
RB0068 OR SMB20068.
Rhizobium meliloti (Sinorhizobium meliloti).
Blasmid 29/ymB (megaplasmid 2).
Bacteria; Proceobacteria; Apphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 66; DB 16; Length 69;
Pred. No. 3.8;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein RSp1175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RŠP1175 OR RS05065.
Ralstonia solanacearum (Pseudomonas solanacearum).
          27;
                                                                                                                                                                                                                                                                                                          A
          Mismatches
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MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=1021;
MEDLINE=21396508; PubMed=11481431;
      17;
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NCBI_TaxID=305;
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             Conservative
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60 VMKVGFRI 67
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Best Local Similarity
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          15;
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AC 092X9
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DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 0
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PROSITE; PS00217; SUGAR_TRANSPORT_2;
SUGAR_TRANSPORT_2;
SUGAR_TRANSPORT, TRANSPORT
SEQUENCE 501 AA; 55546 MM; 23F0B43E944C9AD5 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Aminopeptidase N (EC 3.4.11.2).
                                                                                                                                                                 Last sequence update)
Last annotation update)
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501 AA
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40.0%; Pred. No. 56;
:ive 10; Mismatches
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PROSITE; PSC0041; HTH_ARAC_FAMILY_1; 1.
PROSITE; PS50850; MFS; 1.
                                                                                                           Created)
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PRELIMINARY;
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Job time : 5.24762 secs
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                                                                                    (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicoverpa armigera (Cotton bollworm).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Heliothinae; Helicoverpa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X MEDLINE=21595285; PubMed=11759840; MEDLINE=21595285; PubMed=11759840; MEDLINE=21595285; PubMed=11759840; Marita T., Sasamoto S., A Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki M., Silmpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabara S., Sugimoto M., Takazawa M., Yamada M., Tabara S., Sugimoto M., Takazawa M., Yamada M., Tabara S., Sugimoto M., Takazawa M., Yamada M., Tabara S., Sugimoto M., Takazawa M., Yamada M., Rasuda M., Tabara S., Sugimoto M., Takazawa M., Yamada M., Rasuda M., Tabara S., Sugimoto M., Takazawa M., Yamada M., Tabara S., Sugimoto M., Takazawa M., Yamada M., Tabara S., Sugimoto M., Takazawa M., Yamada M., Rasuda M., Yamada M., Rasuda M., Yamada M., Rasuda M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M.
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                                                                                                                                                            Angelucci C., Akhuret R.J., East P.;
Helicoverpa armigera aminopeptidase N gene APN2.";
Submitted (UNN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY038608; AAR85539.1; -.
R MEROPS; M01.013; -.
R InterPro; IPR001930; Ala peptase.
R InterPro; IPR001052; Zn MTpeptdse.
R Pfam, PP01433; Peptidase M1; 1.
R PRINTS; PR00756; AlaDIPTASE.
R PROSITE; P800142; ZINC_PROTEASE; 1.
Aminopeptidase; Hydrolase.
SEQUENCE 1030 AA; 114505 MW; 258A43E74EFBFCA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 SWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEV 56
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NCBI_TaxID=103690;
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Last annotation update)
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ses 14; Conservative 1
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01-MAR-2002 (TrEMBLrel. 20,
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SEQUENCE 96 AA;
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DT 01.NOV-1996 (TERMELRE]. 01, Created)
DT 01-NOV-1996 (TERMELRE]. 01, Last sequence update)
DE Nef (Negative factor) (F-protein) (27 kDa protein)
DE (Fragment).

ON OTT-2002 (TERMELRE]. 01, Last annotation update)
DE (Fragment).

ON NEF (TERMELRE]. 01, Last annotation update)
ON NEF (TERMELRE]. 01, Last annotation update)
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 AAWB1706
AAW39136
AAY3993
AAY38993
AAB35218
AAB19845
ABU05988
ABG30969
AAU74591
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AAY39176
AAY39081
AAY39033
AAU74592
AAU01901
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AAW32386
AAW81707
AAW84340
AAY39137
AAY38994
AAY03706
AAY03707
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AAW81698
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95US-0523436.
95US-0533634.
96US-0620874.
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   WO9709428-A2
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22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
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2621.664 Million cell updates/sec
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1 TDAATLAQEAGNFERISGDL......VQXSRADEEQQQALSSQMGF
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Compugen Ltd.
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                 GenCore version (c) 1993 - 2003
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                                                                                  sw model
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AAW32376
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AAW64321
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                                                                                  protein search, using
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seq length: 200000000
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Skeiky YAW;

Reed SG,

Houghton R,

Campos-neto A, Dillon DC, Twardzik DR, Vedvick TH;

AAY39118 AAY38981 AAE29717 AAE17581

11 2 3 4 5 9 5 C 8 6

Query Match

Score

Result

(CORI-) CORIXA CORP.

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A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (its variant differing only in conservative substitutions and/or modifications). The present sequence represents and Nuberculosis antigen, TD38-1. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW81747;
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                                                                                                                                                                                                                                                                                                                                                                                    1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                  A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, Tb38-1. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus BSAT-6, are useful in vaccines, preferably when formulated with a M.tuberculosis (for treatment or prevention).
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                            New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yen; immunogen; vaccine; tuberculosis; non specific adjuvant;
testing; M.tuberculosis.
                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                         100.0%; Score 466; DB 18; Length 95; 100.0%; Pred. No. 2.1e-43; ive 0; Mismatches 0; Indels
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Twardzik DR, Vedvick TH;
                                                                                                          English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW32376 standard; Protein; 95
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Best Local Similarity 100.0%;
Marches 95; Conservative C
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95US-0523435.
95US-0532136.
96US-0650280.
                                                                                                        Example 3; Page 124; 168pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
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N-PSDB; AAT91445.
WPI; 1997-192903/17.
N-PSDB; AAT91509.
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                                                                                                                                                                                                                                                                                             95 AA;
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01-SEP-1995;
22-SEP-1995;
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                                                                                                                                                                                                                                                                                             Sequence
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ww immunogenic polypeptide(s) from soluble M. tuberculosis antigens useful for diagnosis of M. tuberculosis infection

Example 3; Page 136; 190pp; English

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This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the
                                                                                        09
                                                                                                                    1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                        1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                 Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA. used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                       .
0
                             Length 95;
                                                          Indels
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                          100.0%; Score 466; DB 18;
100.0%; Pred. No. 2.1e-43;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                       tuberculosis immunogenic polypeptide Tb38-1.
                                                                                                                                                    KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3b; Page 117; 230pp; English.
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96US-0730510.
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           Query Match

Query Match

Best Local Similarity 100...

-hea 95; Conservative
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N-PSDB; AAV64491.
95 AA;
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                                                                                                                                                                                                                                                                                                                           27-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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셤 ò g

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TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQBAANKQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the Mycobacterium tuberculosis antigen
Tb38-1. The invention provides fusion proteins (see AAY32059-71)
containing at least 2 M. tuberculosis antigens such as Tb38-1, e.g.
Tbr-2 (see AAY32063) and a Tb49-Tb38-1 fusion. The new fusion
proteins are useful as vaccines for preventing tuberculosis
(claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis, antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                                                     Tuberculosis; antigen; fusion protein; Tb38-1; diagnosis; therapy;
                                                                                            KOELDEISTNIROAGVOYSRADEEOOOALSSOMGF
                                                             KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis antigen Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campos-Neto A;
                                                                                                                                                                                                 AA.
                                                                                                                                                                                             AAY32097 standard; Protein; 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 4D; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US07717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0056556.
98US-0223040.
                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                           17-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alderson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-601610/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                            vaccine; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09951748-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             components
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                                                                                                                                                                                                                                    AAY32097;
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                                                                                                                                                          RESULT
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                                                                                                  9
                                                                                                                             1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is an antigenic portion of Mycobacterium tuberculosis antigen Tb38-1. A DNA sequence (see AAV44384) coding for antigen Tb38-1 was isolated from a M. tuberculosis strain H37Rv expression library using sera from patients having pulmonary or pleural tuberculosis. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW6421-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant or expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis
                                                                                            1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection
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                  Length 95;
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                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tuberculosis; infection; diagnosis; antigen; Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis antigen Tb38-1 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dillon DC, Houghton R, Lodes MJ; / YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 100.0%; Score 466; DB 19;
Best Local Similarity 100.0%; Pred. No. 2.1e-43;
Matches 95; Conservative 0; Mismatches 0;
                100.0%; Score 466; DB 19;
100.0%; Pred. No. 2.1e-43;
ive 0; Mismatches 0;
                                                                                                                                                                          9
                                                                                                                                                                                                             9
                                                                                                                                                                                               61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 123; 250pp; English.
                                                                                                                                                                                                                                                                                                            95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                            AAW64321 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-US18214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0818111.
96US-0729622.
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
              Query Match
Best Local Similarity 100.
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campos-Neto A, Dillon
Reed SG, Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-251292/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV44384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9816645-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                      09-NOV-1998
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                                                                                                                                                                                                                                                                     RESULT 4
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                                                                      1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                    Gaps
                                    .,
 Length 95;
                                    Indels
100.0%; Score 466; DB 20;
100.0%; Pred. No. 2.1e-43;
ative 0; Mismatches 0;
                                                                                                                                          95
                                                                                                                                                                         61 KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                          61 KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF
                                                                                                                                                                                                              RESULT 6
AAY39118
ID AAY39118 standard; Protein; 95
XX
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1 IDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60

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Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brannon M,
                                                                                                                                                     (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                          WPI; 1999-527416/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     95 AA;
                                                                                                                                                                                                                                       N-PSDB; AAZ19082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200272792-A2.
                                                                                                                                                                                 Campos-Neto A,
                            WO9942118-A2
                                                                                  17-FEB-1999;
                                                                                                              05-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9-SEP-2002
                                                        26-AUG-1999
                                                                                                                                                                                             Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skeiky Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE29717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE2971'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion tuberculosis—immune subjects. AAX192949 to AAX19460 and AAX39033 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigen; diagnosis; detection; infection; antibody; immunisation; vaccine; immunity.
                                                                                                                                                                                                                                                                                                                                                                                           New antigens from Mycobacterium tuberculosis useful in diagnostic
skin tests and protective or therapeutic vaccines or compositions
                                                                                 Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 95;
                                                                                                                                                                                                                                                                                                                          Houghton R;
, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                           M. tuberculosis antigen Tb38-1 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M. tuberculosis recombinant antigen protein Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 466; DB 20; 100.0%; Pred. No. 2.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                                                         Dillon DC, Hendrickson RC, Hc
SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 113; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY38981 standard; Protein; 95
                                                                                                                                                                                                                                                      98US-0072967.
                                                                                                                                                                                                                            99WO-US03268.
                                                                                                                                                                                                                                                                   98US-0025197.
                                                                                                                                            Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-527409/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                         Campos-Neto A,
Lodes MJ, Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95
                                                                                                                                                                      WO9942076-A2
                                                                                                                                                                                                                            17-FEB-1999;
                                                                                                                                                                                                                                                      05-MAY-1998;
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                               05-NOV-1999
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                                                                                                                                                                                                 26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY38981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine; immunity; diagnostic agent; gene therapy; Tb38-1 antigen;
                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                 Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis Tb38-1 antigenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 466; DB 20;
100.0%; Pred. No. 2.1e-43;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                 Hendrickson RC, Ho
YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 159; 323pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guderian J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE29717 standard; Protein; 95
                                                                                                                                                                                                                                               Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAR-2002; 2002WO-US08223
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99WO-US03265
                                                           98US-0072596
                                                                                         98US-0024753
                                                                                                                                                                                                                 A, Dillon DC,
Reed SG, Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with increase the expension of the fusion proteins and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. The diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polymoral sequences of useful as diagnosis to detecting humoral antibodies or call-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as the munogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is Mycobacterium species. These I (Mtb11, 38-1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 466; DB 23;
Pred. No. 2.1e-43;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF
                                             Page 123; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 95; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0818112.
96US-0730510.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campos-Neto A, Dillon
Reed SG, Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-1997;
11-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW81706;
                                             Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                 The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, Leff, MIS, and 6H polynucleotides. Sequences of the invention are useful as vaccines to eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is My tuberculosis TD38-1 antigenic protein. TD38-1 is also referred to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polymucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; Tb38-1; Mtb11; 38-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 466; DB 23; Length 95; 100.0%; Pred. No. 2.1e-43; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium species Tb38-1 (Mtb11; 38-1) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KOELDEISTNIRQAGVOYSRADEEQQQALSSOMGF
                                                                                                                                                              Disclosure; Page 107; 155pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE17581 standard; Protein; 95
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01-FEB-2001; 2001US-265737P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 95; Conservative
WPI; 2002-759844/82.
N-PSDB; AAD47094.
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N-PSDB; AAD28352.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTb11 or 38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium sp
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Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                     Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA
                                                                                                                                                                                                                                                                       1 DC, Houghton R, Lodes MJ;
Twardzik DR, Vedvick TS;
                                                                                                    M. tuberculosis immunogenic polypeptide Tb38-IN
                                                                                                                                diagnosis.
KOELDEISTNIROAGVOYSRADEEOQOALSSOMGF
                                               Ź
                                             AAW81706 standard; Protein; 100
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kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis.
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                                                                                                                                                                                                                                                                                                      AAY39136;
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                                                       Sequence
                                                                              Query Match
                                                                                            Local
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Matches
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                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                                                                                                  AAY39136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This polypeptide comprises a partial sequence of Mycobacterium tuberculosis antigen Tb38-IN. It is encoded by genomic DMA isolated from a M. tuberculosis Strain H37Rv genomic library using a probe derived from clone Tb38-I (see AAV44384). The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW6429-W6439) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic
                                                                                                                                                                                                                                                              TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                       TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                               Gaps
                                                                This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection
    to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
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0
                                                                                                                                                                                    Length 100;
                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tuberculosis; infection; diagnosis; antigen; Tb37-FL.
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Twardzik DR, Vedvick TS;
                                                                                                                                                                                   100.0%; Score 466; DB 19;
llarity 100.0%; Pred. No. 2.2e-43;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                           KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                           95
                                                                                                                                                                                                                                                                                                                                                                                                                                                              tuberculosis antigen Tb38-IN.
                                          Example 3B; Page 138-139; 230pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 145; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   AAW64339 standard; Protein; 100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US18214.
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96US-0729622.
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Reed SG, Skeiky YAW, Twar
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                            100 AA;
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11-OCT-1996;
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                                                                                                                                                             Sequence
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AAW64339
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M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin teers for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T. B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AZI2949 to AAZI29460 and AAY39033 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                        9
                                                                                                                                                                                                                          TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                     1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
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                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antigens from Mycobacterium tuberculosis useful in diagnostic
skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis, M. tuberculosis, antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection;
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                                                 Length 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houghton R;
Vedvick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M. tuberculosis antigen Tb38-IN amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 466; DB 20;
ilarity, 100.0%; Pred. No. 2.2e-43;
Conservative 0; Mismatches 0;
                                                    100.0%; Score 466; DB 19; 100.0%; Pred. No. 2.2e-43;
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YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                       61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF
                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 133-134; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY39136 standard; Protein; 100 AA.
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SG, Skeiky
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immune response; skin test.
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                                                                                                              95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campos-Neto A, Dill
Lodes MJ, Reed SG,
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ses 95; Conserva
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                                                                                     Similarity
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100 AA;
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1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences for members of the esat-6 gene family from Mycobacterium tuberculosis. Th proteins include Rv0287, Rv1036c, Rv3346c, Rv2346c, Rv2553c, Rv2654c, Rv3020c, Rv344dc, Rv3445c, Rv3890c, Rv3891c, Rv3904c and Rv3905c. These can be used to produce vaccines against, and in the diagnosis of, tuberculosis (TB) infection. The present sequence is on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptide encoded by a member of the esat-6-gene family for immunizing against and diagnosis of tuberculosis.
                                                                                                                                       Tuberculosis, TB; vaccine; esat-6 gene family; Rv0287; Rv1036c; Rv1037c; Rv2346c; Rv2348c; Rv2653c; Rv2654c; Rv3020c; Rv3444c; Rv3445c; Rv3890c; Rv3891c; Rv3905c.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 466; DB 22;
Pred. No. 2.2e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                              M tuberculosis Rv3874 protein.
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ilarity 100.0%;
Conservative 0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JUL-2000; 2000WO-DK00398.
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                                                                                                                                                                                                                                                              Mycobacterium tuberculosis
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                         24-APR-2001 (first entry)
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Matches 95; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andersen P,
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                  1 IDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel recombinant antigens and their encoding
                                                              6 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide comprising antigenic portions of M. tuberculosis
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100.0%; Pred. No. 2.2e-43;
live 0; Mismatches 0;
                                                                                                                                                                                   66 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
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Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
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                                                                                                                                                                                                                                                                                                                                             AAY38993 standard; Protein;
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Matches 95; Conservative
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04-MAY-1999; 99US-0132505.

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The present sequence is that of the Mycobacterium tuberculosis MTBM 4 protein. This is 1.0f 8 proteins, i.e. MTBM1-8 (see AAA99035-42) identified as being present in the genome of Kee AAA99035-42) identified as being present in the genome of Mycobacterium bovis. MTBM1-8 represent transmence of the BGG strain of Mycobacterium bovis. W. tuberculosis and BGG and, in particular, for diagnostic methods which discriminate between exposure of a subject to M. tuberculosis and vaccination with BGG. The invention features these MTBM polypeptides, functional fragments of them, DNA encoding them, vectors, transformed cells, and diagnostic, therapeutic, and methods.
                                                                                                                                                                             Novel polypeptide encoded by open reading frames present in Mycobacterium tuberculosis genome and not by the BCG strain of M. bovis, useful as vaccine and for diagnosing tuberculosis infection
                                                      (PUBL-) PUBLIC HEALTH RES INST NEW YORK
                                                                                                                                                                                                                                                         Claim 11; Fig 1; 35pp; English.
                                                                                                                         WPI; 2001-007153/01.
N-PSDB; AAA89038.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 AA;
                                                                                          Gennaro ML;
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Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e-43;
Matches 95; Conservative 0; Mismatches 0; Indels 0

Search completed: November 21, 2003, 16:03:12 Job time : 5.7517 secs

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

Result

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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Davin C.
APPLICANT: Davin C.
APPLICANT: Davin C.
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Wardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND NETHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: COMPOUNDS AND NETHODS FOR IMMUNOTHERAPY
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRASS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                  Sequence
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: 13-MAR: 1997

TLASSIFICATION NUMBER: US/08/818,112

FLING DATE: 13-MAR: 1997

ATTORNEY/AGENT INFORMATION:

NAME: MAK: DAVIA J. 31,392

REGISTRATION NUMBER: 210121.411C6

TELECOMMUNICATION NUMBER: 210121.411C6

TELECOMMUNICATION NUMBER: 2000

TELEFRAX: (206) 622-4900

TELEFRAX: (206) 622-4900

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US-08-818-112-94
US-08-06-6758-94
US-08-06-6758-1
US-08-18-112-94
US-08-18-12-94
US-08-18-12-94
US-08-116-95-10
US-08-116-95-10
US-09-116-492A-10
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100.0%; Score 466; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.1e-46;
Matches 95; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 88, Application US/08818112; Patent No. 6290969; GENERAL INFORMATION:
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    /cgn2 6/ptodata1/iaa/5h_COMB.pep:*
    /cgn2 6/ptodata1/iaa/5B_COMB.pep:*
    /cgn2 6/ptodata1/iaa/6A_COMB.pep:*
    /cgn2 6/ptodata1/iaa/6B_COMB.pep:*
    /cgn2 6/ptodata1/iaa/PCTUS COMB.pep:*
    /cgn2 6/ptodata1/iaa/PCTUS COMB.pep:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-072-596-89
US-08-818-111-115
US-08-056-556-115
US-09-056-556-110
US-09-072-596-110
US-09-072-596-214
US-09-072-596-214
US-09-072-596-214
US-09-072-596-214
US-09-072-596-217
US-09-072-596-117
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US-09-072-596-117
US-09-072-596-117
US-09-116-492A-7
US-09-116-492A-7
US-09-116-492A-12
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US-09-116-492A-12
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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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STRANDEDNESS:
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                            1 TDAATLAQBAGNFBRISGDLKTQIDQVESTAGSLQQQWRGAAGTAAQAAVVRFQBAANKQ 60
TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Jasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Twardaik, Thomas S.
APPLICANT: Twardaik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 148
CORRESPENDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
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SCHWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/018,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTONENTAYAGENT INPOMMATION:
NAME: MAIL, DATIG J. 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REDERENCE/POCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (206) 622-4900
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100.0%; Pred. No. 2.1e-46;
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COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6338852
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
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STATE: Washington
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US-09-056-556-88
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US-08-818-111-89
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Sequence 88, Application US/09056556 Patent No. 6350456 GENERAL INFORMATION: APPLICANT: Reed, Steven G.

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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Damiel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
NAME: MAXL, DAVIA 0
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION NUMBER: 210121.457
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TELECOMMUNICATION NUMBER: 210121.457
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100.0%; Pred. No. 2.1e-46;
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Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.
Matches 95, Conservative
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Washington
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STATE: Washingtor
COUNTRY: USA
ZIP: 98104-7092
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STATE:
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Gaps . 0

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1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
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100.0%; Score 466; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.3e-46;
Matches 95; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                            Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Compounds AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 Indels
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ZIF: 981.04-70.92

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DAY PC COMPALIBLE
ONFRATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAA-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                            ; Score 466; DB 3;
; Pred. No. 2.3e-46;
0; Mismatches 0;
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Patent No. 6338852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
REPRENCE/DOCKET NUMBER: 21012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
INFORMATION FOR SEC IN NO: 110:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 100 amino acids
amino acid
                                               LENGTH: 100 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 95; Conservative
  INFORMATION FOR SEQ ID NO:
                                                                                                                            linear
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US-08-818-112-115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: TARATZIK, Daniel R.
APPLICANT: TARATZIK, Daniel R.
ALITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES.
ADDRESSEE: SED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STRATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
             CURRENT SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION NUMBER: 31.392
REGISTRATION NUMBER: 31.392
REGISTRATION NUMBER: 31.392
REGISTRATION NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFRA: (206) 622-4900
TELEFRA: (206) 622-4900
TELEFRA: (206) 622-631
INFORMATION POR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENDTH: 95 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA

ZIP: 981.04-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAXI, DAVId J
REGISTRATION NUMBER: 31,392
RESPERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 466; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.1e-46;
Matches 95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KÓELDEISTNIRQAGVOYSRADEEQÓQALSSOMGF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 115, Application US/08818112
Patent No. 6290969
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                          SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: siz
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US-09-072-596-89
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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRPQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 214, Application US/09056556
Sequence 214, Application US/09056556
GENERAL INFORMATION: GS50456
GENERAL INFORMATION: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yaair A.W.
APPLICANT: Skeiky, Yaair A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: ADDRESSES: SEED and BERRY LLP STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 100;
Hendrickson, Ronald C. VENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                           CONFUTER READABLE FORM:
COMPUTER: READABLE FORM:
MEDIUM TYPE: FOODPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TOWN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
                                                             NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
STRESSEE: SEED and BERRY LLP
STREST: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 KOELDEISTNIROAGVOYSRADEEQQQALSSOMGF 100
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100.0%; Pred. No. 2.3e-46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INPORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
RELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPRAX: (206) 682-6931
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CRRACTERISTICS:
LENGTH: 100 smino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                     CITY: Seattle
STATE: Washington
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Best Local Similarity
Matches 95; Conserv
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COUNTRY: USA
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US-09-072-596-110
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   APPLICANT:
                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPOUNDS AND METHODS FOR THE PREVENTION AND
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                             66 KOELDEISTNIROAGVOYSRADEEOOOALSSOMGF 100
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                                   61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
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STATE: WASDING.
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"MEDIUM TYPE: ROPPY DE COMPATIBLE
"MEDIUM TYPE: PROPESTIBLE
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                          RESULT 7
US-09-056-556-115
; Sequence 115, Application US/09056556
; Patent No. 6350456
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY !!?
CITCY
CITCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 110, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael R.
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Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (206) 622-490
TELEFAR: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 100 amino acids
amino acid
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Matches 95, Conservative
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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TUBERCULOSIS
                                                                                                                                                                              429 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKO 488
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                                                                                                                                  1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
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                                                                                              .<u>,</u>
                                                Query Match 100.0%; Score 466; DB 4; Length 802; Best Local Similarity 100.0%; Pred. No. 3.5e-45; Matches 95; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky, Yasir A.W.

Skeiky, Yasir A.W.

Dillon, Davin C.

Campos-Neto, Antonia

Houghton, Raymond

Vedvick, Thomas S.

Twardzik, Daniel R.

Lodes, Michael J.

Hendrickson, Ronald C.

INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 802;
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CIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPER: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FLING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/OCKET NUMBER: 210121.417C9
TELECOMMUNICATION INDERARIIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 466; DB 4;
100.0%; Pred. No. 3.5e-45;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                              489 KÓELDEISTNIRQAGVQYSRADEEQQQALSSOMGF 523
                                                                                                                                                                                                                         61 KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                                                                                                        Sequence 346, Application US/09072596
Patent No. 6458366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 346:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 802 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lodes Michae
APPLICANT: Hendrickson,
TITLE OF INVENTION: COMP
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-09-072-596-346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
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      US-09-072-596-209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               429 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 488
                                                                                                                                                                                                                                                                                                                                                                                                            1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 466; DB 4; Length 802;
Best Local Similarity 100.0%; Pred. No. 3.5e-45;
Matches 95; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-May-1998
CLASSIFICATION:
ATTONNEY/AGENT INFORMATION:
NAME: MAKE, DAVIG J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.417C9
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           489 KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
           REGISTRATION NUMBER: 31,392
REFERENCE DOCKET NUMBER: 210121.457
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP. 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 209, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 802 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 622-49
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6300 Colum
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                            ;
US-09-056-556-214
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US-09-072-596-209
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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                        16 ISGDLKTQIDQVESTAGSLQCQWRGAAGTAAQAAVVRFQEAANKQKQELDBISTNIRQAG 75
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                 ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardsk, Thomas S.
APPLICANT: Twardsk, Daniel R.
IIILE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                  Query Match

84.1%; Score 392; DB 3; Length 80;
Best Local Similarity 100.0%; Pred. No. 5.3e-38;
Matches 80; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk Computable.
COMBUTER: IBM PC Compatable.
COPRATICS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/ACBNT INFORMATION:
NAME: Maki, David J. REFRENCES/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEED and BERRY LLP
00 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.1%; Score 392;
                                                      210121.411C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 2101;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 VQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VOYSRADEEQQQALSSOMGF 80
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 112
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                         STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ON NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-818-112-117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                    US-09-116-492A-5
Sequence 5, Application US/09116492A
Sequence 5, Application US/09116492A
Sequence 5, Application US/09116492A
Sequence 5, Application
Sequence 5, Application
Sequence 5, Application
APPLICANT: GICQUEL, BRIGITTE
APPLICANT: BERRHET, FRANCOIS-XAVIER
APPLICANT: BERRHET, FRANCOIS-XAVIER
APPLICANT: RASMUSSEN, PETER B
TITLE OF INVENTION: POINT BERREAL
TITLE OF INVENTION: USING THE SAME
TITLE OF INVENTION: USING THE SAME
TITLE OF INVENTION: USING THE SAME
CURRENT APPLICATION NUMBER: US/09/116,492A
CURRENT APPLICATION NUMBER: 60/252,631
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
VERVION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
VENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.1%; Score 462; DB 4; Length 100; 98.9%; Pred. No. 6.5e-46; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC comparible
COMPUTER: LOW PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENITH Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 KOELDEISTNIROAGVOYSRADEEQOOALSSOMGF 100
                 489 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mycobacterium tuberculosis US-09-116-492A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-818-112-117; Sequence 117, Application US/08818112; Patent No. 6290969
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 98.9'
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: COM
TITLE OF INVENTION: AND
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and B
STREET: 6300 Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Reed, 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 5
LENGTH: 100
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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TREAT
                                                                       16 ISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIRQAG 75
                                                                                                           1 ISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIRQAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIRQAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 ISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIRQAG 75
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND CORRESSES: 241
CORRESPONDENCES: 241
CORRESPONDENCES: SEED and BERN LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98144-7032
COMPUTER: BADDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFBEATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Pacentin Release #1.0, Version #1.30
CURRATION: NUMBER: US/09/056,556
FILING DATE: 07-ARR-1998
CLASSIFICATION: AUTOMARTON:
                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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  100.0%; Pred. No. 5.3e-38; tive 0; Mismatches 0; Indels
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84.1%; Score 392; DB 4; I

Best Local Similarity 100.0%; Pred. No. 5.3e-38;

Matches 80; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 62-6031
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: November 21, 2003, 16:11:38
Job time : 2.0034 secs
                                                                                                                                                                                                                                                                                                                           Sequence 117, Application US/09056556 Patent No. 6350456 GENERAL INFORMATION:
                                                                                                                                                                                                           61 VOYSRADEEQQQALSSOMGF 80
                                                                                                                                                               76 VQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 VOYSRADEEQQQALSSQMGF 95
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Best Local Similarity 100. Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino accor
STRANDEDNESS: single
mobor.OGY: linear
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Sequence 28, Appl Sequence 12, Appl Sequence 12, Appl Sequence 96, Appl Sequence 97, Appl Sequence 97, Appl Sequence 91, Appl Sequence 91, Appl Sequence 10195, Appl Sequence 10195, Appl Sequence 10195, Appl Sequence 10195, Appl Sequence 10195, Appl Sequence 10195, Appl Sequence 10195, Appl Sequence 10195, Appl Sequence 10195, Appl Sequence 10195, Appl Sequence 10195, Appl

Sequence 7, Al Sequence 28, 1 Sequence 12, 1

Sequence

Sequence 109, App Sequence 143, App Sequence 143, App Sequence 143, App Sequence 24, Appl Sequence 19, Appl Sequence 19, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 16, Appl

Sequence 12, Appl Sequence 12, Appl

Sequence 12, Sequence 16, Sequence 49,

OM protein

Run on:

Sequence:

Searched:

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Sequence 88, Application US/10084843

Publication No. US20030143243A1

GENERAL INFORMATION:

Skelky, Yasir A.W.

Dillon, Davin C.

Campos-Netc, Antonio

Houghton, Raymond

Vedvick, Thomas S.

Twardzik, Daniel R.

Lodes, Michael J.

Hendrickson, Ronald C.

TILLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY

AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTY: USA

CONTINE READABLE FOOM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/084,843

FILING DATE: 25-Feb-2002

CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
CITY: Saattle
US-10-084-843-117
US-10-193-002-112
US-10-193-002-112
US-10-140-045-6
US-10-140-045-28
US-10-140-045-28
US-10-140-045-28
US-10-180-045-28
US-10-180-045-39
US-10-084-843-98
US-10-084-843-98
US-10-084-843-98
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US-10-084-843-98
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US-10-084-843-98
US-10-084-843-98
US-10-084-843-98
US-10-084-843-98
US-10-084-843-98
US-10-088-732A-47
US-10-088-732A-47
US-10-088-732A-47
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US-10-098-732A-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
APPLING DATE: 05-MAY-1998
ATTONEY/AGENT INFORMATION:
NAME: MAKi, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
    US-10-084-843-88
                                                                                                                                                 118
117
100.5
                                                                                                                                                                                                                         Sequence 88, Appl
Sequence 89, Appl
Sequence 115, Appl
Sequence 110, Appl
Sequence 639, Appl
Sequence 8, Appli
Sequence 10, Appl
Sequence 214, Appl
Sequence 214, Appl
Sequence 354, Appl
Sequence 354, Appl
Sequence 354, Appl
Sequence 354, Appl
Sequence 354, Appl
Sequence 354, Appl
Sequence 354, Appl
Sequence 354, Appl
Sequence 156, Appl
Sequence 157, Appl
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Sequence 157, Appl
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Sequence 157, Appl
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Sequence 157, Appl
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1 TDAATLAQEAGNFERISGDL.....VQXSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA:*

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18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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US-10-084-843-88
US-10-084-843-115
US-10-084-843-115
US-10-084-843-115
US-10-193-002-110
US-10-185-460-8
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US-10-185-460-8
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US-10-183-114
US-10-185-460-10
US-10-185-460-10
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                                                                                                                                                                                                                                                                   666188 seqs, 182559486 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                                                US-09-688-672A-10
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Perfect score:
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Database :

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Goderian, Jeffrey
APPLICANT: Corporation
TITLE OF INVENTION: Hererologous Fusion Protein Constructs Comprising of TITLE OF INVENTION: Leishmania Antigen
FILE REPERENCE: 0.44058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campos.Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendzickson, Ronald C.
Hendzickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
                                                                                                                                                          Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 95;
                                                                                                                                                                                                      Indels
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                                                                                                                                                     Query Match 100.0%; Score 466; DB 12; Best Local Similarity 100.0%; Pred. No. 1.9e-43; Matches 95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 466; DB 12;
100.0%; Pred. No. 1.9e-43;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                      61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: Tb38-1 or 38-1 (MTb11)
US-10-098-732A-35
                                                    TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 89:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 35, Application US/10098732A Publication No. US20030175294A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 115, Application US/10084843 Publication No. US20030143243A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
                            STRANDEDNESS: single
       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 95, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Skeiky, Yasir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Reed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-084-843-115
                                                                                                        US-10-193-002-89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
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Twardzik, Dannel R.

Lodes, Michael J.

Hendrickson, Ronald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF

TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                      Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 466; DB 12; 100.0%; Pred. No. 1.9e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 KOELDEISTNIRQAGVOYSRADEEQQQALSSOMGF 95
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNE; Maki, David U.
NAME: Maki, David U.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-0ul-2002
CLASSIFICATION: <ur>
CHASSIFICATION DATA:

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FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-10-084-843-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 89, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 95 amino acids
                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 89
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington
                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-193-002-89
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Gaps

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Sequence 639, Application US/10080170
Publication No. US20030129601A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: COLE, S.T.
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495.0218
CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT APPLICATION NUMBER: 60/270,123
PRIOR APPLICATION NUMBER: 60/270,123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 100;
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100.0%; Pred. No. 2e-43;
ive 0; Mismatches 0;
                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPRAIN SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-741-2002
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
ATTORNSY/AGENT INFORMATION:
NAME: MAX., DAVID G.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 110: SEQUENCE CHARACTERISTICS:
                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 95; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 639
LENGTH: 100
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Best Local Similarity
Matches 95; Conserv
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Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TILLE OF INVENTION: COMPONDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12; Length 100;
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                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                           ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 KOELDEISTNIRQAGVOYSRADEEQQQALSSQMGF 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELECHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 115: US-10-084-843-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 110, Application US/10193002
Publication No. USZ0030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 115:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                  STATE: Washington
                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 98104-7092
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Best Local Similarity
Matches 95; Conserva
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APPLICANT: Seed, Steven G.
APPLICANT: Seed, Steven G.
APPLICANT: Seed, Steven G.
APPLICANT: Seed, Steven G.
APPLICANT: Seed, Steven G.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Seed G.
APPLICANT: Campos-Neto, Seed G.
APPLICANT: Campos-Neto, Seed G.
APPLICANT: Campos-Neto, Seed G.
APPLICANT: Campos-Neto, Seed G.
APPLICANTON: TUNGER: 1999-04-07
FRIOR APPLICANTON NUMBER: US 08/942,578
FRIOR FILING DATE: 1998-02-18
FRIOR PRIOR PELING DATE: 1998-02-18
FRIOR PELING DATE: 1998-02-18
FRIOR PELING DATE: 1998-02-18
FRIOR APPLICANTON NUMBER: US 09/025,197
FRIOR FILING DATE: 1998-02-18
FRIOR APPLICANTON NUMBER: US 09/026,556
FRIOR FILING DATE: 1998-02-18
FRIOR APPLICANTON NUMBER: US 09/026,556
FRIOR APPLICANTON NUMBER: US 09/026,556
FRIOR APPLICANTON NUMBER: US 09/026,556
FRIOR APPLICANTON NUMBER: US 09/026,556
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FRIOR APPLICANTON NUMBER: US 09/026,556
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GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Cantonio Articles of Notations of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens
FILE REPERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/10/359,460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 466; DB 9; Length 358; Best Local Similarity 100.0%; Pred. No. 9.6e-43; Matches 95; Conservative 0; Mismatches 0; Indels
66 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
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US-09-287-849-8
                                                                                                                                                                                                                                                                    Sequence 8, Application US/09287849
Patent No. US20020009459A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
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LENGTH: 358
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APPLICANT: Reed, Stewn G.
APPLICANT: Reed, Stewn G.
APPLICANT: Billon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Addreson, Mark
APPLICANT: Campos Neto, Autonio
APPLICANT: Campos Neto, Autonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: end Their Uses
FILE REPERENCE: 014058-009000S
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT PILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/941,578
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,566
PRIOR APPLICATION NUMBER: US 09/025,566
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLOGOWRGAAGTAAQAAVVRFQEAANKQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:bi-fusion OTHER INFORMATION: protein TbH9-Tb38-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 100.0%; Score 466; DB 12;
1 Similarity 100.0%; Pred. No. 9.6e-43;
95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 KOELDEISTNIROAGVOYSRADEEOOOALSSOMGF 358
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PRIOR APPLICATION NUMBER: US/09/287,849
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-03-13
PRIOR PELICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR PRIOR APPLICATION NUMBER: US 09/025,566
PRIOR FILING DATE: 1998-04-07
PRIOR PRIOR PRIOR DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PALENTIN VET: 2.1
SEQ ID NO 8
LENGTH: 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MOD_RES
COCATION: (254)
COTHER INFORMATION: Xaa = any amino acid
MS-10-359-460-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/09287849 Patent No. US20020009459A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reed, Steven G.
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SEQ ID NO 10
LENGTH: 802
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Best Local 9
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429 TDAATLAQEAGNFERISGDLKTQIDQVBSTAGSLQGQWRGAAGTAAQAAVVFFQEAANKQ 488
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Lodes, Michael J.
Hendrickson, Rould C.
Hendrickson, Robert C.
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION NUMBER: US/10/084,843
FLING DATE: 25-Feb-2002
CLASSIPICATION: CURROWN-
PRIOR APPLICATION OF TO THE COMPONENT OF TO THE COMPONENT OF TO THE COMPONENT OF TO THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMPONENT OF THE COMP
                                                                                                                                                                                         489 KOELDEISTNIROAGVOYSRADEEOOOALSSOMGF
                                                                                                                 61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
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ADDRESSEE: SEED and BERRY
                                                                                                                                                                                                                                                                                                                                 US-10-084-843-351
; Sequence 351, Application US/10084843
; Publication No. US20030143243A1
; GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 05-MAY-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 95; Conserv
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                                                                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                                                                                         1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                             Gaps
           ; OTHER INFORMATION: Description of Artificial Sequence:tetra-fusion US-09-287-849-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houghton, Raymond
Vedvick, Thomas S.
Twatdzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                             0
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                                                                                                                     Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
MEDLUM TYPE: Floppy disk
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION NUMBER: US/09/072,967
FILING DATE: US/09/072,967
FILING DATE: OS-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAMM: MAKH, DAVIG J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
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                                                                                                                                                                                         0
                                                                                                             Score 466; DB 9;
Pred. No. 2.6e-42;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                         61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
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SEQUENCE DESCRIPTION: SEQ ID NO: 214:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 214, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
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                                                                                                                 Query Match
Best Local Similarity 100.0%;
Matches 95; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SULT 10
-10-084-843-214
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Version #1.30

701 Fifth Avenue

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429 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 488
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                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                    .
                                                                                                                                                                                                                                                                                        Length 802;
                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                             DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       523
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                                                                                                                                                                                                                                                                                                               2.6e-42
                    REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               489 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                             Score 466; DE
Pred. No. 2.66
); Mismatches
                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 351:
REGISTRATION NUMBER: 31,392
                                                                                                                                       LENGTH: 802 amino acids
                                                                               (206) 682-6031
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0
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100.0%;
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                                                                                                INFORMATION FOR SEQ ID NO: 351
SEQUENCE CHARACTERISTICS:
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1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60

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Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-10-359-460-10
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                                                                                                                  NEKAL INFORMATION
NEKAL INFORMATION
SREIKY, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIF: 98104-705A
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
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100.0%; Score 466; DB 12;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-UU1-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 209: US-10-193-002-209
                                                           Sequence 209, Application US/10193002 Publication No. US20030135026A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FELEPHONE: (206) 622-4900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Washington
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                    RESULT 12
US-10-193-002-209
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US-10-193-002-346
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, Sequence 346, Application US/10193002 , Publication No. US20030135026A1 , GENERAL INFORMATION:

APPLICANT: Reed, Steven G. Skeiky, Yasir A.W.

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429 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 488
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APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
Twardzik, Daniel R.

Twardzik, Daniel R.

Lodes, Michael J.

Hendrickson, Ronald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF

TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: SOO Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 466; DB 12;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               489 KQELDEISTNIRQAGVQYSRADEBQQQALSSQMGF 523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-WAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-011-2002
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 346:
US-10-193-002-346
                                                                                                                                                                                                                                                                                        STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
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66 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                    Search completed: November 21, 2003, 16:38:12
Job time : 4.70522 secs
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Squence 5, Application US/10140045

Squence 6. Application US/10140045

Publication No. US20300928991

GENERAL INFORMATION:
APPLICANT: GLOUGLE, BRIGITER
APPLICANT: ADDERSENS, PETER B

APPLICANT: ADDERSENS, PETER B

APPLICANT: ARABRESEN, PETER B

TITLE OF INVENTION: POLYNUCLECTIDE FUNCTIONALLY CODING FOR THE LHP PROTEIN FROM MYCOE

TITLE OF INVENTION: TUBERCULOSIS, ITS BIOLOGICALLY ACTIVE DERIVATIVE FRAGMENTS, AS W

TITLE OF INVENTION: USING THE SAME

TITLE OF INVENTION: USING THE SAME

TITLE OF INVENTION: UNMBER: US/09/116,492A

PRIOR PLICATION NUMBER: US/09/116,492A

PRIOR PELICATION NUMBER: US/09/116,492A

PRIOR PELING DATE: 1998-07-16

PRIOR PELING DATE: 1997-07-16

NUMBER OF SEQ ID NOS: 39

SEQ ID NO 5

LENGTH: 100

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 TDAATLGGEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:tetra-fusion
US-10-359-460-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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100.0%; Score 466; DB 12; Length 802;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

99.1%; Score 462; DB 15; Length 100;
Best Local Similarity 98.9%; Pred. No. 5.5e-43;
Matches 94; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAV
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     CURRENT APPLICATION NUMBER: US/10/359,460
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/287,849
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
SRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PAECHLIN VET: 2.1
SEQ ID NO 10
LENGTH: 802
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61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

November 21, 2003, 15:57:31 ; Search time 1.98186 Seconds (without alignments) 4609.825 Million cell updates/sec Run on:

Title: Perfect score:

US-09-688-672A-10 466 1 TDAATLAQEAGNFERISGDL......VQYSRADEEQQQALSSQMGF 95 Sequence:

BLOSUM62 Scoring table:

283308 segs, 96168682 residues Gapop 10.0 , Gapext 0.5 Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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SUMMARIES		H70802	T10032	T35661	B59103	T38435	E70836	B70600	T43214	G70857	A47334	833068	A59287	T44704	G87116	A61231	521801	KRSHL2	T42722	S05408	S33124	F75559	D29674	AB1873	JC6549	H82503	B75310	A42184	D84335	533479
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	Query Match		37.1	ö	σ.	σ,	œ	ω.	œ,	œ	۲.	۲.	۲.	ζ.	ζ.	۲.	ζ.	7	Ģ.	ý.	ý.	œ	ů.	ů.	ŝ	œ	S.	ů.	'n.	ري ري
	Score	9	173	•	٥.	σ	87.5	86	æ	84.5	•	80	α	φ.	79.5	φ.	o,	79	78	94	97	~		74.5			74	74	73.5	m.
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ferredoxin-NADP(+)	periplasmic olidop	unknown protein [i	hypothetical prote	hypothetical prote	uncharacterized sm	keratin-like prote	probable exonuclea	8.9K linker polype	keratin, type II,	biphenyl-2,3-diol	secreted 45 kd pro	qeneral stress pro	methyl-accepting c	laminin B1k chain	protein J - Yersin
AB2321	AD1824	H96760	F96673	S48385	G96905	I38025	T03465	A24691	S29094	DAPSPC	G95258	B98124	D87536	A53612	T14652
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440	552	745	1313	1679	103	257	1238	80	503	293	392	392	555	1170	1492
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73.5	73.5	73.5	73.5	73.5	73	73	73	72.5	72	71.5	71.5	71.5	71.5	71.5	71.5
30	31	32	33	34	32	36	37	38	9	40	41	42	43	44	45

## ALIGNMENTS

_	RESOLT 1
	H70802 .
	hypothetical protein Rv3874 - Mycobacterium tuberculosis (strain H37RV)
	C;Species: Mycobacterium tuberculosis
	C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text change 20-Jun-2000
	C;Accession: H70802
	R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
	; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
	Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
	Nature 393, 537-544, 1998
	A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
	A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
	A;Reference number: A70500; MUID:98295987; PMID:9634230
	A;Accession: H70802
	A; Status: preliminary; nucleic acid sequence not shown; translation not shown
	A, Molecule type: DNA
	A;Residues: 1-100 <col/>
	A;Cross-references: GB:AL022120; GB:AL123456; NID:g3261558; PIDN:CAA17966.1; PID:g296022
	A, Experimental source: strain H37Rv
	C; Genetics:
	A,Gene: Rv3874
	100.0%;
	rest Local Similarity 100.0%; Pred. No. 96-36; Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	OV I TDAATIAORAGNERPISGDI.KTOTOAONEGAGI.GGWPGBAGTAAATAFBAGFAG
	72
	DD. 6 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 65
	QY 61 KQELDEISTNIRQAGYQYSRADEBOQQALSSOMGF 95
	Db 66 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
	RESULT 2

RESULT 2 T10032

Argotherical protein MLCB628.13c - Mycobacterium leprae
C;Species: Mycobacterium leprae
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C;Species: Mycobacterium leprae
C;Accession: T1002
R;Eiglmeier, K.; Honore, N.; Woods, S.A.; Caudron, B.; Cole, S.T.
Mol. Microbiol. 7, 197-206, 1993
A;Fitle: Use of an ordered cosmid library to deduce the genomic organization of Mycobact
A;Fitle: Use of an ordered cosmid library to deduce the genomic organization of Mycobact
A;Fitle: Use of an ordered cosmid library to deduce the genomic organization of Mycobact
A;Fitle: Use of an ordered from GB/EMBL/DDBJ
A;Reference number: Z16917, MUD:93188700, PMID:8446027
A;Residues: L100 <EIG>A;Residues: L100 <EIG>A;Residues: L100 <EIG>A;Residues: L100 <EIG>A;Cross-references: EMBL:Y14967; NID:92370268; PIDN:CAA75210.1; PID:92370280

37.1%; Score 173; DB 2; Length 100; Query Match

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probable transcription regulator Rv0287 - Mycobacterium tuberculosis (strain H37RV) C.Species: Mycobacterium tuberculosis (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 (C.Date: 17-Uul-1998 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-Oct-1999 #text_change 22-
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A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: i-750 <MCD>
A;Cross-references: EMBL:AL009227; PIDN:CAA15821.1; GSPDB:GN00066; SPDB:SPAC27D7.02c
A;Experimental source: strain 972h-; cosmid c27D7
                                                                                                                                                                                                                                                         coiled coil protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T38432
R;McDougall, R.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, December 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 QEAG--NFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 90; DB 2; Pred. No. 1.4; 18; Mismatches
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62 MMFNILQELDKIAVELERAAVKFREADE 89
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28.2%;
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Best Local Similarity 28.2%
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z21793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
A;Gene: SPDB:SPAC27D7.02c
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Best Local S
Matches 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
T35661
probable chromosome associated protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Bote: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 02-Jun-2000
C;Accession: T35661
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
A;Accerace number: 221585
A;Accession: T3560
A;Accession: T3560
A;Accession: T3561
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A,Residues: 1-410 <OKI>
A,Cross-references: GB:AF065404; NID:g4894216; PIDN:AAD32402.1; PID:g4894314
A,Experimental source: strain Sterne
C,Genetics:
A,Gene: pXO1-98
                                                                                                                                                                                                     6 TERAILIQQAAQFDQIASGLSQERNFVDSIGQSFQNTWEGQAASAALGALGARFDEAMQDQ
                                                                                                                                             1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
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Best Local Similarity 29.5%; Pred. No. 0.67;
Matches 26; Conservative 14; Mismatches 27; Indels 2
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                                                        Indels
         37.9%; Pred. No. 4.4e-09;
tive 20; Mismatches 39;
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                                                                                                                                                                                                                                                                                                                                                                              66 IRQLESIVDKLNRSGGNYTKTDDEANQLLSSKMNF 100
                                                                                                                                                                                                                                                                                                                          61 KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
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         Best Local Similarity 37.99
Matches 36; Conservative
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A, Status: preliminary, nucleic acid sequence not shown, translation not shown A, Molecule type: DNA A, Molecule type: DNA A, Molecule type: 1-97 cCOL> A, Residues: 1-97 cCOL> A, Cross-references: GB: ALO21287, GB: AL123456; NID: G3261508, PIDN: CAA16105.1; PID: e123776 A, Experimental source: strain H37Rv
              A,Molecule type: mRNA
A,Residues: 733-874,'E',876-916,'S',918-1038,1040-1047,'S',1049-1283,'E',1285-1347,'E',1
A,Cross-references: EMBL:M30398; NID:g159876; PIDN:AAA29413.1; PID:g159877
C;Gene: ovt1
C;Keywords: leucine zipper:
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Reference number: A7050; MUID:98295987; PMID:9634230
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A, Cross-references: GB:LO7879; NID:G308884; PIDN:AAA29254.1; PID:G308885
A, Cross-references: GB:LO7879; NID:G308884; PIDN:AAA29254.1; PID:G308885
A, Experimental source: MHG/MSK/82/BA-2,C1
A, Note: sequence extracted from NCBI backbone (NCBIN:122864, NCBIP:122865)
C, Superfamily: unassigned kinesin-related proteins; kinesin motor domain homology
                                                                                                                                                                                                                                                                                                                             63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable PE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                              6 LAQEAGNFERISGDLKTQIDQVESTAGSLQGQ-----WRGAAGTAAQAAVV-----RFQE
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                                                                                                                                                                                                                                                 Query Match
18.5%; Score 86; DB 2;
Best Local Similarity 25.5%; Pred. No. 9.8;
Matches 25; Conservative 22; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 84.5; DB Pred. No. 0.49; 7; Mismatches
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ilarity 34.9%;
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Best Local Similarity
Matches 29; Conserv
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hypothetical protein Rv3905c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70600
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-54, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MJDE:9829597; PMID:9634230
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DMA
A;Residues: 1-103 cCOL-
A;Cross-references: GB:294121; GB:AL123456; NID:g3261736; PIDN:CAB08096.1; PID:e312272;
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
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Best Local S:
Matches 21
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Conserved hypothetical protein Mil661 [imported] - Mycobacterium leprae
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CiSpecies: Mycobacterium leprae
CiSpecies: Mycobacterium leprae
CiSpecies: Mycobacterium leprae
CiSpacesion: G87116
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Eutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Residues preliminary
A;Molecule type: DNA
A;Residues: 1-247 <STO>
A;Cross-references: GB:AL450380; NID:g13093432; PIDN:CAC30614.1; GSPDB:GN00147
                                                                                                                                      1044 DLKATQETVDDLERVKRDLEEQLRRKEAEIGGLSGKFEDEQGLVAQ-----LQRKIKELQ 1098
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                                           DAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein MLCB1243.13 [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Accession: T44704 R;Parkhill, J; Barrell, B.G.; Rajandzeam M.A. Submitted to the EMBL Data Library, May 1998 A;Reference number: 222830 A;Reference number: 222830 A;Reference number: 222830 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Reference: EMBL:ALO23635; PIDN:CAA19194.1 A;Residues: 1-245 <PAR> A;Residues: 1-245 <PAR> A;Residues: 1-245 <PAR> A;Residues: 1-245 <PAR> A;Residues: 1-245 <PAR> A;Reperimental source: Cosmid B1243
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C,Superfamily: Mycobacterium leprae hypothetical protein MLCB1243.13
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C;Superfamily; Mycobacterium leprae hypothetical protein MLCB1243.13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 AANKOKQELDEISTNIRQAGVQYSRADEE---QQQALSSQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 AANKQKQELDEISTNIRQAGVQYSRADEE---QQQALSSQ 92
                                                                                                                                                                                                                                                                                                                   DB
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                                                                                                                                                                                                                                                  62 QELDEISTNIRQAGVQYSRADEEQQQALSSQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 27.0%
Matches 27; Conservative
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Matches 27; Conserv
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C.Species: Schistosoma mansoni
C.Species: Schistosoma mansoni
C.Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 08-Sep-2000
C.Accession: A59287
R.Weston, D.S.; Schmitz, J.; Kemp, M.; Kunz, W.
Mol. Biochem. Parasitol. 58, 161-164, 1993
A;Title: Cloning and sequence characterization of a complete myosin heavy chain cDNA from A;Accession: A59287; MUD:93211444; PMID:8459827
A;Accession: A59287
A;Accession: A59287
A;Accession: MSP287
A;Accession: MSP287
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833068
myosin heavy chain - fluke (Schistosoma mansoni) (fragment)
N.Alternate names: surface antigen, 200K
C;Species: Schistosoma mansoni
C;Date: 22-Nov-1993 #sequence_revision 06-Sep-1996 #text_change 13-Feb-1998
C;Accession: 83306
R;Soisson, L.M.A.; Masterson, C.P.; Tom, T.D.; McNally, M.T.; Lowell, G.H.; Strand, M. A;Reference number: A46514; MUD:93056536; PMID:1431131
A;Reference number: A46514; MUD:93056536; PMID:1431131
A;Residues: 1-527 - SOID.
A;Residues: 1-527 - SOID.
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                                                                                                                                                                                                                                                                                                                                                                                                              4 ATLAQEAGNFERISGDLKTQIDQV------ESTAGSLQGQWRGAAGTAAQAAVVR 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQK 61
                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                            Length 955;
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ilarity 22.8%; Pred. No. 33;
Conservative 21; Mismatches 44; Indels
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A;Note: the authors translated the codon CAA for residue 346 as
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP; surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 527;
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                                                                                                                                                                                            17.5%; Score 81.5; DB 2; Length 9 ilarity 31.0%; Pred. No. 11; Conservative 12; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            918 EATAAAKSSAEQDR--ENTRAALEQQLRDSEERAAELASQ 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 FOEAANKOKOELDEISTNIRQAGVQYSRADEEQQQALSSQ 92
C;Keywords: ATP; nucleotide binding; P-loop
F;13-398/Domain: kinesin motor domain homology <KMOT>
F;122-129/Region: nucleotide-binding motif A (P-loop)
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22.8%; Pred. No. 8;
tive 21; Mismatches 4
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A;Cross-references: GB:L01634; PIDN:AAA29905.1
A;Experimental source: strain Brazilian LE
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Best Local Similarity
Matches 31; Conserval
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Matches 21; Conserva
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A; Molecule type: mRNA
A; Molecule type: mRNA
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A; Molecule type: mRNA
A; Molecule type: mNA
A; Molecule type: mNA
A; Cross-references: GB: MG9180; NID:g189029; PIDN:AAA61765.1; PID:g189030
B; Sacz, C.G.; Myers, J.C.; Shows, T.B.; Leinwand, L.A.
R; Sacz, C.G.; Myers, J.C.; Shows, T.B.; Leinwand, L.A.
A; Secondary Sci. 10 S.A. 87, 1164-1168, 11990
A; Title: Human nonmuscle myosin heavy chain mRNA: generation of diversity through altern
A; Reference number: A34876; MUID:90138958; PMID:1967836
                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 12-May-1994 #sequence_revision 14-Jul-1994 #text_change 19-Apr-2002
C;Date: 12-May-1994 #sequence_revision 14-Jul-1994 #text_change 19-Apr-2002
C;Accession: A61231; A34876; I52562; I61692
R;Simons, M; Wang, M; McBride, O.W.; Kawamoto, S.; Yamakawa, K.; Gdula, D.; Adelstein, Circ. Res. 69, 530-539, 1991
A;Title: Human nonmuscle myosin heavy chains are encoded by two genes located on differe A;Reference number: A61231; MUID:91316803; PMID:1860190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Title: Identification and overlapping expression of multiple unconventional myosin gen
A:Reference number: A55758; WUID:94294418; PMID:8022818
A:Accession: 161692
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Superfamily: myosin heavy chain; myosin motor domain homology

Superfamily: myosin heavy chain; myosin motor domain homology

Keyvords: actin binding; ATP, coiled with homology chain: myosin motor domain homology chain:

184-764/Domain: myosin motor domain homology chain:

185-565/Region: actin binding #status predicted

186-640/Region: actin binding #status predicted

1887-1938/Domain: coiled coil #status predicted

18837-1277/Domain: S1 #status predicted coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Residues: 1.52,'EAI',56-659,'T',661-868,'T',870-930,'C',932-1239,'KG',1242-1337 <RES>,Cross-references: GB:M81105; NID:g188988; PIDN:AAA59888:1; PID:g553596
Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Nolecule type: mRNA
|Residues: 715-1961 <SAE>
|Scriptures: 715-1961 <SAE>
|Cross-references: GB:M1013; NID:g189035; PIDN:AAA36349.1; PID:g189036
|Toothaker, L.E.; Gonzalez, D.A.; Tung, N.; Lemons, R.S.; Le Beau, M.M.; Arnaout, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lood 78, 1826-1833, 1991
Title: Cellular myosin heavy chain in human leukocytes: isolation of 5' cDNA clones,
Reference number: IS2562; MUID:92003925; PMID:1912569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'n
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C;Map position: 22q1.3-22q13.1
C;Map position: 22q1.3-22q13.1
C;Map voids meavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino a
C;Keywords: actin binding motif A (P-loop)
F;14-181/Region: nuclectide-binding motif A (P-loop)
F;52-565/Region: actin binding #status predicted
F;626-640/Region: actin binding #status predicted
F;837-1238-Domain: coiled coil #status predicted coil
F;837-1238-Domain: coiled coil #status predicted clamy>
F;1278-1961/Domain: light meromyosin #status predicted clamy>
F;1258-1961/Domain: light meromyosin #status predicted
F;125/Modified site: MG,NG,NG-trimethyllysine (Lys) #status predicted
F;694,704/Active site: Cys #status predicted
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Wolecule type: mRNA
Residues: 182-218 «BEM»
Cross references: GB:L29141; NID:g457249; PIDN:AAA20904.1; PID:g531134
                                                                                                                                                                                                                                                                Alternate names: cellular myosin heavy chain; myosin type 9; NAMHC-A Contains: myosin ATPase (EC 3.6.4.1)
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SINRAQSECDRL---IENGNISYEKAIQEGIKEQQRLVSQ 177
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Molecule type: mRNA
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llarity 21.7%; Pred. No. 37;
Conservative 23; Mismatches
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                                                                                                                                                                                                                        myosin heavy chain nonmuscle form A - human
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Best Local Similarity
Matches 34; Conserv
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GenCore version 5.1.6
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November 21, 2003, 15:51:11; Search time 1.12018 Seconds (without alignments) 3988.226 Million cell updates/sec US-09-688-672A-10 466 1 TDAATLAQEAGNFERISGDL......VQYSRADEEQQQALSSQMGF 95 OM protein - protein search, using sw model Title: Perfect score: Run on:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

ery tch Length DB ID			Ω. I
) L	MYCLE		083084 mycobacteri
103 1	_MYCTU		0
.5 2022 1	ONCVC		σ
.5 955 1	LEICH		P46865 leishmania
.1 245 1 YT27	_MYCLE		Q9cbs6 mycobacteri
.1 1960 1 MYH9_			P35579 homo sapien
.7 1325 1 G160_			mus π
.3 491 1 K2M2			P15241 ovis aries
.3 2349 1 TPR_H	HUMAN		_
.2 440 1 FENR	ANAVA		anapa
.2 1961 1 MYH9	9 RAT		
.0 80 1	L ANASP		
.8 440 1 FENR	ANASO		i.
.8 440 1	ANASP		anabaena
.8 16/	PERST		P40457 saccharomyc
1 11	MASLA		
.6 1947 1	CAEEL		
.5 502 1	SHEEP		P25691 ovis aries
.3 292 1 1	_PSES1		P17297 pseudomonas
.3 1172 1 LMB3	HUMAN		
.2 1938 1 MYSD_			
.1 78 1 PYS1			P50035 synechococc
.1 189 1	MANSE		
.1 373 1 CK13	HUMAN		_
.1 845 1 Y4FA	A RHISN		_
.1 1959 1 MYH9	CHICK		
.0 186 1 APL3	GALME		~
.0 512 1	ENTAE		~
.9 24	THALME		Q9hhc2 halobacteri
.9 457 1			,
232 1	E_LEUM!	m	Q10419 leuconostoc

P48667 homo sapien	P33741 halobacteri	P48668 homo sapien	Q10973 mycobacteri	P12608 synechococc	P21758 bos taurus	P33292 pichia past	Q9nqx4 homo sapien	09bv73 homo sapien	Q8xgj3 salmonella	P13509 alcaligenes	P06159 human parai
K2CD_HUMAN	HTR1 HALN1	K2CE HUMAN	YT27 MYCTU	IRPA_SYNP7	MSRE_BOVIN	PEXS PICPA	MYSC HUMAN	CEP2 HUMAN	SYFA SALTY	CZCC_ALCEU	NCAP_PI3H4
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384	535	563	245	356	453	576	1742	2442	327	417	515
14.8	14.8	14.8	14.7	14.7	14.7	14.7	14.7	14.7	14.6	14.6	14.6
ტ ტ	o W	69	68.5	68.5	68.5	68.5	68.5	68.5	68	68	68
3.4	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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requires a license agreement (See http://www.isb-sib.ch/announce/
                            or send an email to license@isb-sib.ch).
                                                                                            EMBL; ALS83917; CAC29558.1; -. PIR; T10032; T10032.
Leproma; ML0050; -.
                                                                                                                                                                                                                    99 AA; 10833 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
                                                                       EMBL; Y14967; CAA75210.1;
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 37.9<sup>5</sup>
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                        Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1769,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eiglmeier K., Garnier T., De Rossi E., Fsihi H., Cole S.T., Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 AA; 10663 MW; EBCAE6A996C5489D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 466; DB 1;
100.0%; Pred. No. 5.3e-36;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Massive gene decay in the leprosy bacillus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
MLOOSO OR MLCB628.13C.
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-!- SIMILARITY: BELONGS TO THE ESAT6 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 AA
     SIMILARITY: BELONGS TO THE ESAT6 FAMILY
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                                                                                                                                                                                                                                           EMBL, AF004671, AAC83445.1; -.
EMBL, AL022120, CAA17966.1; -.
EMBL, AE007190, AAK48366.1; -.
EMBL, AF418984, AAL14999.1; -.
                                                                                                                                                                                                                                                                                                                          PIR, H70802; H70802.
TIGR; M73988; --
Tuberculist; Rv3874; --
Antigen; Complete proteome.
INT_MET 0
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Les 95; Conservative
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                                                                                                                                                                                                                                                                                                  1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                     5 TEAAILTÕQAAQFDQIASGLSQERNFVDSIGQSFÖNTWEGQAASAALGALGRFDEAMQDQ
                                                                                                                                                                                                                        Gaps
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann W.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Deloher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole genome comparison of Mycobacterium tuberculosis clinical and
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0
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                       37.1%; Score 173; DB 1; Length 99; 37.9%; Pred. No. 2.3e-09; iive 20; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laboratory strains.";
submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE ESAT6 FAMILY.
BY SIMILARITY.
859B484F7EFE5A8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 IRQLESIVDKLNRSGGNYTKTDDEANOLLSSKMNF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative ESAT-6 like protein 13.
RV3905C OR MT4024 OR MTCYISF10.06.
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A47334; A47334.
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955 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leishmania chagasi.
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Best Local Similarity
Matches 31; Conserv
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SEQUENCE
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                     2 DAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Triteeraprapab S., Richie T.L., Tuan R.S., Shepley K.J., Dinman J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
NCBI_TaxID=6282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 733-866 FROM N.A.
MEDLINE=89127417; PubMed=2464764;
Donelson J.E., Duke B.O.L., Moscre D., Zeng W., Erondu N.E.,
Lucius R., Renz A., Karam W., Flores G.Z.;
"Construction of Onchocerca volvulus cDNA libraries and partial
characterization of the cDNA for a major antigen.";
Mol. Biochem. Parasical. 31:241-250(1988).
-!- FUNCTION: MAY BE A MYOFIBRILLAR PROTEIN.
                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neubert T.A., Scott A.L.;
"Modecular cloning of a gene expressed during early embryonic development in Onchocerca volvulus.";
Mol. Biochem. Parasitol. 69:161-171(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 2022;
                                                                                                                                                                                                                              18.5%; Score 86; DB 1; Length 103; 23.9%; Pred. No. 0.2; ive 20; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 COLLED COIL (POTENTIAL).
237341 MW; B7132AACF1520317 CRC64;
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ED COIL (POTENTIAL).
ED COIL (POTENTIAL).
D COIL (POTENTIAL).
                                                                                 TIGR; MT4024; -
TUGR; MT4024; -
Tuberculist; Rv3905c; -
Hypothetical protein; Complete proteome.
SEQUENCE 103 AA; 10460 MW; 3994E272A7BDFF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1991 (Rel. 18, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2022 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 QELDEISTNIRQAGVQYSRADEEQQQAL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 LGLSMLAAALAHAGAGYQHNETASAQVL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 86;
Pred. No.
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MEDLINE=95287898; PubMed=7770081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U12681; AAA80009.1; -. EMBL; J03995; AAA29412.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.5%;
25.5%;
MBL; Z94121; CAB08096.1; -. MBL; AEC07193; AAK48388.1; IR; B70600; B70600.
                                                                                                                                                                                                                                                            Local Similarity 23.9
les 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2022 AA;
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Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Major antigen.
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                                                                                                                                                                                                                                 Query Match
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ONCVO
                              EMBL;
                                                                                                                                                                                                                                                               Best Loca
Matches
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Gaps

10;

41; Indels

22; Mismatches

Conservative

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                                                   1752 LDEEKRTMENILHETALQREAIESSLNALERENKELHRNCAQLQQQIAQLELENGNRLIQ 1811
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6 LAQEAGNFERISGDLKTQIDQVESTAGSLQGQ----WRGAAGTAAQAAVV-----RFQE 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
NCBL_TaxID=44271;
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MOTOR DOMAIN2; RINESIN MOTOR DOMAIN2; 1.

MOTOC protein; Microtubules; ATP-binding; Coiled coil; Repeat.

DOMAIN 399 KINESIN-MOTOR (BY SIMILARITY).

MODAIN 426 >955 COILED COIL (POTENTIAL).

NP BIND 122 129 ATP (POTENTIAL).

DOMAIN 704 >955 7 X 39 AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular characterization of a kinesin-related antigen of Leishmania chagasi that detects specific antibody in African and American visceral leishmaniasis."; Proc. Natl. Acad. Sci. U.S.A. 90.775-779 (1993).
-!- DEVBLOPMENTAL STACE: PREDOMINANT IN AMASTIGGTES.
-!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burns J.M. Jr., Shreffler W.G., Benson D.R., Ghalib H.W., Badaro Reed S.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106168 MW; 8CA76815BE84C6E9 CRC64;
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ilarity 31.0%; Pred. No. 5.4;
Conservative 12; Mismatches 44;
                                                                                                                                    56 AANKOKOELDEISTNIRQAGVOYSRADEEQQQALSSQM
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Kinesin-like protein K39 (Fragment).
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Incerpro; 1PR001752; kinesin_motor.
Pfam; PF00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=MHOM/BR/82 / Isolate BA-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93133867; PubMed=8421715;
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79 TESESLLSHARAEADKILSDAKSQVDRMASEARQHSERMLGDAREESIRIATVAKREYEA 138
858 ATLEQQLRESEERAAELASQLESTTAAKMSAEQDRESTRATLEQQLRDSEERAAELASQL 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IDPATLAGEA-GNFERISGDLKTQIDQVESTAGS----LQGQWRGAAGTAAQAAVVRFQE 55
                                                                                                                                                                                                                                                                                                     MEDLINE-21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honoren N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Barrell B.G.,
"Massive gen-decay in the leprosy bacillus.";
"Massive gen-decay in the leprosy bacillus.";
"Mature 409:1007-1011(201).
"In TUBERCULOSIS RV2927C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYH9 HUMAN STANDARD; PRT; 1960 AA.
P35579; O60805;
01-JUN-1994 (Rel. 29, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Myosin heavy chain, nonmuscle type A (Cellular myosin heavy chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.1%; Score 79.5; DB 1; Length 245; 27.0%; Pred. No. 1.9;
                                                                                                                                                                                                                           Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein, Complete proteome.
SEQUENCE 245 AA, 27087 MW, C984D9A5FA49697A CRC64;
                                                  918 EATAAAKSSAEQDR--ENTRAALEQQLRDSEERAAELASQ 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 FQEAANKOKQELDEISTNIRQAGVQYSRADEEQQQALSSQ 92
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                                                                                                                            905085; 060467;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FES-2003 (Rel. 41, Last annotation update)
Hypothetical protein Mil661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AL023635; CAA19194.1; -.
EMBL; AL583923; CAC30614.1; ALT_INIT.
                                                                                                                    PRT;
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                                                                                                                    STANDARD;
                                                                                                                                                                                                                Mycobacterium leprae.
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Leproma; ML1661; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       NCBI_TaxID=1769;
                                                                                                                    YT27 MYCLE
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YT27_MYCLE
ID _YT27_M
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Best Local Similarity 21.7
Matches 34; Conservative
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P55937;
01-NOV-1997 (
01-NOV-1997 (
15-DEC-1998 (
                                                                                                                                                                                                                                                                          Deafness.
DOMAIN
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G160_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                               VALIANT DENALT HIS-70S.
MEDLINE=20489856; PubMed=11023810;
Lalwani A.K., Goldstein J.A., Kelley M.J., Luxförd W., Castelein C.M.,
Mhatre A.N.;
"Human nonsyndromic hereditary deafness DFNA17 is due to a mutation in
                                                                                                                                                                            MEDLINE=20428192; PubMed=10973259;
Seri M., Cusano M., Gangarossa S., Caridi G., Bordo D., Lo Nigro C.,
Ghiggeri G.M., Ravazzolo R., Savino M., Del Vecchio M., d'Apolito M.,
Iolascon A., Zelante L.L., Savoia A., Balduini C.L., Noris P.,
Magrini U., Belletti S., Heath K.B., Babcock M., Glucksman M.J.,
Aliprandis E., Bizzaro N., Desnick R.J., Martignetti J.A.;
MATTATIONS in MYH9 result in the May-Hegglin anomally, and Fechtner and
                                                                                                                                                                                                                                                                                                              VAKIANTS MHA ILE-1155 AND LYS-1841.

MEDLINE-20428193; PubMed=10973260;

Kelley M.J., Jawien W., Ortel T.L., Korczak J.F.;

"Mutation of MYH9, encoding non-muscle myosin heavy chain A, in
May-Hegglin anomaly.";

Nat. Genet. Z6:106-108(2000).

-1- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS,

CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
nonmuscle myosin heavy chain mRNA: generation of diversity
                                                                                                                                                      VARIANTS MHA/FINS/SBS LYS-93; CYS-702; CYS-1165; HIS-1424 AND
            through alternative polyadenylylation.";
Proc. Natl. Acad. Sci. U.S.A. 87:1164-1168(1990).
                                                                                                               nonmuscle myosin MYH9.";
Am. J. Hum. Genet. 67:1121-1128(2000).
                                                                                                                                                                                                                                                                          Sebastian syndromes.";
Nat. Genet. 26:103-105(2000).
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HSSP, P10587, 1BR2.
Genew, HGNC:7579, MYH9.
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EMBL; EMBL;

MIM;

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1738 LEEEQGNTELINDRLKKANLQIDQINTDLNLERSHAQKNENARQQLERQNKELKVKLQEM 1797
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Myosin; ATP-binding; Calmodulin-binding; Actin-binding;
Coiled coil; Alkylation; Multigene family; Disease mutation;
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E - K (IN MHA).

/FTIG=VAR 010797.

EAI -> RGH (IN REF. 3).

T -> S (IN REF. 3).

T -> M (IN REF. 3).

C -> Y (IN REF. 4).
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/FTIG=VAR 010794.
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/FTIG=VAR 010795.
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/FTIG=VAR 010791.
R -> C (IN FTNS).
/FTIG=VAR_010792.
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Last sequence update)
Last annotation update)
GO; GO:005860; C:non-muscle myosin; TAS.
InterPro; IPR000048; IQ_region.
InterPro; IPR001609; Myosin_head.
InterPro; IPR004009; Myosin_head.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR002928; Myosin_tail.
Pfam; PF00612; IQ; 1.
Pfam; PF0013; Myosin_head; 1.
Pfam; PF00136; Myosin_head; 1.
Pfam; PF00135; Myosin_tail; 1.
Pfam; PF00135; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODO; PR0010555; Myosin_head; 1.
SWART; SM00015; IQ; 1.
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The amino acid sequence of component 7c, a type II intermediate
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C -> G OR S.
C -> S.
F -> Y.
S -> V.
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Q -> H.
CG -> GC.
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LINKER 12.
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                                                                                                                                                                                InterPro; IPR001664; IF.
InterPro; IPR003054; Keratin_II.
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                                                                                                                                                                                                                         PRINTS; PRO1276; TYPE2KERATIN.
PROSITE; PS00226; IF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53681 MW;
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Best Local Similarity 22...
Best Local 19; Conservative
                                                                                                                                                                                                              Pfam; PF00038; filament;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 AAAAQHQDQNQEANGEVRSRRDSICSSVSMESSLAEPQDELLQILKDKRRLEGQVEALSL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SLQGQWRGAAG 43
                                                                                                                                                                                                                                        BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                          "Cloning and molecular characterization of cDNA encoding a mouse male-enhanced antigen-2 (Mea-2): a putative family of the Golgi autoantigen.";

DNA Seq. 7:71-82(1997).

-I- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN SPERMATOGENESIS AND/OR TESTIS DEVELOPMENT. PROBABLY IDENTICAL WITH THE SEROLGGICALLY DETECTABLE MALE ANTIGEN (SDM).

-I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS. TRANSCRIPTS CAN FOUND IN SPERMATIDS DURING SPERMATOGENESIS. NO EXPRESSION IN LEYDIG CELLS, SPERMATOGENESIS. NO EXPRESSION IN LEYDIG CELLS, SPERMATOGENESIS.

-I- SIMILARITY: HIGH, TO HUMAN GOLGIN-160.

-I- CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-19 OR MET-30 IS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
11-OCT-2001 (Rel. 40, Last annocation update)
Keratin, type II microfibrillar, component 7C.
Ovis aries (Sheep).
Markaryota: Netacoca: Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Eovidae; Caprinae; Ovis.
                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 TAAQAAVVRFQEAANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQM 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D. 122.7.
WGP; MGI:96982 T42722.
WGD; WGI:96983; Golga3.
GO; GO:0005793; C:ER-Golgi intermediate compartment; IDA.
GO; GO:0000139; C:Golgi membrane; IDA.
GO; GO:000515; P:protein binding activity; IPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90026244; PubMed=2803231;
Sparrow L.G., Robinson C.P., McMahon D.T.W., Rubira M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     )4 POLY-ALA.
149880 MW; 3230636962C687B0 CRC64;
 Golgin-160 (Male-enhanced antigen-2) (MEA-2)
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                                                                                           SEQUENCE FROM N.A.
STRAINS-CD-1; TISSUB=Testis;
MEDIJNE=97217683; PubMed=9063644;
Kondo M., Sutou S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D78270; BAA19612.1; -.
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                             Mus musculus (Mouse)
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es 28; Conserv
                                                                 NCBI_TaxID=10090;
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               GOLGAS OR MEAZ
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12 NFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNI
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MEDLINE=93064711; PubMed=1437155; Mitchell P.J., Cooper C.S.; Mitchell P.J., Cooper C.S.; The human tyr gene encodes a protein of 2094 amino acids that has extensive colled-coil regions and an acidic C-terminal domain."; Oncogene 7:2329-2333(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.3%; Score 76; DB 1; Length 491; 22.9%; Pred. No. 8.5; ive 23; Mismatches 39; Indels
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01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                          Intermediate filament; Coiled coil; Keratin.
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AA.

440

STANDARD;

MEDLINE=95096166; PubMed=7798308;

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SEQUENCE FROM N.A.
STRAIN=PCC 7937 / ATCC 29413;
Mannan R.M., Matthijs H.C.P., Pakrasi H.B.;
"Cloning and molecular characterization of the petH gene in the cyanobacterium Anabaena variabilis ATCC 29413 ";
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Reduced ferredoxin + NADP(+) = oxidized
                                                                                                                                                                                                                                                                                               Anabaena variabilis.
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
NCBI_TaxID=1172;
                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
FESSEP-2007 (Rel. 42, Last annotation update)
FESSEP-2007 (Rel. 42, Last annotation update)
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01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/TPRID282.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                             Byrd D.A., Sweet D.J., Pante N., Konstantinov K.N., Guan T., Saphire A.Cs., Mitchell P.J., Cooper C.S., Aebi U., Gerace L.; "Tpr, a large coiled coil protein whose amino terminus is involved in activation of oncogenic kinases, is localized to the cytoplasmic surface of the nuclear pore complex."; J. Cell Biol. 127:1515-1526(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THYMUS, SPLEEN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPONENTS, INCLUDING P62.
TISSUE SPECIFICITY: HIGHEST IN TESTIS, LUNG, THYMUS, SPLEEN AN BRAIN, LOWER LEVELS IN HEART, LIVER, AND KIDNEY.
DISEASE: INVOLVED IN TUMORIGENIC REARRANGEMENTS WITH THE MET, OR RAF GENES.
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18 POLY-SER.
265600 MW; AFDD6885CEDCA9EF CRC64;
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26.2%;
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1833 183
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2349 AA;
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Best Local Similarity
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SEQUENCE
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-!- COFACTOR: FAD.
-!- SUBCELLULAR LOCATION: May be bound to the thylakoid membrane or anchored to the thylakoid-bound phycobilisomes.
-!- SIMILARITY: WITH OTHER SPECIES FNR.
-!- SIMILARITY: Contains 1 cpcD-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
Lactr-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, nonmuscle type A (Cellular myosin heavy chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY) CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01383; CpcD; 1.
Pfam; PF00667; FAD binding_1; 1.
Pfam; PF00667; FAD binding_1; 1.
PFNNTS; PR00406; CYTBSENDTASE.
PRINTS; PR00371; FPNCR.
ProDom; PD002828; CpcD-11ke_C; 1.
Oxidoreductase; Flavoprotein; NADP; FAD; Thylakoid; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.2%; Score 75.5; DB 1; Length 440; ilarity 30.0%; Pred. No. 8.4; Conservative 15; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22; Indels
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NADP (RIBOSE PART)
; 660BAA2DCF59BB6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001683; CpcD-like.
InterPro; IPR001834; Cyt_B5 reductase.
InterPro; IPR0018397; FAD_binding.
InterPro; IPR001709; FPN_Cyt_redetse.
InterPro; IPR001433; Oxred_FAD/NAD(P).
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HSSP; P21890; 1QUE.
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Best Local Similarity
Matches 18; Conserv
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NP BIND
SEQUENCE
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Q62812;
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MYH9_RAT
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2 DAATLAQEAGNFE-----RISG-----DLKTQIDQVESTAGSLQGQWRGAA 42

006

Gaps

24;

16; Mismatches 39; Indels

Pred. No.

28; Conservative

Matches

à В ò

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01-APR-1988 (Rel. 07, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                            NCBI_TaxiD=103690;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Local S.
21;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FENR_ANASO
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                 셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                   SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (WHC), 2 ALKALI LIGHT CHAIN SUBUNITS (WLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

DOMAIN: THE RODLIKE TALL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

SIMILARITY: Contains I IQ domain.
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                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Choi O.H., Park C., Itch K., Adelstein R.S., Beaven M.A.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS,
CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
CAPPING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----KQELDEISTNIRQAGVQYSRADEEQQQALSSQ 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 ALKYLATION (SH-1) (POTENTIAL).
34 ALKYLATION (SH-2) (POTENTIAL).
226336 MW; 9B9876D9681FB19E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Calmodulin-binding, Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLLED COLL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING.
type A) (Nonmuscle myosin heavy chain-A) (NPMHG-A) MYH9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50096; IQ; 1.
Woseln, ATP-binding; Calmodulin-binding; Actin
Colled coil; Alkylation; Multigene family.
DOMAIN MYSSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.2%; Score 75.5; Di
22.8%; Pred. No. 41;
Sive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000048; IQ_region.
InterPro; IPR001609; Myosin_head.
InterPro; IPR001609; Myosin_N.
InterPro; IPR0012028; Myosin_X.
Pfam; PF00612; IQ; 1.
Pfam; PF00763; Myosin, head; 1.
Pfam; PF007063; Myosin, head; 1.
Pfam; PF0176; Myosin_Lail; 1.
PRINTS; PR00193; MYOSINHEAYY.
PRODOM; PD000355; Myosin_head; 1.
SMART; SM00125; MYSC; 1.
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174 18
654 67
694 69
704 70
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                                                                                                                  NCBI_TaxID=10116;
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Best Local Simi]
Matches 26; (
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PYS1_ANASP
ID _PYS1_ANASP
AC P07124;
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MOD_RES
SEQUENCE
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DOMAIN
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01.APR-1988 (Rel. 07, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Phycocyanin-associated, rod
Furchilssone 8.9 kDa linker polypeptide, phycocyanin-associated, rod
CPCD OR ASR0531.
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-87246520; PubMed=3109890;
Belknap W.R., Haselkorn R.;
"Cloning and light regulation of expression of the phycocyanin operon
of the cyanobacterium Anabaena.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21134097, PubMed=11237320, Glazer A.N.; Murphy V.T., Wedemayer G.J., Glazer A.N.; "Recombinant phycobilistoretains Recombinant C-phycocyanins equipped with affinity tags, oligomerization, and biospecific recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21595265; PubMed=11759840; Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Tanguranbe A., Targuranbe M., Iriguranbe M., Kanemabe A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Kishida Y., Kohara M., Matsumoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.0%; Score 74.5; DB 1; Length 80; larity 35.6%; Pred. No. 1.7; Conservative 10; Mismatches 21; Indels
                                                                                                                                                                                                                      Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
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-!- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
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01-077-1994 (Rel. 30, Last sequence update)
01-575-25P-2003 (Rel. 42, Last annotation update)
Ferredoxin--NADP reductase (EC 1.18.1.2) (FNR).
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EMBL; AF178757; AAG09319.1; -.
EMBL; AP003582; BAB72489.1; -.
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1E64;
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1BJK;
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     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation the Buropean Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its concent is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lb-sib.ch).
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**MEDLINE=20508220; PubMed=11053838;

*Menales R., Kachalova G., Vellieux F., Charon M.-H., Frey M.;

*Morales R., Kachalova G., Vellieux F., Charon Detween the Crystallographic studies of the interaction between the ferredoxin.NADP+ reductase and ferredoxin from the cyanobacterium anabaena: looking for the elusive ferredoxin molecule.";

**Anabaena: looking for the elusive ferredoxin molecule.";

**Acta Crystallogr. D 56:1408-1412(2000).

**C. I CATALYTIC ACTIVITY: Reduced ferredoxin + NADP(+) = oxidized ferredoxin + NADPH.

**C. I CATALYTIC ACTIVITY: Reduced ferredoxin + NADP(+) = oxidized ferredoxin + NADPH.

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                                                               SEQUENCE FROM N.A.
MEDLINE-93344523; PubMed-8343609;
Fillat M.F., Flores E., Gomez-Moreno C.;
"Homology of the N-terminal domain of the petH gene product from
Anabaena sp. PCC 7119 to the CpcD phycobilisome linker polypeptide.";
Plant Mol. Biol. 22:725-729(1993).
                                                                                                                                                                             SEQUENCE OF 137-440 FROM N.A.
MEDLINE=91088322; PubMed=2124680;
Fillat M.F., Bakker H.A.C., Weisbeek P.J.;
"Sequence of the ferredoxin-NADP(+)-reductase gene from Anabaena PCC
                                                                                                                                                                                                                                                                                                                                              Sancho J., Peleato M.L., Gomez-Moreno C., Edmondson D.E., "Purification and properties of ferredoxin-NADP+ oxidoreductase from the nitrogen-fixing cyanobacteria Anabaena variabilis."; Arch. Biochem. Biophys. 260:200-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20114461; PubMed=10651039;
Mayoral T., Medina M., Sanz-Aparicio J., Gomez-Moreno C.,
Hermoso J.A.,
"Structural basis of the catalytic role of Glu301 in Anabaena PCC
7119 ferredoxin-NADP+ reductase revealed by x-ray crystallography.";
Proteins 38:60-69.(2000).
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MEDLINE=99119186; PubMed=9923134;
MEDLINE=99119186; PubMed=9923134;
Martinez-Julivez M., Hermoso J., Hurley J.K., Mayoral T.,
Sanz-Aparidio J., Tollin G., Gomez-Moreno C., Medina M.;
Role of Arglot and Arg264 from Anabaena PCC 7119 ferredoxin-NADP+
reductase for optimal NADP+ binding and electron transfer.";
Biochemistry 37:17680-17691(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 137-440.
MEDLINE=97045988; PubMed=8890910;
Serre L., Vellieux F.M.D., Medina M., Gomez-Moreno C.,
Fontecilla-Camps J.C., Frey M.;
"X-ray structure of the ferredoxin:NADP+ reductase from the
crystallographic studies of NADP+ binding at 2.25-A resolution.";
J. Mol. Biol. 263:20-39(1996).
 Anabaena sp. (strain PCC 7119).
Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc.
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                                                                                                                                                                                                                                                                                                              STRAIN=1403.46;
MEDLINE=88132819; PubMed=3124746;
                                                                                                                                                                                                                                                                                                SEQUENCE OF 152-183.
                 Bacteria, Cyanoba
NCBI_TaxID=1168;
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                                                                                                                                                                                                                                                                                                                                                                                          33 SLQGQWRGAAGTAAQAAVVRFQBAANKQKQELDEISTNIRQAG-----VQYSRADEEQQQ 87
                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBCELLULAR LOCATION: May be bound to the thylakoid membrane or anchored to the thylakoid-bound phycobilisomes.
-i- SIMILARITY: WITH OTHER SPECIES FNR.
-i- SIMILARITY: Contains 1 cpcD-like domain.
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HASP: Wildray), Lark..

InterPro; IPR001685; CpcD-like.

InterPro; IPR001034; Cyt_B5_reductase..

InterPro; IPR00101709; FPN Cyt_redctse..

InterPro; IPR0011709; FPN Cyt_red_FAD/NAD(P)..

Pfam; PF00175; NAT binding 1; 1..

Pfam; PF00175; NAT binding 1; 1..

PRINTS; PR00466; CpcD-like C; 1..

R ProDom; PD002828; CpcD-like C; 1..

R ProDom; PD002828; CpcD-like C; 1..

R ProDom; PD002828; CpcD-like C; 1..

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Bacteria: Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2013 (Rel. 42, Last annotation update)
F15-Redoxin--NADP reductase (EC 1.18.1.2) (FNR)
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30.0%; Pred. No. 13;
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HSSP; P21890; 1B2R.
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BB07AA1B99295C98 CRC64;
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1 Similarity 30.0%; Pred. No. 13;
18; Conservative 15; Mismatches
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O8fs24 corvnebacte	09zbd2 streptomyce				042657 schizosacch	053692 mycobacteri	O53267 mycobacteri	O8vi87 mycobacteri	Q921b9 mus musculu	077248 spodoptera	O8ed18 shewanella	O9f5nl rhizobium m			
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08FS24	324		
Π	Q8FS24	PRELIMINARY; PRT; 106 AA.	
AC	Q8FS24;		
DŢ	01-MAR-2003	(TrEMBLrel, 23, Created)	
ĽΩ	01-MAR-2003	(TrEMBLrel. 23, Last sequence update)	
Ľ	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)	
E	Hypothetical	protein.	
2 0	CEUSSZ.		
S C	Corynebacter	Corynebacterium efficiens.	
ט ס ס	Bacteria; Ac	Bacceria; Actinobacteria; Actinobacteridae; Actinomycetales;	
òò	NOBI TaxID=152794	ringae, corynabacterraceae, corynabacterram. 152794.	
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RP	SEQUENCE FROM N.A.	OM N.A.	
RC	STRAIN=YS-31	STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;	
RA	Kawarabayasi	i Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,	
RA	Ikeo K., Suz	zuki M., Mashima J., Itoh T., Yamaqishi A., Nishio Y.,	
RA	Usuda Y., Su		
RI	"The entire	genomic sequence of Corynebacterium efficiens YS-314.";	
RL	Submitted (M	Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.	
DR	EMBL; AP0052	EMBL; AP005215; BAC17392.1;	
Š	Hypothetical	l protein; Complete proteome.	
S	SEQUENCE 1	SEQUENCE 106 AA; 11382 MW; 73AF6CDBEA7838A6 CRC64;	
ÕÅ	Query Match Rest Local Similarity	24.5%; Score 114; DB 16; Length 106;	
ΣĚ	Matches 23;	a	,
ò	1 TDA	TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ	09 3
QQ	7 TES	TESDVMLATAĞQVDDTMDQVQNELSRLRGVVDSVRGSWAĞQAQVSFDALMNRWNDSARQL	9
ò	61 KQE	KOELDEISTUIROAGVOYSRADEEQQQALSSQMG 94	
Dp	67 QEA	GEALDSISTNIRANARSFDSTEADNAQAFSAVGG 100	

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RESULT 2

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691 ECAALVEELGERRRAADREKSSVAQ---QLGRLAGQARGAAGEAERSAAAAERAQEALDK 747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Stretcomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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STRAIN=A3(2) / M145.
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Thomson N.R., James K.B., Harris D.B., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete genome sequence of the model actinomycete Streptomyces
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SEQUENCE 1186 AA; 128723 MW; CB11027815373E99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Murphy L., Harris D.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                Last sequence update)
Last annotation update)
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                             1186 AA
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Pfam; PF02463; SMC_N; 1.
PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
                                                                                                                                                                   Putative chromosome associated protein
                                                                                      Created)
                             PRT;
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33.0%;
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Best Local Similarity 55..
Best Acal 31; Conservative
                                                                                   01-MAY-1999 (TrEMBLrel. 10,
                             PRELIMINARY;
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                             Q9ZBQ2;
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1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
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Pridmore R.D., Arigoni F.;
Pridmore R.D., Arigoni F.;
Pridmore R.D., Arigoni F.;
Pridmore R.D., Arigoni F.;
Pridmore Sequence of Bifidobacterium longum reflects its adaptation
to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
EMBL, AE0146114, AAUS3700.1;
Hypothetical protein; Complete proteome.
SEQUENCE 96 AA; 10431 MW; 7D02BE38C6BIF6IC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 ERI---SGDLKTQIDQVESTAG-----SLQGQWRGAAGTAAQAAVVRFQEAANKQKQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                    Bifidobacterium longum.
Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger
Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
Pridmore R.D., Arigoni F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 108;
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19.8%; Pred. No. 0.6;
ive 26; Mismatches 47; Indels
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01-07T-2002 (TrEMBLrel. 22, Last sequence update)
01-07T-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein Cgl0579.
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Last annotation update)
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27.3%; Pred. No. 0.53;
tive 17; Mismatches 37;
AA.
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
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96
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                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=NCC 2705;
MEDLINE=22294977; PubMed=12381787;
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PRELIMINARY;
                                                     01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                                                                                            Hypothetical protein
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RESULT 3 Q8G878

20; Gaps

RESULT 5 Q9X367

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550 KQAGENHYSNLSSDYETQIKSLESSL------TNSOAECVSFOEKINELNSOID 597
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                                                                                                                                                                                                 DB 3; Length 750;
                                                                                                                                                                                                                                    23; Indels
                            STRAIN-972h.;
Wood V., Barrell B.G., Rajandream M.A.;
Submitted (BCE-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AL009227, CAA1821.1; -.
GeneBB SPombe; SPAC27D7.02c; -.
InterPro; IPR000237; GRIP_domain.
Pfam; PF01465; GRIP_1.
SEQUENCE. 750 AA; 87265 MW; A469AD95C5787042 CRC64;
                                                                                                                                                                                             19.3%; Score 90; DB 3
28.2%; Pred. No. 6.3;
tive 18; Mismatches
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Best Local Similarity 28.2%,
".hes 24; Conservative 1
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les 29, Conserv
                 FROM N.A.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-A2012; PLASMID-PXO1;
MEDLINE=22061436; PubMed=12004073;
MEDLINE=22061436; PubMed=12004073;
MEDLINE=22061436; PubMed=12004073;
Med Tables S. L., Pop M., Shumway M., Umayam L., Jiang L.,
Holtzapple E., Busch J.D., Smith K.L., Schupp J.M., Solomon D.,
Keim P., Fraser C.M.;
"Comparative Genome Sequencing for Discovery of Novel Polymorphisms in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                            STRAIN=Sterne; PLASMID=virulence plasmid PX01;
MEDLINE=9945483; PubMed=10515943;
Okinaka R.T.; Cloud K., Hampton O., Hoffmaster A.R., Hill K.K.,
Keim P., Koehler T.M., Lanke G., Kunano S., Mahillon J., Manter D.,
Martinez Y., Ricke D., Svensson R., Jackson P.J.;
"Sequence and organization of pX01, the large Bacillus anthracis
plasmid harboring the anthrex toxin genes.";
"Jacketiol. 181:6509-6515(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
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                                                                                                                                                                                        Plasmid virulence plasmid PX01, and Plasmid pX01.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=972h-; McDougall R.; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
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Bacillus anthracis...

Bacillus anthracis...

Science 296:2028-2033(2002).

EMBL, AF065404, AAD324022.1; -..

EMBL, AE011900, AAM36135.1; -..

FROSITE; PS00678; WD-REPEATS...

PROSITE; PS00678; WD-REPEATS...

Hypothetical protein; Plasmid.

SEQUENCE 410 AA; 45798 MW; FIOBCO4607575C7D CRC64;
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                                                                                                   Last sequence update)
Last annotation update)
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01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Coiled coil protein with GRIP domain.
SPAC27D7.02C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 -----QELDEISTNIRQAGVQYSRADE
                                                                                  Created)
                                                                            01-NOV-1999 (TrEMBLrel. 12, Cr. 01-NOV-1999 (TrEMBLrel. 12, La 01-NAR-2003 (TrEMBLrel. 23, La PXOI-99 (Hypothetical protein)
                                              PRELIMINARY;
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                                                                                                                                                                      anthracis.
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                                            Q9X367
Q9X367;
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SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harris
                                                                                                                                                                                                                                                                                                                                                                                                                               Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeler K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Bashama D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd W. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandram M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Bociphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                Churcher C., Har
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 97;
                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL021930; CAA17362.1; -.
EMBL; AE006937; AAK44524.1; -.
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Hypothetical protein, Complete proteome.
SEQUENCE 97 AA, 9778 MW, 927527DA610A1637 CRC64;
                                                  annotation update)
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Pred. No. 1.1;
8; Mismatches 43;
       Last sequence update)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation updat Hypothetical 9.8 kDa protein (PE family protein) RNG97 OR MTV035.15 OR MT0300.
Mycobacterium tuberculosis.
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RESULT 6

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29; Conservative
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Best Local Similarity
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APOLP-III.
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Local Sim
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Q921B9
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SORRERERE
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X MEDLINE=895987; PubMed=9634230;

XA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

A Cole S.T., Brosch R., Parkhill J., Garnier T., Councr R.,

A Gordon S.V., Basham D., Brown D., Chillingworth T., Connor R.,

A Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Cliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

A Sulston J.B., Taylor K., Whitehead S., Barrell B.G.,

RT "Deciphering the biology of Mycobacterium tuberculosis from the

RI Ordice 393:537-544(1998...)

RE EMBL, ALO21287; CAA16105.1; -.

DR EMBL, ALO21287; CAA16105.1; -.
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                                                 18 FAAKAGLMRHTIGQAEQQAMSAQAFHQGESAAAFQGAHARFVAAAAKVNTLLDIAQANLG 77
                    FERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIR 72
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Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
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Bacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae, Mycobacterineae,
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                                                                                                       73 OAGVOYSRADEEQOQALSSOMGF 95
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                                                                                                                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel. 06,
01-JUN-1998 (TrEMBLrel. 06,
01-OCT-2002 (TrEMBLrel. 22,
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Best Local Similarity
Matches 29; Conserv
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Q8VJ87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 FAAKAGLMRHTIGQAEQQAMSAQAFHQGESAAAFQGAHARFVAAAAKVNTLLDIAQANLG 82
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"Evolutionarily conserved mouse tpr is a single-copy gene located on chromosome l.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L. Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.;
                                                                                                                        "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                          DB 16; Length 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
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                                                                                                                                                                                                                                                                                                                                                                                                44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1200 AA; 138973 MW; 616663FBA6B267D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC'2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ298076; CAC40701.1; -
InterPro; IPR005613; AIP3.
Pfam; PF03915; AIP3.
NON_TER 1200 1200
                                                                                                                                                           laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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01-DEC-2001 (TrEMBirel. 19, Last sequence update)
01-OCT-2002 (TrEMBirel. 22, Last annotation update)
Nuclear pore complex-associated protein Tpr (Fragment)
                                                                                                                                                                                                                                                                              102 AA; 10372 MW; 03CB984D6633D2E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                    18.1%; Score 84.5; DE 34.9%; Pred. No. 2.2; tive 7; Mismatches
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Amory L.M.;
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MEDLINE=22297666; Pubmed=12368813;
MEDLINE=22297666; Pubmed=12368813;
Read T.D., Eisen J.A., Seehadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Todoson R.J., Durkin A.S., Haft D.H., Kolnary J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Walther J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis.";
Eukaryota; Metazoa; Arthropoda; Hexapoda; Ineecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Amphipyrinae; Spodoptera.
NCBL TaxID=69820;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 914;
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QBED18,
QBED16,
QBED16,
QBED16,
QBED18,
QBED18,
QBED18,
Q1-MAR-2003 (TEMBirel. 23, Last sequence update)
Q1-MAR-2003 (TEMBirel. 23, Last annotation update)
Prophage LambdaSo, tail length tape meausure protein.
H OR SO293
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llarity 31.2%; Pred. No. 51;
Conservative 14; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nat. Biotechnol. 20:1118-1123(2002).
EMBL; AE015734; AAN55966.1; -.
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Best Local Similarity 26.7%
Matches 27; Conservative
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Matches 20; Conserv
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SEQUENCE 914 AA
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625
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SEQUENCE FROM N.A.
Muschler P.F. Scharf B., Schmitt R.,
Muschler P. Scharf B., Schmitt R.,
Muschyl-accepting chemotaxis protein McpU of Sinorhizobium meliloti.",
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF312876; A4G34154.1;
InterPro, IPR004010; Cache.
InterPro, IPR004010; Cache.
InterPro, IPR004089; Chmtaxis_transd.
InterPro, IPR003669; HAMP.
InterPro, IPR003122; TarH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     570 AVVAQBVRELAQRSANAAKEİKALITİSGEQVHSGVTLVGD----TGRALQAIVVEVQEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATLAGEAGNFERISGDLKTQIDQVESTAG-----SLQGQWRGAAGTAAQAAVVRFQE-
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Schistosomatoidea, Schistosomatidae, Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Induction of protective immunity in mice using a 62-kDa recombinant fragment of a Schistosoma mansoni surface antigen.";
J. Immunol. 149:3612-3620(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Puerto Rican;
MEDLINE=93056536; PubMed=1431131;
Soisson L.M., Masterson C.P., Tom T.D., McNally M.T., Lowell G.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 707;
                                                                                                                                         Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Sinorhizobium.
NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            626 NKHVSAIVTATREOSTGLOFINTAVNTMDOGTOONAAMVEOOTAAS 671
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Pfam; PF02203; TarH; 1.
SMART; SM00304; HAMP; 1.
SMART; SM00203; NA; 1.
SMART; SM50211; CHEMOTAXIS_TRANSDUC_2; 1.
SEQUENCE 707 AA; 74391 MW; A82D7762FD81FFCC_CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAX-2003 (TrEMBLrel. 23, Last annotation update)
                                                                 Last sequence update)
Last annotation update)
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  707 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
17.3%; Score 80.5; D
Best Local Similarity 31.1%; Pred. No. 42;
Matches 33; Conservative 11; Mismatches
                                                                                                         Methyl-accepting chemotaxis protein McpU.
                                              Created)
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Schistosoma mansoni (Blood fluke)
                                       01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2003 (TrEMBLrel. 23,
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Pfam; PF00672; HAMP; 1.
PRELIMINARY;
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01-NOV-1996 (TrEMBLrel
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STRAIN=Puerto Rican;
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Search completed: November 21, 2003, 16:08:11 Job time : 5.6746 secs
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                                                                                                                                                                                                                                                                                                                                                                                         2 DAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQK 61
                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota, Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
NCBI_TaxID=6183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=Brazilian LB;
STRAIN=Brazilian LB;
STRAIN=Brazilian LB;
STRAIN=Brazilian LB;
Weblins 23211444; PubMed=8459827;
Weston D.S., Schmitz J., Kemp M., Kunz W.;
"Cloning and sequence characterization of a complete myosin heavy chain cDNA from Schistosoma mansoni.";
MOI. Biochem. Parasitol. 58:161-164(1993).
EMBL; L01634; AAA23905.1;
HSSP; P08739; IMND.
                                                                                                                                                                                                                                                                                                          17.2%; Score 80; DB 5; Length 528; 22.8%; Pred. No. 34; tive 21; Mismatches 44; Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 TRIQELEEDLEAERAARSKAEKSRQQ-LESEL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 QELDEISTNIRQAGVQYSRADEEQQQALSSQM 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1940 AA
              InterPro; IPR001648; IQ_region.

InterPro; IPR001609; myosin_head.

DR InterPro; IPR002938; Myosin_tail.

InterPro; IPR00533; Tropomyosin.

PR Pfam; PF00612; IQ; 2.

R Pfam; PF00612; Myosin_head; 1.

R Pfam; PF01576; Myosin_head; 1.

R PRINTS; PR00194; TROPOMYOSIN.

SMART; SM00118; IQ; 1.

PROSITE; PS001182; GLAB ADENYLATION; 1.

NOW TER
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InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin, head.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR000533; Tropomyosin.
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Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_Lail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRINTS; PR00194; TROPOMYOSIN.
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 22.8%
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SEQUENCE
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17.2%; Score 80; DB 5; Length 1940; 22.8%; Pred. No. 1.4e+02;

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                      2 DAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQK 61
 6; Gaps
21; Conservative 21; Mismatches 44; Indels
                                                                                         62 QELDEISTNIRQAGVQYSRADEEQQQALSSQM 93
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AAW32449 standard; Protein; 391 AA
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1 MVDFGALPPEINSARMYAGP.....SGVLRVPPRPYVMPHSPAAG 391
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1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop.10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Mycobacterium tube	. Mycobacterium tube	M. tuberculosis im	Mycobacterium tube	M. tuberculosis an	M. tuberculosis re	Mycobacterium spec	M. tuberculosis an	Mycobacterium sp.
SUMMARIES	AAW32449	AAW32381	AAW81702	AAW64335	AAY39132	AAY38989	AAY04778	AAU01888	AAE29707
DB	181	18	13	13	20	20	20	22	23
% Query Match Length DB	391	391	391	391	391	391	391	391	391
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                                  New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also
                                                                                                                 (or
                                                                                                   A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (of its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TbH-9FL The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins BSAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or prevention).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gen; immunogen; vaccine; tuberculosis; non specific adjuvant;
testing; M.tuberculosis.
                                                                                                                                                                                                                                         100.0%; Score 1949; DB 18; Length 391; 100.0%; Pred. No. 4.8e-143; ive 0; Mismatches 0; Indels 0;
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                                                                                Example 3; Page 138-139; 168pp; English.
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  WPI; 1997-192903/17
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for diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TDH-9PT The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
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100.0%; Pred. No. 4.8e-143;
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96US-0680573.
95US-0523435.
95US-0532136.
96US-0620280.
96US-0658800.
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Best Local Similarity 100.0
                                                                                                                                                                                                                                                      Campos-neto A, Dillon D
Twardzik DR, Vedvick TH;
                                                                                                                                                                                        CORP.
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N-PSDB; AAT91455.
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TbH-9FL.

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tuberculosis strain H37Rv.

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us-09-688-672a-26.rag

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Tuberculosis; infection; diagnosis; antigen;
                                                                                                                                       Mycobacterium tuberculosis antigen TbH-9FL.
                                               AAW64335 standard; Protein; 391
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                                                                                                                                                                                                                                                                                                                             13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                            11-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                        Campos-Neto
                                                                                                          09-NOV-1998
                                                                                                                                                                                                                                                                23-APR-1998
                                                                            AAW64335;
                                                                                                                                                                                                                                                                                                                                                                                                                       SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61. SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunishing against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVDFGALPPEINSARMYAGPGSASIVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LIATNLIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 MYSMANNHMSMINSGVSMINISSMIKGFAPAAAAQAVQIAAQNGVRAMSSIGSSIGSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                          Tuberculosis, immunogenic; soluble, antigen, protective immunity, TB, vaccine, pharmaceutical; infection, diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - use to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
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100.0%; Pred. No. 4.8e-143;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                             Houghton R, Lodes MJ; ik DR, Vedvick TS;
                             M. tuberculosis immunogenic polypeptide TbH-9FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3B; Page 128-129; 230pp; English
                                                                                                                                                                                                                                                                                                             Campos-Neto A, Dillon DC, Hou
Reed SG, Skeiky YAW, Twardzik
                                                                                                                                                                                                  97WO-US18293
                                                                                                                                                                                                                              97US-0818112
96US-0730510
                                                                                                          Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                           Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 391, Conservative
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                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391 AA;
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                                                                                                                                      WO9816646-A2
                                                                                                                                                                                                  07-OCT-1997;
                                                                                                                                                                                                                                13-MAR-1997;
11-OCT-1996;
27-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MYDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This polypeptide comprises Mycobacterium tuberculosis antigen TDH-9FL. It is encoded by genomic DNA (see AAV44395) isolated from tw. tuberculosis strain H37kv genomic DNA (see AAV44395) isolated from clone TDH-9 (see AAV44371). The invention relates to compositions and methods for diagnoshing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, or an immunogenic portion of an M. polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using primers, for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                          New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1949; DB 19;
Pred. No. 4.8e-143;
; Mismatches 0;
                                                                                                                                                        DC, Houghton R, Lodes M
Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 133-135; 250pp; English.
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and diagnosis of tuberculosis
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97US-0818111.
96US-0729622.
                                                                                                                                                    Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 391; Conservative
                                                                                                                                                                                         Skeiky YAW,
                                                                                         (CORI-) CORIXA CORP.
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                LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
                                                                 The present invention describes polypeptides comprising an immunogenic are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments. can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion tuberculosis-immune subjects. AA219249 to AA219460 and AAX39033 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antigens from Mycobacterium tuberculosis useful in diagnostic
skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis, M. tuberculosis, antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Houghton R;
                                                                                                                                                                                                                                                                  M. tuberculosis antigen TbH-9FL amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campos-Neto A, Dillon DC, Hendrickson RC, Ho
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                   GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                       GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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                                                                                                                                                                                         AAY39132 standard; Protein; 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0025197
                                                                                                                                                                                                                                                                                                                     immune response; skin test.
                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
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Best Local Similarity 100.
Matches 391; Conservative
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N-PSDB; AAZ19305.
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                                                                                                                                                                                                                                          LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
                                                                                                                                                                                                                                                               This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                   LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPENTSAGG
                                                                             181 LLEQAAAVEEASDTAAANQLANNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                    LLEQAAAVEEASDTAAANQLMMNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Houghton R;
Vedvick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M. tuberculosis recombinant antigen protein TbH-9FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dillon DC, Hendrickson RC, HosG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                           GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                         GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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98US-0024753
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Lodes MJ, Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine, immunity
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18-FEB-1998;
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                                                                                                                       181
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                                                                                                                                                                                                                                                                                                                                    361
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Length 391;

100.0%; Score 1949; DB 20;

Query Match

1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 60 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG

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methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection.
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                                                                                                                                                                                                                                                                                                                                      LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
                                                                                                                                                                                                                                                                                                                                                                MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
                                                                                                                                                                                                                                                                                                                                                                                MYSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                             LGGGVAANLGRAASVGSLSVPQAWAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
                              as Mtb39A), an M. tuberculosis antigen. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency
                                                                                                                                                                                                              9
                                                                                                                                                                                           1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                         MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                             LIAINLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                  LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLILPFEEAPEMTSAGG
                                                                                                                                                                                                                                   SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                       SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                      Gaps
                   sequence represents Mycobacterium tuberculosis TbH9 (also known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccine; immunity; diagnostic agent; gene therapy; TbH9FL antigen
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                                                                                                                                              Length 391;
                                                                                                                                                                     Indels
                                                                                                                                               9; DB 22;
4.8e-143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TbH9FL antigenic protein.
                                                                                                                                               100.0%; Score 1949;
100.0%; Pred. No. 4.8
                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
Page 151-152; 168pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guderian J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE29707 standard; Protein; 391
                                                                                                                                                          100.08;
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                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 391, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                            391 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium sp
                                                                                                        disease, AIDS.
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 Example 2;
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous bolynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agants and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is
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                                                                                                     New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIP, Mis or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microogganisms e.g. Leishmania and Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mysmannhmsminsgysmintlssmikgfapaaaaqayqiaaqngyramssigssigssg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATILIPFEEAPEMTSAGG
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tuberculosis; infection; vaccine; MTB39; TbH9 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 391;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium sp. TbH9FL antigenic protein.
                                                                                                                                                                                                                                                                                            Disclosure; Page 86-87; 155pp; English.
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Best Local Similarity 100.
Matches 391, Conservative
WPI; 2002-759844/82.
N-PSDB; AAD47082.
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301 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Di-antigen fusion protein, termed Mtb59f, composed of the antigens TbH9 and Ra35. The fusion protein is expressed in host cells using a vector carrying a polymucleotide (see AA22026) comprising the coding sequences for the 2 antigens. The invention provides fusion proteins (see AA32059-71) containing at least 2 Mr ubscrulosis antigens. The new fusion proteins and polymucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed) for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-Mr tuberculosis antibodies), monitoring more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis
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0
                                                                                                                                                                                                                                                                                                                                                                   antigen; fusion protein; Mtb59f; TbH9; Ra35;
                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis antigen fusion protein Mtb59f.
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100.0%; Pred. No. 8.1e-143;
ive 0; Mismatches 0;
                                               GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                     361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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                                                                                                                                                                                                                                                                                                                                                                                         diagnosis; therapy; vaccine; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Met/His tag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                          AAY32070 standard; Protein; 596
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391; Conservative 0;
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/note= "TbH9"
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                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
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/note=
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N-PSDB; AAZ20205.
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Best Local Similarity
Matches 391; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  596 AA;
                                                                                                                                                                                                                                                                                                                                                                   Tuberculosis;
                                                                                                                                                                                                                                                                               17-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
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                                                                                                                                                    RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and creatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting hunoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a non-human patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. WTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is Mycobacterium species
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                                                                                                                                                                                                                                                                                                                                                          Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 83; Page 102-103; 136pp; English.
                                                                                                                                                                                                                                                    Skeiky Y, Reed S, Alderson M;
                                                                                                                                           20-JUN-2000; 2000US-0597796.
                                                                                                     20-JUN-2001; 2001WO-US19959
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Best Local Similarity 100.
Matches 391; Conservative
                                                                                                                                                                                                                                                                                             2002-147798/19.
                                                                                                                                                                                                            (CORI-) CORIXA CORP.
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                 WO200198460-A2
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N-PSDB; AAD28344.
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Matches 391; Conserv
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01-FEB-2001;
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                                                                                                                                                                                                      LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
                                                                                                                                                                                                                                             LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 248
                                                                                                                                                                                                                                                                                      MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
                                                                                                                                                                                                                                                                                                                             249 MYSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG 308
                                                                                                                                                                                                                                                                                                                                                                    LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
                                                                                                                                                                                                                                                                                                                                                                                              New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and
                                                                                                                                                MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                         LIATNLLGQNTPALAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPENTSAGG
                                                                               SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium sp. MTB59F fusion protein.
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Chimeric - Mycobacterium tuberculosis.
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N-PSDB; AAD47086.
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microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusic polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is MTB59F fusion protein. This fusion protein comprises Ra35 protein from Mycobacterium tuberculosis and TbH9 protein from Mycobacterium sp.
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losis; infection; vaccine; MTB59F; TbH9-Ra35 protein.
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                                                                                                                                                                                                                                                   Length 596;
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Pred. No. 8.1e-143;
Mismatches 0;
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                                                                                                                                                                                                                       polynucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or call-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. WIB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is Mycobacterium species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89
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                                                                       The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nuclectides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention are useful for eliciting an immune response in a mammal, e.g., human, immunised with BCG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the
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Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in
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100.0%; Pred. No. 8.1e-143;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigenic fusion protein Tb59-Ra35 (Mtb59f).
                                                     5; Page 114-115; 136pp; English.
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                                                                                                                                                                                                                                                                                                                                               MTB59F (TbH9-Ra35) fusion protein.
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The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protein coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents an M. tuberculosis fusion protein
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Fusion protein; tuberculosis; Mycobacterium tuberculosis; tuberculostatic; immunogen; vaccine; Tb59-Ra35; Mtb59f.
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                                                                                   - Mycobacterium tuberculosis
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597
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                                                                                                                                                                                        'label= OTHER
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97US-0942578.
98US-0025197.
98US-0056556.
98US-0223040.
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Best Local Similarity 100.
Matches 391, Conservative
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SKEIKY Y A.
DILLON D C.
ALDERSON M.
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07-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a recombinant Mycobacterium tuberculosis tri-antigen fusion protein, termed Mtb61f, composed of the antigens TDH9, DPV and MTI. The fusion protein is expressed in host cells using a vector carrying a polynucleotide (see AA220203) comprising the coding sequences for the 3 antigens. The invention provides fusion proteins (see AAY32059-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polynucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                     Tuberculosis, antigen, fusion protein, Mtb61f, TbH9, DPV, MTI, diagnosis, therapy, vaccine, immunogen.
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                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis antigen fusion protein Mtb61f.
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98US-0223040.
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APPLICANT: Reed, Steven G.
APPLICANT: Red, Steven G.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
ITILE DE INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
ITILE OF INVENTION: LAD INGENOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED: and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                             Sequence
                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                     Sequence
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CITY: Seattle
COMPTRY: USA
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPATION:
COMPUTER: IBM PC COMPATION:
COMPUTER: IBM PC COMPATION:
COMPUTER: IBM PC COMPATION:
COMPUTER: IBM PC COMPATION:
COMPUTER: IBM PC COMPATION:
COMPUTER: IBM PC COMPATION:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REPREMENCE/DOCKET NUMBER: 210121.411C6
TELEPHONE: (206) 682-601
INFORMATION FOR SEQ 1D NO: 107:
US-08-095-734-2
US-08-444-623-2
US-08-441-869-2
US-09-342-563-2
US-09-342-08267-2
US-09-073-009-14
US-09-072-591A-20437
US-09-072-591A-20437
US-09-252-991A-20437
US-09-864-0368-3
US-08-864-0368-47
US-09-894-998A-47
US-08-861-464-8
US-08-861-464-8
US-08-334-8
US-09-323-433A-8
US-09-323-433A-8
US-09-334-736E-1
US-08-9911-364-1
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100.0%; Pred. No. 2.7e-154;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 107, Application US/08818112 Patent No. 6290969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 391; Conservative
    single
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TOPOLOGY: linear
    4444400044402750000
    Sequence 107, App
Sequence 102, App
Sequence 102, App
Sequence 2, Appl
Sequence 111, App
Sequence 111, App
Sequence 111, App
Sequence 116, App
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991, APP
991, APP
992, APP
1126, APP
1142, APP
115, APP
115, APP
116, APP
117, APP
116, APP
116, APP
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116, APP
116, APP
                                                                                                                                November 21, 2003, 15:58:31; Search time 8.24558 Seconds (without alignments) 2006.354 Million cell updates/sec
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1 MVDFGALPPEINSARMYAGP......SGVLRVPRRPVVMPHSPAAG 391
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Sequence 9
Sequence 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Issued_Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                      GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-09-818-111-102
US-09-072-596-102
US-09-072-596-102
US-08-818-111-106
US-08-818-111-106
US-08-818-111-106
US-08-818-111-104
US-08-818-111-104
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US-08-818-111-91
US-09-072-596-92
US-09-072-596-92
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US-09-072-596-92
US-09-072-596-92
US-09-072-596-92
US-09-072-596-92
US-09-073-009-142
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US-08-311-731A-208
US-08-818-112-114
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                                                                                                                                                                                                                                                                                                                                                 328717 segs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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us-09-688-672a-26.rai

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STRANDEDNESS:
TOPOLOGY: 111
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                                                 120
                                                                       SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
                                                                                                                        121 LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSAGG 180
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1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 60
                                                 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentUI Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13 MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                         GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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NAME: Maki, David J.
REGISTRATION WUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 102, Application US/08818111
Patent No. 6338852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206) 682-6931
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
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amino acid
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US-08-818-111-102
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Patent No. 6350456

GENERAL INFORMATION

APPLICANT: Reed, Steven G.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND

NUMBER OF SEQUENCES: 241

CORRESPONDENCE ADDRESS:
                                                           .
0
      Length 391;
                                                           Indels
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APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J. 31,392
REGISTRATION NUMBER: 21,392
REGISTRATION NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 682-6931
100.0%; Score 1949; DB 4;
100.0%; Pred. No. 2.7e-154;
ive 0; Mismatches 0;
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6300 Columbia Center, 701 Fifth Avenue
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WIDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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amino acid
   Query Match
Best Local Similarity 100.0
Matches 391; Conservative
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CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
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301 LGGGVAANIGRAASVGSLSVPQAWAAANQAVTPAARALPITSLTSAAERGPGQMLGGLPV 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 LIATNILGONTPALAVNEAEYGEMWAQDAAMFGYAAATATATATLLPFEEAPEMTSAGG
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                                                                                                                                                                                                                                                               1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                                                                                    Length 391;
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99.7%; Pred. No. 1.7e-153;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                100.0%; Score 1949; DB 4;
100.0%; Pred. No. 2.7e-154;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                                                            LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 99.7 Matches 390; Conservative
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Matches 391; Conservative
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                                                                                                                                         US-09-072-596-102
                                                                                                                        TOPOLOGY:
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US-09-223-040-2
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                                                                                 Gaps
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                                      Length 391;
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APPLICANT: Reed, Steven G.
APPLICANT: Reid, Yasir A.W.
APPLICANT: Campos Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Lodes, Michael R.
APPLICANT: Lodes, Michael J.
APPLICANT: Rendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 99104-7092
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
                                    Score 1949; DB 4;
Pred. No. 2.7e-154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                 100.0%; Scot.
100.0%; Pred. No. z..
0; Mismatches
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMOMICATION INFORMATION:
TELEPHONE: (206) 622-4900
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05-MAY-1998
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Patent No. 6458366
                                  Query Match
Best Local Similarity 100.(
Matches 391, Conservative
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CLASSIFICATION:
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US-09-072-596-102
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STATE: Wa
COUNTRY:
US-09-056-556-10
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ADDRESSEE:
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                           SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                  LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
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APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCUNTRY: USA
ZIP: 98104-7092
COMPUTER: RELABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Date of the compatible
COMPUTER: Date of the compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/818,112
FILING DATE: 13-MAA-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAAI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/POCKET NUMBER: 210121.411C6
TELEPHONE: (206) 622-601
TELEPHONE: (206) 622-601
TELEPHATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 anino acids
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6300 Columbia Center, 701 Fifth Avenue
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Patent No. 6290969
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Dillon, Davin C.
Campos-Neto, Antonio
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ADDRESSEE: SEED and
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APPLICANT:
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Length 396;

DB 3;

84.8%; Score 1652.5;

Query Match

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61 SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
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                                                                            1 MVDFGALPPEINSARMYAGPGSASIVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                            Gaps
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APPLICANT: Campos-Neco, Anconia
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
CORRESPONDENCE ADDRESS:
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTONNEY/AGENT INFORMATION:
NAME: Maki, David 1 31,392
REGISTRATION NUMBER: 210121.417C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 GLPVGQMGARAG--GGLSGVLRVPPRPYVMPHSPAAG 391
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     Pred. No. 1.3e-129;
                         19; Mismatches
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Patent No. 6338852
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
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Dillon, Davin C.
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84.98;
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
Best Local Similarity 84.9
Matches 337; Conservative
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                7;
                                                                                                                                                             Length 396;
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APPLICANT: Dillot, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Hodylck, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Lodes, Michael J.
APPLICANT: Hondrickson, Ronald C.
TITLE OF INTENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF WINNER, OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
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APPLICATION NUMBER: US/09/072,596
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                                                                                                                                                    84.8%; Score 1652.5; DB 4
84.9%; Pred. No. 1.3e-129;
iive 19; Mismatches 34;
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05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 106, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAK!, DAVIG J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                              Query Match
Best Local Similarity 84.9%
Matches 337; Conservative
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STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
            TYPE: amino acid
STRANDEDNESS:
                                                                  TOPOLOGY:
US-09-056-556-111
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                                                                                                                                                                                                                                                                      US-09-08-510-11, Application US/09056556

| Sequence 111, Application US/09056556
| Patent No. 6350456
| GENERAL INFORMATION:
| APPLICANT: Read, Steven G. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Dillon, Davin C. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
| CORRESPONDENCE ADDRESS: 241
| CORRESPONDENCE ADDRESS: 241
| CORRESPONDENCE ADDRESS: 241
| CORRESPONDENCE ADDRESS: 341
| CORRESPONDENCE ADDRESS: 341
| CORRESPONDENCE ADDRESS: 341
| CORPUTER FARDABLE FORM: Amaington CONNTRY: USA 21P: 19104-7092
| COMPUTER READABLE FORM: MEDIUM TYPE: FLEPPY disk COMPUTER READABLE FORM: PC-DOS/NS-DOS SOFTWARE: PREFICI POPPY disk COMPUTER READABLE FORM: PC-DOS/NS-DOS SOFTWARE: PREFICI POPPY DATA: O7-APR-1998 CEASIFICATION NUMBER: 21,309/056,556 FILING DATE: O7-APR-1998 CEASIFICATION NUMBER: 21,302 REFRENCE/DOCKET NUMBER: 21,302 REFRENCE/DOCKET NUMBER: 21,302 REFRENCE/DOCKET NUMBER: 21,302 REFRENCE/DOCKET NUMBER: 21,204 CEASIFICATION NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 REFRENCE/DOCKET NUMBER: 21,305 RE
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                                                                                                                           DB 4; Length 396;
                                                                                                                  84.8%; Score 1652.5; DB 4; Length
84.9%; Pred. No. 1.3e-129;
ive 19; Mismatches 34; Indels
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                                                                                                            Query Match
Best Local Similarity 84.99
Matches 337; Conservative
STRANDEDNESS:
TOPOLOGY: linear
                                 ; TOPOLOGY:
US-08-818-111-106
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COMPUTER READABLE FORM:
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SOFTWARE: PatentI
                                                                                                                                                                                                                                                            linear
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COMPUTER: IB
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US-08-818-112-109
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US-08-818-111-104
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                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                         DB 4; Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 109, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos Natir A.W.
APPLICANT: Campos Nation Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                          Indels
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COUNTRY: MASHINGSON
ZIP: 98104-7092
COMPUTER READABLE FORM:
NEDIUM TYPE: Floppy disk
COMPUTER: 1BM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
CORRESSED: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                          34;
                                                                                                                                                                                                        Query Match

84.8%; Score 1652.5; DB 4
Best Local Similarity 84.9%; Pred. No. 1.3e-129;
Matches 337; Conservative 19; Mismatches 34;
   210121.417C9
REFERENCE/DOCKET NUMBER: 2101
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
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                                                                                                                      TYPE: amino acid STRANDEDNESS:
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US-09-072-596-106
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US-08-818-112-109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 359;
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APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
CORRESPONDENCE: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 76.3%; Score 1486.5; DB 3; Length Best Local Similarity 84.2%; Pred. No. 7.2e-116; Matches 303; Conservative 16; Mismatches 36; Indels
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                                                                                                                                     210121.411C6
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Patent No. 6338852
GENERAL INFORMATION:
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6300 Columbia Center,
                                                ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGIESTRATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 2101:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campos-Neto, Antonia
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Dillon, Davin C.
                                                                                                                                                                                                         TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, Steven G. APPLICANT: Skeiky, Yasir A. WAPPLICANT: Dillon, Davin C. APPLICANT: Campos-Neto, Anto APPLICANT: Houghton, Raymonn APPLICANT: Vedvick, Thomas S. APPLICANT: Twardzik, Daniel
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                    : 359 amino acids amino acids
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TUBERCULOSIS
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APPLICANT: Reed, Steven G.

APPLICANT: Skeiky, Yasır A.W.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Twardaik, Thomas S.

APPLICANT: Twardaik, Daniel R.

APPLICANT: Hendrickson, Ronald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and RPDPL.
                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                       76.3%; Score 1486.5;
84.2%; Pred. No. 7.2e
                                                                                                                                                                                                                                                                                                                                                                                                                    16; Mismatches
                          ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELETAX: (206) 682-691
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 104, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION;
                                                                                                                                                                                                                                 LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Matches 303; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washing
           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                         US-09-056-556-109
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Patent No. 6350456

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle washington
COUNTRY: USA
ZIP: WASHINGTON
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                  76.3%; Score 1486.5; DB 4; 84.2%; Pred. No. 7.2e-116; ive 16; Mismatches 36;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAXI, DAVIG J. 392
REFRENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: (206) 622-4900
TELEPRAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 104:
LENGTH: 359 amino acids
                                                                                                                                                                                                                                                                                             LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 84.2*
Matches 303; Conservative
                                                                                                                                                                                                                                                                                                                                                                       linear
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US-09-056-556-109
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SV 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 VSSIANNHMSMMGTGVSMTNTLHSMLKGLAP-AAAQAVETAAENGVWAMSSLGSQLGSSL 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SSAGLMAAAASPYVAWMSVTAGQAQLTAAQVRVAAAAAYETAYRLTVPPPVIAENRTELMT
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                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 91, Application US/08818112
| Fatent No. 6290969
| GENERAL INFORMATION:
| APPLICANT: Reed, Steven G. |
| APPLICANT: Skeiky, Yasir A.W. |
| APPLICANT: Olilon, Davin C. |
| APPLICANT: Campos-Neto, Antonio APPLICANT: Houghton, Raymond |
| APPLICANT: Vedvick, Thomas S. |
| APPLICANT: Vedvick, Thomas S. |
| APPLICANT: Trile OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY |
| TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS |
| MINDER OF SEQUENCES: 153
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                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 359;
                                                                                                                                                                                                                                                                                                                                                                                  ; Score 1486.5; DB 4; Length; Pred. No. 7.2e-116; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                 210121.41709
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-WAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORWATION:
NAME: MAK! David J.
RECISTRATION NUMBER: 310121.417C
TELECHONINICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-4900
TELEFAX: (206) 622-631
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                  76.3%;
84.2%;
                                                                                                                                                                                                                                                              LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 84.25
Matches 303; Conservative
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US-09-072-596-104
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US-08-818-112-91
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APPLICANT: Callon, Davin C.
APPLICANT: Gampos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Target, Daniel R.
APPLICANT: TARGET S.
APPLICANT: TARGET S.
CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 13-MAR-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 31,392

REGISTRATION NUMBER: 31,392

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 31,392

REFERENCE/CORTION INFORMATION:

TELEPRAX: (206) 622-4900

TELEPRAX: (206) 622-4900

INPORMATION FOR EAQ 10 0:

SEQUENCE SEQ ID NO: 91:

SEGUENCE SEQ ID NO: 91:

SEGUENCE 263 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6300 Columbia Center, 701 Fifth Avenue
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Sequence 92, Application US/08818111

Parent No. 6338852

GENERAL INFORMATION:
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APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
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74 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGGNTPA 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 IAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
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APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/POCKET NUMBER: 210121.417C6
FILECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6931
FILEPHONE: (206) 682-6931
FILEPHONE: ARAACTERISTICS:
LENGTH: 263 amino acids
FYPE: amino acid
STRANDEDRESS: single
TOPOLOGY: linear
US-08-818-111-92
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Search completed: November 21, 2003, 16:11:39 Job time : 9.24558 secs

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; Search time 15.2499 Seconds (without alignments) 4680.740 Million cell updates/sec
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1949
1 WVDFGALPPEINSARMYAGP......SGVLRVPPRPYVMPHSPAAG
                                                                                                                                                                                                                                                                                                                                           Published Applications AA:*

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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                November 21, 2003, 16:08:22 ; Search
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Maximum Match 100%
Listing first 45 summaries
                                                         protein search, using sw model
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2 US-10-084-843-109
2 US-10-104
2 US-10-38-002-104
2 US-10-359-460-8
2 US-10-359-460-8
2 US-10-103-002-92
2 US-10-103-002-92
2 US-10-103-002-92
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US-09-791-171-92 US-09-804-980-92

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Ouery Natch Length DB ID Description

No. Score Match Length DB ID Description

2 1949 100.0 391 12 US-10-084-843-107 Sequence 102, App 2 100.0 391 12 US-10-193-002-102 Sequence 102, App 4 1949 100.0 396 12 US-10-088-732A-14 Sequence 26, Appl 5 1949 100.0 596 12 US-10-359-460-26 Sequence 26, Appl 6 1949 100.0 596 12 US-10-359-460-26 Sequence 22, Appl 7 1949 100.0 596 12 US-10-359-460-22 Sequence 22, Appl 8 1949 100.0 600 9 US-10-359-460-22 Sequence 22, Appl 10 1949 100.0 600 9 US-10-359-460-22 Sequence 22, Appl 10 1949 100.0 600 9 US-10-359-460-22 Sequence 22, Appl 10 1944 99.7 729 12 US-10-359-460-2 Sequence 65, Appl 11 1944 99.7 729 12 US-10-359-460-2 Sequence 65, Appl 11 1944 99.7 729 12 US-10-359-460-2 Sequence 16, Appl 13 1944 99.7 729 12 US-10-088-732A-16 Sequence 16, Appl 13 1944 99.7 729 12 US-10-359-460-2 Sequence 16, Appl 14 1652.5 84.8 396 12 US-10-0193-002-106 Sequence 106, Appl 15 1652.5 84.8 396 12 US-10-193-002-106 Sequence 106, Appl 15 1652.5 84.8 396 12 US-10-193-002-106 Sequence 106, Appl 15 1652.5

RESULT 1  US-10-084-843-107  Sequence 107, Application US/10084843  Publication No. US20030143243A1  GENERAL INFORMATION:  APPLICANT: Reed, Steven G.  Campoos-Neto, Antonio  Houghton, Raymond  Vedvick, Thomas S.  Twardzik, Daniel R.  Lodes, Machael G.  Machael G.  Machael G.  Machael G.  Machael G.  Machael G.  Machael G.  Machael G.  Machael G.  Machael G.  Machael G.  Machael G.  Machael G.	Hendrickson, Ronald C.  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INMUNOTHERAPY AND DIAGNOSIS OF TUBERCULOSIS NUMBER OF SEQUENCES: 355 CORRESPONDENCE ADDRESS: ADDRESSED: SEED and BERRY LLP STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle STATE: Washington COUNTRY: USA ZIP: 98104-7092	COMPUTER READABLE FORM:  MEDLINM TYBE: Floppy disk COMPUTER: IBM PC compatible OPERATURG SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NATA: APPLICATION NABER: US/10/084,843 FILING DATE: 25-Feb-2002 CLASSIFICATION: <unimal control="" control<="" of="" th="" the=""></unimal>
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APPLICANT: Brannon, Mark
APPLICANT: Brannon, Jeffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIATNILGGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSAGG
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                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                    APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDENESS: single TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 102: US-10-193-002-102
                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/10098732A Publication No. US20030175294A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 391 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-098-732A-14
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Houghton, Raymond
Vedvick, Thomas S.
Twardik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
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STREET: 6300 Columbia Center, 701 Fifth Avenue
STRATE: Washington
                      REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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                                                                                                                                                                                                                                            ; SEQUENCE DESCRIPTION: SEQ ID NO: 107: US-10-084-843-107
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 102, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                               LENGTH: 391 amino acids
                                                                                                                INFORMATION FOR SEQ ID NO: 107: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
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ADDRESSEE: SEED ar
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US-10-193-002-102
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GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Bacid Steven G.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: and Their Uses
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TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION NUMBER: US 08/818,112
PRIOR FILING DATE: 1999-04-07
PRIOR PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR PLILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
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   ; SEQ ID NO 26
; LENGTH: 596
; LENGTH: 596
; CRANISM: Artificial Sequence
; FATURE: PETURE
; CTHER INFORMATION: Description of Artificial Sequence:bi-fusion US-09-287-849-26
                                                                                                                                                                                                                                                                                                        Length 596;
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100.0%; Score 1949; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 391; Conservative 0; Mismatches 0;
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US-10-359-460-26
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APPLICANT: Seelky Yasir A.W.
APPLICANT: Dillon. Davin C.
APPLICANT: Dillon. Davin C.
APPLICANT: Dillon. Davin C.
APPLICANT: Corisa Corporation.
APPLICANT: Compos-Neto, Antonio
APPLICANT: Corisa Corporation.
TITLE OF INVENTION: Fuelon Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: And Their Uses
FILE REFERENCE: 014058-00902087.849
FILE REFERENCE: 014058-00902087.849
CURRENT APPLICATION NUMBER: US 08/918,112
PRIOR APPLICATION NUMBER: US 08/918,112
PRIOR APPLICATION NUMBER: US 09/92,578
PRIOR PILNOR DATE: 1997-10-01
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
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100.0%; Pred. No. 7.1e-146;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: MTB39 full length (TbH9FL)
US-10-098-732A-14
               60/275,837
                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26, Application US/09287849 Patent No. US20020009459A1
PRIOR APPLICATION NUMBER: US 60
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.'
Matches 391; Conservative
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US-09-287-849-26
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TITLE OF INVENTION: Testing Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REPREBNEE: 014058-00902008
CURRENT APPLICATION NUMBER: 020/09/287,849
CURRENT FILING DATE: 1999-04-07
FRICA PAPLICATION NUMBER: US 08/818,112
FRICA FILING DATE: 1997-03-13
FRICA FILING DATE: 1997-03-13
FRICA FILING DATE: 1997-10-01
FRICA FILING DATE: 1997-10-01
FRICA FILING DATE: 1998-04-07
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APPLICANT: Skeiky, Yasix A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos Neto, Antonio
APPLICANT: Corixa Corporation
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ORGANISM: Artificial Sequence
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APPLICANT: Brannon, Mark
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Leishmania Antigen
TITLE OF INVENTION: Leishmania Antigen
TITLE OF INVENTION: Leishmania Antigen
TITLE OF INVENTION: Leishmania Antigen
CURRENT APPLICATION NUMBER: US 10/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 80
                                                                                                                                                                                                                                                                                                               SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                                      ; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion US-10-359-460-26
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COTHER INFORMATION: Description of Artificial Sequence:bi-fusion
FORTHREN INFORMATION: protein TbH9-Ra35 (designated MTB59F)
(S-10-098-732A-20
                                                                                                                                                    Length 596;
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100.0%; Pred. No. 1.2e-145;
ive 0; Mismatches 0;
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US-10-098-732A-20
US-10-098-732A-20
Sequence 20, Application US/10098732A
Publication No. US20030175294A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
ORGANISM: Artificial Sequence FEATURE:
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Matches 391; Conservative
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LIATNILGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of Mycobacterium tuberculosis Antigens
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                                                                                                        LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
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                                           129 LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATALLPFEEAPEMTSAGG
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US-10-359-460-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                   GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 399
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APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dilon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: and Their Uses
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TITLE OF INVENTION: and Their Uses
CURRENT FILING DATE: 1993-04-07
PRIOR PELING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
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; Publication No. US20030147911A1
; GENERAL INFORMATION:
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                         188
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129 LIATNILGQNTPALAVNEAEYGEWWAQDAAAMFGYAAATATATILPFEEAPEMTSAGG
                                                                                             189 ILEQAAAVEEASDTAAANQIMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                               249 WUSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
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OTHER INFORMATION: Description of Artificial Sequence:WTB72FMutSA
OTHER INFORMATION: (Ral2-TbH9-Ra35MutSA)
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100.0%; Score 1949; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.6e-145;
Matches 391; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                   369 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 399
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ORGANISM: Artificial Sequence
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Skeiky, Yasir A.W. Dillon, Davin C.
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LENGTH: 729
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US-10-359-460-2
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442 IGGGVAANLGRAASVGSLSVPQAWAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 501
                                                                                                                                                          Sequence 65, Application US/10098732A

| Sequence 65, Application US/10098732A
| Publication No. US20030175294A1
| GENERAL INFORMATION:
| APPLICANT: Skeiky, Yasir
| APPLICANT: Brannon, Mark
| APPLICANT: Brannon, Mark
| APPLICANT: Coriza Corporation
| TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
| TITLE OF INVENTION: Leishmania Antigen
| TITLE OF INVENTION: Leishmania Antigen
| TITLE OF INVENTION: Leishmania Antigen
| TITLE OF INVENTION: Leishmania Antigen
| FILE REFERENCE: 014058-01201005
| CURRENT APPLICATION NUMBER: US 60/275,837
| FRIOR FILING DATE: 2001-03-13
| NUMBER OF SEQ ID NOS: 80
| SEQ ID NO 65
| LENGTH: 930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:MTB72F-MAPS OTHER INFORMATION: (1954) fuesion construct, TB MTB72F (Ra12-TbH9-Ra35) OTHER INFORMATION: linked to Leishmania thiol-specific antioxidant OTHER INFORMATION: (TSA or MAPS)
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Best Local Similarity 100.0%; Pred. No. 2.2e-145;
Matches 391; Conservative 0; Mismatches 0; Indels 0;
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                                       GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                             502 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 532
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ORGANISM: Artificial Sequence
                                                                                                                                                        US-10-098-732A-65
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Sequence 2, Application US/09287849 Patent No. US20020009459A1

RESULT 11 US-09-287-849-2

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Pred. No. 3.9e-145;
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APPLICANT: DILLON, MARK
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Cargos-Neto, Antonio
APPLICANT: Cargos-Neto, Antonio
APPLICANT: Cargos-Neto, Antonio
APPLICANTON: Fusion Proceiens of Myco;
TITLE OF INVENTION: and Their Uses
FILE REFRENCE: 014058-003008
CURRENT PRILING DATE: 1999-04-07
PRIOR PLILNG DATE: 1997-03-13
PRIOR PLILNG DATE: 1997-10-01
PRIOR PLILNG DATE: 1997-10-01
PRIOR PLILNG DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR PLILNG DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR APPLICATION NUMBER: US 09/056,566
PRIOR PLILNG DATE: 1998-04-07
PRIOR PLILNG DATE: 1998-12-30
PRIOR PLILNG DATE: 1998-12-30
PRIOR PLILNG DATE: 1998-12-30
PRIOR PLILNG DATE: 1998-12-30
PRIOR PLILNG DATE: 1908-12-30
PRIOR PLILNG DATE: 1908-12-30
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; Publication No. US20030147911A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.7%;
Matches 390; Conservative
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
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Gaps

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61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
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                                                                                                                                                                                                                                                                                                                                             Description of Artificial Sequence:tri-fusion protein MTB32-MTB39 fusion)
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ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1944; DB 12;
Pred. No. 3.9e-145;
0; Mismatches 1;
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                      FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
FRIOR APPLICATION NUMBER: US 60/275,837
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
LENGTH: 729
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Skeiky, Yasir A.W.
Dayloo, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vodyick, Thomas S.
Twardzik, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND ME
TITLE OF INVENTION: Leishmania Antigen
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                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.77
Matches 390; Conservative
                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
OTHER INFORMATION:
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                 APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protises of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their uses
TITLE REFERENCE: 014058-009020US
CURRENT PAPLICATION NUMBER: US/10/359,460
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/287,849
PRIOR APPLICATION NUMBER: US/09/287,849
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR PILING DATE: 1997-03-13
PRIOR PILING DATE: 1997-10-01
PRIOR PILING DATE: 1997-10-01
PRIOR PAPLICATION NUMBER: US 09/025,197
PRIOR PAPLICATION NUMBER: US 09/025,56
PRIOR APPLICATION NUMBER: US 09/025,56
PRIOR APPLICATION NUMBER: US 09/025,56
PRIOR APPLICATION NUMBER: US 09/025,56
PRIOR APPLICATION NUMBER: US 09/025,56
PRIOR APPLICATION NUMBER: US 09/025,56
PRIOR FILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-04-07
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99.7%; Pred. No. 3.9e-145;
live 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.7
Matches 390; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2
LENGTH: 729
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261 180 360

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121 LIATNLLGONTPAIAVNEAEYGEMWAQDAAAWFGYAATAATATEALLPFEDAPLITNPGG 180
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                                                                                  METHODS FOR DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34; Indels
                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 98104-7032
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                     ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
STTY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 GLPLGQLINSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
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84.9%; Pred. No. 1.9e-122;
live 19; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATIÓN NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/10/193,002
FILING DATE: 10-U11-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 106:
Transfall, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND ITUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 396 amino acids
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                                                                                                                                                     CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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Best Local Similarity 84.99
Matches 337; Conservative
                                                                                                                              SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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Best Local Similarity 84.9%; Pred. No. 1.9e-122;
Matches 337; Conservative 19; Mismatches 34; Indels
                                                                              COMPUTER: IBM PC_compatible
COMPUTER: IBM PC_compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||:||:
|GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
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                                                                                                                                                                                                                                                                                                                        NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
PILING DATE: 05-WAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                  APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Peb-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 111:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 106, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Netc, Attonia
Houghton, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 111:
           ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
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US-10-193-002-106
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Gaps

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GenCore version 5.1.6
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November 21, 2003, 15:57:31; Search time 8.15692 Seconds (without alignments) 4609.825 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-688-672A-26 1949 1 WVDFGALPPEINSARMYAGP.....SGVLRVPFRPYVMPHSPAAG 391 Title: Perfect score: J Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	probable PPE prote	probable PPE prote	PPE	PPE	PPE	PPE	PPE	y pr	probable PPE prote	PPE	PPE	PPE	probable PPE prote	PPE	PPE	PPE	PPE	PPE	PPE	PPE	PPE L	PPE	PPE	BBE	PPE	BPE	PPE prot	PPE	probable PPE prote
SUMMARIES	Ωï	B70608	07	C70568	9	6	9	9	H87056	9	9	5	9	6	9	8	5	9	a	ന	រោ	D70922	w	A70504	706	05	708	09	വ	œ
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B70524	C70830	A70931	D70676	B70987	C70780	F70846	E70663	A70762	B70969	H70552	F70675	E70808	E70946	F70825	A70647
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	22.6 487														
22.7	22.6	22.6		22.0	21.9	21.7	21.7	21.4	21.4	21.3	21.3	21.3		21.1	21.0

## ALIGNMENTS

9

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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium-tuberculosis
C;Species: Mycobacterium-tuberculosis
C;Species: Mycobacterium-tuberculosis
C;Species: T-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Spacession: G70929
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comoor, R.; Davies, R.; Devihin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Familin, N.; Holroyd, S.; Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atcession: G70929
A;Accession: G70929
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A;Accession: G70929
A;Accession: G70929
A;Accession: Dxalminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Corss-references: GB:AL123456; NID:g3250699; PIDN:CAA17711.1; PID:e1254600
A,Molecule type: DNA
A,Residues: 1-393 «COL»
A,Cross-references: GB:Z95390, GB:AL123456, NID:g3261766, PIDN:CAB08702.1, PID:e316074, A,Experimental source: strain H37Rv
C,Genetics: A,Gene: PPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSSGLGAGVAANLGRAASVGSLSVPPAWAAANQAVTPAARALPLTSLTSAAQTAPGHMLG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SSAGLMAAAASPYVAWMSVTAGQAQLITAAQVRVAAAAYETAYRLTVPPPVIAENRTELMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSS----LGSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 VSSIANNHMSMMGTGVSMTNTLHSMLKGLAP-AAAQAVETAAENGVWAMSSLGSQLGSSL
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40.0%; Score 779.5; DB 2;
Best Local Similarity 43.7%; Pred. No. 4.3e-39;
Matches 179; Conservative 65; Mismatches 129;
                                                                                                                                                                                                                                                                   Score 1583; DB 2;
Pred. No. 1.4e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 GLPLGH-SVNAGSGINNALRVPARAYAIPRTPAAG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357 GLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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                                                                                                                                                                                                                                                                   81.2%;
81.5%;
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Best Local Similarity 81.5
Matches 322; Conservative
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                                                                                                                                                                           probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: H7041
R;Oble, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Natucter, 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Accession: H7041
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C.Speciess: Mycobacterium tuberculosis

C.Speciess: Mycobacterium tuberculosis

C.Speciess: Mycobacterium tuberculosis

C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C.Accession: C70568

R.Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitchead, S.; Barrell, B.G.

A.Fitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; PMID:9634230

A.Stetus: preliminary; nucleic acid sequence not shown; translation not shown
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; Pred. No. 6.4e-91;
18; Mismatches 34;
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   GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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Best Local Similarity 85.1%;
Matches 338; Conservative 1:
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C)Species: Mycobacterium tuberculosis
C)Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C)Accession: H70931
R)Cole, S.T., Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor. R.; Davies, R.; Devlin, K.; Feltwell, T.; Gantles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70931
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DMS
A;Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17728.1; PID:e1254618
A;Genetics:
A;Genetics:
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: 17-011-1998 #sequence_revision 17-011-1998 #text_change 22-Oct-1999
C;Accession: B70331
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 AAQSAAIAHATGASAGAQOTTLSQLIAAIPSVLQGLSSSTAATFASGPSGLLGIVGSGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 WLDKLWALLDPN-----SNFWNTIASSGLFLPSNTIAPFLGLLGGVAAADAAGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 JATNLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 KLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSM-TNTLS---SMLKGFAPAAAQAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 OTAAQNGVRAMSSLGSSL----GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 AARAL---PLTSLTSAAERGPGQMLGGLPVGQMGARAGGGLSGVLRVPP----RPYVMPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFOSVVWGLTVGSWIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 IATNVLGONAPATAATEAQYAEMWSQDAMAMYGYAGASAAAT-QLTPFTEPVQTTNASGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 LGEATSG-----GLGGALVAPLGSAGGLGGTVAAGLGNAATVGTLSVPPSWTAAAPLASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 37.8%; Score 737.5; DB 2; Best Local Similarity 42.6%; Pred. No. 1.3e-36; Matches 181; Conservative 60; Mismatches 123;
| | : | : | : | 353 AAEAPGALFGEMALSSLAGRALAGTAVRSGAGAARV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPAAG 403
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C;Species: Mycobacterium tuberculosis
C;Decies: Mycobacterium tuberculosis
C;Decies: Mycobacterium tuberculosis
C;Decies: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: A70932
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, G.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MUD:98295987; PMID:9634230
A;Reference number: A70500; MUD:98295987; PMID:9634230
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-409 cCOLb
A;Residues: 1-409 cCOLb
A;Residues: 1-409 cCOLb
A;Residues: 1-409 cCOLb
A;Residues: 1-409 cCOLb
A;Residues: PIDN:CAAI7729.1; PID:e125461
A;Genetics:
C;Genetics:
A;Genetics: PPE
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                                                                                                                                                                                                                                                                                                                                                                      GDAAKGLPGLGGMLG----GGPVAAGLGNAASVGKLSVPPVWSGPLPGSVTPGAAPLPVS 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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                                                                                                                                                         180 GTQAAAVATAAGTAQSTLTEMITGLPNALQSLTSPLLQSS-NGPLSWLWQILFGTPNPPT
                                                                                                                                                                                                                                                            LEQAAAVEEASDIAAA-----NQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPH
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                                                                                                                                                                                                                      -----TVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAA
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                     IATNLLGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGL
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                                                                                                                    182 LEQAAAVEEASDTAAA--NQLMNNVPQALQQLAQPTQGTTPSSKLGGLWK-
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llarity 44.7%; Pred. No. 2.2e-37;
Conservative 53; Mismatches 138; Indels
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Best Local Similarity
Matches 177; Conserv
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180 179 214 239 272 298 332 358 388 418

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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: G;Species: Mycobacterium tuberculosis
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.;
Nature 393, 537-544, 1998
A;Reference number: A70500; MyID:98295987; PMID:9634230
A;Reference number: A70500; MyID:98295987; PMID:9634230
A;Reference number: A70500; MyID:98295987; PMID:9634230
A;Residues: 1-408 <COL>
A;Residues: 1-408 <COL>
A;Residues: 1-408 <COL>
A;Cross-references: GB:Z74024; GB:Ali23456; NID:g3250700; PIDN:CAA98377.1; PID:e1301025; A;Genetics:
A;Genetics:
A;Genetics:
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                                                MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                    61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                          180 LAQEVVEEVVEEVVEEVVEEVVEBVVEARQAISQAALDQAVNEGMEATVVPQVDQQVNVDVATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 TQGTTPSSKLGG--LWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 QTAVPDSSSAAAPQLWGGFAQHLSPINDTLSMINNHAGMANAGLSLVNGMGSAMKSLAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 AAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 AATRALSPARVAVATESESAPILGGGLPWAPMVPGGGSGTGGVNTALRLQPRAFVMPRNP
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                                                                                                                                                                                                                                                                                                                                                                                                                    181 L-----VPQALQQ----LEQAAAVEEASDTAAANQLMNN-----VPQALQQ----LAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 TTTKAAESAFKAMGSAVQSTGRGILGSSSGGHVTAQLGRAASIGSLRVPQTWTTASQPVT
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Best Local Similarity 41.8%; Pred. No. 1.1e-34;
Matches 182; Conservative 47; Mismatches 134; Indels
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C:Species: Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: H87056
R:Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HG
R:Davies, R.M.; Butherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, R.; A;Reference number: A86909; MUID:21128732; PMID:11234002
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Reference number: D70931
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-423 <COL>
A; Residues: 1-423 <COL>
A; Residues: 1-423 <COL>
A; Residues: 1-504
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A; Residues: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17722.1; PID:e125461
A; Generics:
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A;Residues: 1-421 <STO>
A;Cross-references: GB:AL450380; NID:g13093150; PIDN:CAC31563.1; GSPDB:GN00147
C;Genetics:
A;Gene: ML1182
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41.1%; Pred. No. 3.4e-36;
iive 55; Mismatches 160; Indels 34;
                                                                                                                                                                                                                                                                                                                                                                                          Length 423
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41.8%; Pred. No. 1.7e-36;
tive 50; Mismatches 123; Indels
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Matches 182; Conservative
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                                                                                                                               probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C,Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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Matches 168; Conservative
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Acession: B70625
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S;
Rajandream, M.A.; Rogers, V.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 39; S37-544, 1998
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Residues: 1-391 cCOL.
A;Residues: 1-391 cCOL.
A;Residues: 1-391 cCOL.
A;Residues: 1-391 cCOL.
A;Gene: PPE
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: PPE
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                                                                                                                                                                                                                    --SGLGGGVAANLGRAASVGSLS 319
                                                                                                                                                                                                                                                                                                                                    VPQAWAAANQAVTPAARALP---LISLISAAERGPGQMLGGLPVGQMGARAGGGLSGVLR 376
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                                                                                                                                                                                                                 QAVQTAAQNGVRAMSSL--GSSLGS---
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Best Local Similarity 42.3'
Matches 166; Conservative
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: C70931
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. adjandresm, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
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36.0%; Score 702; DB 2; Le
39.1%; Pred. No. 1.7e-34;
ive 61; Mismatches 145;
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227 237 291 331

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Cipeciaes Mycobacterium tuberculosis (Strain H3/KV)
Cipeciaes Mycobacterium tuberculosis
Cipeciaes Mycobacterium tuberculosis
Cipeciaes Mycobacterium tuberculosis
Cipeciaes Mycobacterium tuberculosis
Cipeciaes Mycobacterium tuberculosis
Cipeciaes Mycobacterium tuberculosis
Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeglen, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A,Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A,Authors: Anoson, Mycobacterium tuberculosis from the complete genome A,Aecession: A70646
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A;Residues: 1-380 <COL>
A;Cross-references: GB:Z83867; GB:AL123456; NID:g3261695; PIDN:CAB06278.1; PID:e291015; A;Experimental source: strain H37Rv
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                                                                                                                                                                                                                                                                                                               ------WKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQ 276
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                                   180 AGQAAATGQATALASGTNAVTTALSSAAAQFPFDIIPTLLQGLA--TLSTQYTQLMGQLI
                                                                                                                                                                                                                                                                                                                                                238 NAIFGPTGATTYQNVFVTAANVTKFSTWANDAMSAPNLGMTEFKVF-----WQPPPAPE
                                                                                                                                                                                                                                                                                                                                                                                                                     277 AVQTAAQNGVRAMSSLGSSLG----SSGLGGGVAANLGRAASVGSLSVPQAWAAANQAV
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     62 SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
                                                                                                          IATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Uul-1998 #sequence_revision 17-Uul-1998 #text_change 22-Oct-1999
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C;Accession: 17-Uul-1998 #text_change 22-Oct-1999
C;Authors: Sqares, R.; Parkhill, G.; Feltwell, T.; Gentles, S.; Hamin, N.; Holroyd, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
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A;Residues: 1-468 *COL>
A;Cross-references: GB:AL022021; GB:AL123456; NID:93250699; PIDN:CAA17730.1; PID:e125462
A;Experimental source: strain H37Rv
C;Genetics: A;Gene: PPE
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70931
A;Accession: C70931
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A;Genetics:
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 MSSLGSSLG----SSGLGG---GVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPL 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 -SALGAGLGLRSAISSGLGSTAPAISAGASQAGSVGGMSVPPSWAAATPAIRTVAAVFSS 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 ATQGVAVAQAVGASAGN-ARSLVSEVLEFLA--TAGTNYNKTVASLMNAVTGVPYASSVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
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                                                                                                                                                                                                                                                                    Length 463;
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al Similarity 40.9%; Pred. No. 2.8e-33;
164; Conservative 59; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                        Indels
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; Pred. No. 1.2e-33;
48; Mismatches 136;
                                                                                                                                                                                                                                                                      35.3%;
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Best Local Similarity 42.8*
Matches 174; Conservative
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Best Local Similarity
Matches 164; Conservat
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12;

Gaps

28;

179 238

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121 120

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RESULT 15
G70881
probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
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C;Accession: G70881
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Decipharing the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 LEQAAAVEEASDTAAANQ-----LMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSP--H 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 ITFVQNAINGAVN----TTAWFVMATIPNAVFLGHAFAALNPATVTAAADAVPAAAAG 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAGLMVAAASPYVAWMSVTAGOAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGSSLGSSGLGG-GVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAABRG 350
290 GAASVGNTVLASVGRANSIGQLSVPPSWAAPSTRPVSALSPAGLTTLPGTDVAEHGMPG- 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS 61
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                                                                                   349 -VPGVPV-----AAGRASGVLPRYGVRLTVMAHPPAAG 380
                                               354 MLGGLPVGQMGARAGGGLSGVL-RVPPRPYVMPHSPAAG 391
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Search completed: November 21, 2003, 16:09:54 Job time : 9.15692 secs

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us-09-688-672a-26.rsp

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 21, 2003, 15:51:11; Search time 4.61043 Seconds (without alignments) 3988.226 Million cell updates/sec Run on:

US-09-688-672A-26 1949 1 WVDFGALPPEINSARMYAGP......SGVLRVPPRPYVMPHSPAAG 391 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SIMMARIES

		Q11031 mycobacteri		-									Q50703 mycobacteri			rattı		P47033 saccharomyc	O60641 homo sapien	P28284 herpes simp	P76072 escherichia	P35658 homo sapien	Q05233 mycobacteri	P12021 sus scrofa	Q9fec4 chlamydomon	P52172 drosophila	P24856 notothenia	Q10169 schizosacch	Q24523 drosophila		P51611 mesocricetu	-	P71789 mycobacteri	
SUMMARIES	ID	YD61 MYCTU	YS92 MYCTU	YI02_MYCTU	Y442 MYCTU	m			Y096 MYCTU	YU18 MYCTU	YU21_MYCTU	YY29_MYCTU	YY25 MYCTU	ELS MOUSE	YY26 MYCTU	ELS RAT	ELS HUMAN	PRY3_YEAST	A180_HUMAN	ICPO_HSV2H	STFR_ECOLI	N214_HUMAN	VG26_BPML5	APMU_PIG	RAA3_CHLRE	SRP_DROME	ANP_NOTCO	YAUG SCHPO	BUN2_DROME		$\overline{}$	YI36 MYCTU	'o'	YM96_YEAST
	Length DB	96	08	63	87		78		63	34	3.5	78	92	0.0	32	54	30	31	907 1	825	20	060	836	010	783	79	06	54	11	577	0	7.7	432	0
о́ю	Query Match L	5.	ė.	S.	ζ,	ä	•	φ.	ġ	ġ	è.	ς.	ä	•	•	•	•	•	6.9	•	٠		•	•	•	•	•	•	•	•	•	6.3		•
	Score	65	0	688.5	4	•	418	4.	24.	$^{\circ}$	21.	33.	٠	53.	51.	S	•	39.	133	٠	ന	ጣ	m	m	$^{\circ}$	2	•	12	125.5	$^{\prime\prime}$	12	123.5	$^{\circ}$	7
	Result No.		7	m	4	Ŋ	9	7	80	σν	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P45805 alcaligenes P35828 caulobacter	Ogul36 homo sapien P52591 rattus norv	P10105 drosophila Q05140 rattus norv	P23314 xanthomonas P13709 drosophila	P58938 xanthomonas Q92798 chlamydia p	Q13492 homo sapien P03764 bacteriopha
ALCEU CAUCR	2236_HUMAN P121_RAT	DROME	XANCP ROME	XANAC	HUMAN AMBD
1 HYF1_ 1 SLAP	1 Z236 1 P121	1 HMLA 1 A180_	1 EXPR 1 FSH D	1 BCSC 1 Y808	1 PICA 1 STF L
394 1025	1845	635 915	580 2038	1508	652 774
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122 121.5	121.5	119.5	118.5 118.5	118	117
9.84 13.84	34	დ ტ ო ო	40 41	4 4 2 8	4.4 5.0

## ALIGNMENTS

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EMBL; Z74024; CAA98377.1; --
EMBL; AE007119; AAK47285.1; --
PIR; G70925; G70925.
TIGR; MT2959;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 182; Conservative
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AC 51951
D Y102 MYCTU
AC 30-MAY-2000
DT 30-MAY-2000
DT 16-OCT-2001
DE Hypothetical
GN RV1802 OR MT
OS Mycobacteriu,
OC Bacteria; Ac Corynebacter
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Feterson J., Dedson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                     1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                        MVDFGALPPEINSARMYAGPGSASLVAAAKMWDSVASDLFSAASAFQSVVWGLTTGSWIG
                                                                                                                                                                                                                                                                                                  61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                              LIATNILIGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATATLLIPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 MYSMANNHMSMINSGVSMINILSSMLKGFAPAAAAQAVQTAAQNGVRAMSS----LGSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSSGLGGGVAANLGRAASVGSLSVPQAWAANQAVTPAARALPLTSLTSAAERGPGQMLG
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglineier K., Gas S., Barry C.E. III, Tekaia F., Backon S.V., Eiglineier K., Gas S., Barry C.E. III, Tekaia F., Davies R., Davies R., Davies R., Davies R., Millingworth T., Comnor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Stalton J.E., Taylor K., Whitchead S., Barrell B.G.; Deciphering the blology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                                       Gaps
                                                                                                                                   7;
                                                                                        DB 1; Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                   34; Indels
                     A -> AT (IN REF. 2).
6AFAE0D7B5F668D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 GLPVGOMGARAG--GGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
                                                                                        Score 1656.5; DB Pred, No. 4.8e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical PPE-family protein Rv2892c.
Mycobacterium tuberculosis.
                                                                       85.0%; Sco. No. 4.0.
85.1%; Pred. No. 4.0.
44e 18; Mismatches
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Hypothetical protein; Complete proteome.
CONFLICT 158 159 TA -> AT (1
SEQUENCE 396 AA; 40015 MW; 6AFAE0D7E
                                                                                                             al Similarity 85.1
338; Conservative
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Y892_MYCTU
1D Y892_MYCTU
DT 10-00T-1996
DT 11-DEC-1998
DT 16-00T-2001
DE HYPOCHECICAL
ON MYCODACTERIO
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 LEQAAA-----VEEASDIAAANQLMNN-----VP--QALQQ-LAQPIQGITPSSKL---
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genome comparison of Mycobacterium tuberculosis clinical and
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
14-OCD-2001 (Rel. 40, Last annotation update)
RV1802 OR MT1851 OR MTV049.24.
Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.2%; Score 705; DB 1; Length 408; 41.8%; Pred. No. 4.4e-34; Live 47; Mismatches 134; Indels
                           laboratory strains.";
Submitted (APR-2011) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARIY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLGK; MILLOLD,
TUBECULIST; RV2892c; -
TUBECULIST; RV2892c; -
TOTAL PRO00033; PPE; 1.
FFAM; PF00823; PPE; 1.
Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 56 76 POTENTIAL.
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TIGR; MT0458; -.

Tuberculist; Rv0442c; -.

InterPro; IPR000030; Microbac_PPE.

InterPro; IPR002989; Mycobac_pentapep.

Pfam; PF01469; Pentapeptide_2; 5.
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EMBL; AL021322; CAA17399.1; --
EMBL; AE006948; AAK44681.1; --
PIR; C70830; C70830.
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87137260; PubMed=3029018;
                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=Erdmann;
                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                          NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                 Shinnick T.M.
                                                                                                             RESULT 4
Y442_MYCTU
ID Y442_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 MSSLGSSLG:----SSGLGG---GVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPL 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 LEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVS--PHRSPI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
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                                                  MEDLINE-98255987; PubMed=9634230; Garnier T., Churcher C., Harris I Gordon S.V., Eiglmeier K., Gas S., Barry C. E. III. Tekaia F., Badcock R., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Kelton B., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Murphy L., Complete genome sequence."; Mccobacterium tuberculosis from the Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                "Whole genome comparison of Mycobacterium tuberculosis clinical and
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                                                                                                                                                                                                                                                                                                                                                           laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
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EMBL; AE007044; AAK46123.1; -.
EMBL; AE007044; AAK46123.1; -.
EIR; AT0831; C70931.
TIGR; MT1851; -.
TUBECCLLIST; RV1802; -.
InterPro; IPR000030; Microbac_PPE.
Ffam; PF00823; PPE; 1.
Hypochetical protein; Complete proteome.
CONFLICT 401 401 8 -> L (IN REF. 2).
SEQUENCE 463 AA; 46021 MW; EB64828BF09FA551 CRC64;
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Best Local Similarity
Matches 174; Conservat
                           FROM N.A.
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284 -SALGAGLGIRSAISSGLGSTAPAISAGASQAGSVGGMSVPPSWAAATPAIRTVAAVFSS 342
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Eiglmeler K., Gas S., Barry C.B. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Rutter S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.B., Taylor K., Whitehead S., Barrell B.G.,
"Deciphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence.";
Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The 65-kilodalton antigen of Mycobacterium tuberculosis."; J. Bacteriol. 169:1080-1088(1987).
                                                                                                                                                                                                                                                                                                                                                                                                    341 TSLTS--AAERGPGQML-----GGLPVGQMGARAGGGLSGVLRV
                                                                                                                                                                    laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
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                                                                                                                                                                                                                                                           126 TWWFGQNAPALMDVEAAYEQWWALDVAAMAGYHFDASAAVAQLAPWQQV--LRNLGIDIG 183
                                                                                                                                                                                                                                                                                                           184 KWGQINLGFGNTGSGNIGNNNIGNGNIGSGNTGTGNIGSGNTGSGNLGLGNLGDGNIGFG 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                   340 ITSLTSAAERGPGQM----LGGLPVGQMGARAG--GGLSGVLR--VPPRPYVMPHSPAA 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                          341 EAALVSSAGYATGGMSTAALSSGILASALGSTGGLQHGLANVLNSGLTNTPVAAPASAPV 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98295987, PubMed=9634230,
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.; Harris D.,
Cole S.T., Brosch R., Parkhill J., Gas S., Barry C.E. III, Tekaia F.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Elrown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Sulston J.E., Taylor K., Whitehead S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                     64 GLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIA
                                                                                                                                                                                                  --GLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLG-----GLW
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                                                                                                                                     FGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSA
                                                                                                              Gaps
                                                                                                              58;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                      Length 487;
                                                                                                              180; Indels
            1 protein; Complete proteome.
40 40 E -> K (IN REF. 2).
96 96 I -> T (IN REF. 1).
211 211 G -> GNNNIG (IN REF. 1).
487 AA; 47247 MW; 97234DSB316C8C7F CRC64;
                                                                                     22.8%; Score 444; DB 1; 32.1%; Pred. No. 6.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical PPE-family protein Rv0878c.
Mycobacterium tuberculosis.
                                                                                                              48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      443 AA
                                                                                                              Conservative
Pfam; PF00823; PPE; 1.
Hypothetical protein; Cor
CONFLICT 40 40
CONFLICT 96 96
CONFLICT 211 211
SEQUENCE 487 AA; 47247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 OGPAAAAAAAAAPYLSWLNAATARAEGAAAGAKAAAAVYEAARAATAHPALVAANRNQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 MILIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSA
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                                      rieiscnmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L. Beicher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.;
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                                                                                                                                                                                              "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --MGNSGD--
                                                                                                                                                                                                                         laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.9%; Score 426.5; DB 1; Length 443; 31.2%; Pred. No. 5.8e-18; ive 56; Mismatches 132; Indels 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 X 10 AA APPROXIMATE REPEATS.
C58BEC607F0675E2 CRC64;
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POTENTIAL.
POTENTIAL.
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ALA-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tuberculist; Rv0878c; -.
Tuberculist; Rv0878c; -.
InterPro; IPR000030; Microbac_PPB.
InterPro; IPR0002899; Mycobac_pentapep.
Pfam; PF01469; Pentapeptide_2; 4.
Pfam; PF00823; PPB; 1.
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EMBL, AB06977, AAK45143.1, ALT_INIT.
PIR, C70780, C70780
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125; Conservative
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TRANSMEM 15 39
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443 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=H3TRY;

MEDILINE=9829997; PubMed=9634230;

A Gordon S.V., Biglmeier K., Gas S., Barry C.E. III, Tekaia F.,

A Gordon S.V., Barjam D., Brown D., Chillingworth T., Connor R.,

A Badcock K., Barjam D., Brown D., Chillingworth T., Connor R.,

A Davies R., Deviin K., Fkrogh A., McLean J., Moule S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Oliver S., Seeger K., Skelton S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

T Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
Bacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.4%; Score 418; DB 1; Length 678; 31.9%; Pred. No. 2.9e-17; ive 48; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY; BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane; Complete proteome.
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180 200 POTENTIAL.
258 258 D -> G (IN REF. 2).
678 AA; 66736 MW; 209F1593D52533A2 CRC64;
                                                                                                                                      01-0cT-1996 (Rel. 34, Created)
15-UTL-1999 (Rel. 38, Last sequence update)
14-0cT-2001 (Rel. 40, Last unctation update)
17-0cthetical PPE-family protein Rv1548c.
RV1548C OR MT1599 OR MTCY48.17.
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EMBL; AE007026; AAK45866.1; ALT_INIT.
PIR; A70762; A70762.
TIGR; MI1599; --
Tuberculist; Rv1548c; --
Tuberculist; Rv1548c; --
Tuberculist; Rv1548c; --
Tuberculist; PR000030; Microbac_PPE.
InterPro; IPR000309; Mycobac_Pentapep.
Pfam; PF01469; Pentapeptide_2; II.
Pfam; PF01823; PPE; I.
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                                                                            STANDARD;
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TRANSMEM 14 34
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Q10778;
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SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 121 

62

2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS

Best Local Similarity 31.9 Matches 106; Conservative

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Query Match

Gaps

38;

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SEQUENCE FROM N.A.
MEDILTE-9323938; PubbMed=8478104;
MEDILTE-9323928; Brooks L.A., Dockrell H.M., de Smet K.A.L.,
Thompson J.K., Hussain R., Stoker N.G.;
"Sequence and immunological characterization of a serine-rich antigen
Erom Woodbacterium leprae.
Infect. Immun. 61:2145-2153(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21128732; PubMed=11234002;
Cole S.T., Eiglaneier K., Parkhill J., James K.D., Thomson N.R.,
Muheeler P.R., Honore N. Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.; tevens K., Taylor K., Whitehead S., Woodward J.R.,
Massive gene decay in the leprosy bacillus.";
Mature 409:1007-1011(2001)
Mature 409:1007-1011(2001)
                                                                                                                                                           PHRSPISNM--VSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMS
                                                            122 IATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG-
                                                                                              121 VASNILGONAPAIAAVEAVYEOMWAADVAAMLGYHGEASAVALSLTPFTPSPSAAATPGG
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MEDLINES-85020554; PubMed=7934845;
Rinke de Wit T.F. Clark-Curtiss J.E., Abebe F., Kolkon A.H.J., Jonson A.A.M., Thole J.E.R.;
A Wycobacterium leprae-specific gene encoding an immunologically recognized 45 kba protein ";
Mol. Microbiol. 10:829-838(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Serine-rich antigen (25L) (45 kDa protein)
SRA OR MIOA11 OR MICLI383.14.
Mycobacterium leprae.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterium: Mycobacteriaes, Mycobacterium.
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InterPro, IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
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EMBL; AE006922; AAK44327.1;
PIR; H70750; H70750.
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245
276
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463 AA;
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les 112;
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2 X 6 AA REPEATS OF S-V-A-Q-S-E.
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773;
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189 S -> L (IN REF. 2).

191 H -> D (IN REF. 2).

292 P -> L (IN REF. 2).

42466 MW, 5COC2BEOD6E6A9D8 CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical PPE-family protein Rv0096.
Mycobacterium tuberculosis.
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                 EMBL, U00015, AAC43220.1; -. EMBL, X68431, CAA48480.1; -. EMBL, Z21552, CAA79950.1; -. EMBL, Z97179; CAB09938.1; -.
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Matches 115; Conser
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Baloinformatics and the FWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CDC 1551 / Oshkosh,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 AIPPEVHSGLLSAGCGPGSLLVAAQQWQELSDQXALACAELGQLLGEVQASSWQGTAATQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bishai W.;
"Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLURAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 FFGINTVPIALNEADYVRMWLQAADTMAAYQAVADAATVAVPSTQPAPPIRAPGG
MEDIATES 982997; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harra Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy Hornbyy T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton S., Squares S., Squares T., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
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an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                         Local Similarity
les 115; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1773;
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                              ---GGLW-----KTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLK----GF 269
                                                         ------TLSALTALSALIHLLNLPPAGL 275
                                                                                        APAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQ 329
----DAADTRLDVLSSIGQLIRDI---LDFIANPYKYFLEFFEQFGFSPAVTVVLALVAL 229
                                                                                                                   -----LGPGDQWGANLAVAVTPATAAVP----GGSP 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reductase.
-!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts
in positions 294; 337 and 355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann T.D., DeBoy R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bishal W.; "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=9829587; PubMed=9634230; Carnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Elgimeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Eromn D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd (Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seber K., Krogh A., McLean J., Squares R., Ruter S., Seeger K., Skelton S., Squares S., Squares R., Slston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Isolate 50410;
Batki A.H., Dale J.W.;
Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
-:- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
-:- CAUTION: In strain Oshkosh the gene for this protein is incerrupted in position 307 by an IS6110 element.
-:- CAUTION was originally (Ref.3) thought to be a dihydrofolate
                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                     368
                                                                                                                                                                      309 PISNPAPAAPSSNSVGSASAAPGISYAVPGLAPPGVSSGPKAG 351
                                                                                                                                                   330 AVTPAARALPLISLISAAERGPG---QMLGGLPVG-QMGARAG
                                                                                                                                                                                                                                                                   P31500; 053265;
01-0UL-1993 (Rel. 26, Created)
28-FEB-2003 (Rel. 40, Last sequence update)
Hypothetical PPE family protein Rv3018c.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                         434 AA
                                                         230 QLYDFLWYPYYASYGLLLLPFFTP--
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                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                    276 LPIAAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 LLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 GGPLLGALAAVVPGVAGLAGVAGLAAL-PAVGAA--AGAPAALVGSVAPVSGGVVSPQA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 ASPPEVHSALLSAGPGPGSLQAAAAGWSALSAEYAAVAQELSVVVAAVGAGVWQGPSAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 MVAAASPYVAWMSVIAGQAELIAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 AAVEEASDTAAAN------QLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 ILGFNIIGFIITLASNAQLLTEFAINASYVAVGLLYAIAGVIDIVVEWVIGNLFGVVPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----PAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASV-GSLSVPQA
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MEDLINE=9825987, PubMed=9634230;

MEDLINE=9825987, PubMed=9634230;

Gordon S.V., Brosch R., Parkhill J., Garnier T., Churcher C., Harris J Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Chillingworth T., Connor R., Badcock K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandraem M.A., Rogers J., Sulter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 WAAANQAVTPAARALPLTSLTSAAERGPGOMLGGLPVGOMGARAGGGLSGV 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---RSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFA-----
                                                                                                                                                                                                                                                                                                                                                                                                       41D673C4BD389DD6 CRC64;
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16-0CT-2001 (Rel. 40, Created)

16-0CT-2001 (Rel. 40, Last sequence update)

Hypochetical PPE-family protein Rv3021C/Rv3022c.

RV3021C/RV3022C OR MT3106 OR MTV012.35C/MTV012.36C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.6%; Score 324; DB 1; Lularity 28.0%; Pred. No. 4.7e-12; Conservative 56; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       435
                                                                                                                                                                                                                                                                                      InterPro; IPR00030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
Hypothetical protein; Complete proteome.
EMBL, AL021287, CAA16103.1; -...
EMBL, AE07129; AAK47427.1; ALT SEQ.
EMBL, XS927129; AAK47430.1; ALT SEQ.
EMBL, XS9271; CAA41961.1; ALT FRAME.
PIR, E70857; E70857.
TIGR, MT3109; -...
TUGR, MT3109; -...
Tuberculist; Rv3018c; -...
                                                                                                                                                                                                                                                                                                                                                                                                   434 AA; 43029 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 IPAEYISNIIYEGPGADSLSAAAEQLRLMYNSANMTAKSLTDRLGELQE-----NWK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Deloper A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=9829587; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hensby T., Jagels K., Krogh A., McHean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.0%; Score 233.5; DB 1; Length 178; larity 35.9%; Pred. No. 3e-07; Conservative 25; Mismatches 76; Indels 15.
                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein, Complete proteome.
SEQUENCE 178 AA; 19811 MW; 8BEIFC025ABFBEA6 CRC64;
                                                                                                                                                                            178 AA
                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical PRP-family protein RV3429.
RV3429 OR MT3S33 OR MTCY77.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tuberculist; Rv3429; -.
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE007158; AAK47873.1; -. PIR; C70975; C70975.
TIGR; MT3533; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z95389; CAB08678.1; -.
      386 GTAGKESVGQPAGL 399
                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=CDC 1551 / Oshkosh;
                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65;
                                                                                                                                                                         YY29 MYCTU
006246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bishai W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EVED outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.cib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----AALVGSVAPVSGGVVSPQARLVS--AVEPAPASTSVSVL--ASDRGAGAL--GF-V 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
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                                                                                                               SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterschmann R.D., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 ALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 MVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 FVAAYVPYVAWLVQASADSAAAGEHEAAAAGYVCALAEMPTLPELAANHLTHAVLVATN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 MSMTNSGVSMTNTLSS-----MLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 AVAAATITPFPFGELAKFLEMAAQAFTEVGELIMKSAEAWAVGFVELITGLVNFEP---
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                                                                                                                                                                                                                                                                                                                    "Whole genome comparison of Mycobacterium tuberculosis clinical and
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.5%; Score 321.5; DB 1; Length 435; 26.5%; Pred. No. 6.6e-12; ive 53; Mismatches 159; Indels 107;
                                                                                                                                                                                                                                                                                                                                         laboratory strains...;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
-!- CAUTION: Ref. 1 sequence differs from that shown due to a frameshift in position 82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGE; MT3106; -.
TUBERCULIST; RV3021c; -.
TUBERCULIST; RV3021c; -.
INTERPOSIT RV30030; MICTOBAC_PPE.
PFam; PF00823; PPE; 1.
HYPOTHELICT 299 G -> A (IN REF. 2).
CONFLICT 299 LAGV -> VTGL (IN REF. 2).
CONFLICT 326 L -> V (IN REF. 2).
SEQUENCE 435 AA; 42876 MW; 3B157643EAAB484A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 LLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL021287; CAA16106.1; ALT FRAME.
EMBL; AL021287; CAA16107.1; ALT_FRAME.
EMBL; AE007129; AAK47435.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 VAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADAVERYLQWLSKHSSQLKHAAWVINGLANAYNDTRRKVVPPBEIAANREERRRLIASNV 123
                                             GSSSDLMADAAGRYLDWLTKHSRQILETAYVIDFLAYVYBETRHKVVPPATIANNREEVH 116
                            ILIAINLIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATILLPFEEAPEMTSAG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 LPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSAGLM 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 IPAEYISNIIYEGPGADSLFFASGQLRELAYSVETTAESLEDELDELD-ENWKGSSSDLL 63
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98295987; PubMed=9634230;

A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.T., Brosch R., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Reltwell T., Gentles S., Hamiln N., Holroyd S., A Davies R., Jagels K., Kregh A., McLean J., Moule S., Murphy L., A Coliver S., Seeger K., K., Skelton S., Squares R., Staters S., Seeger K., K., Skelton S., Squares R., Suleton J.E., Taylor K., Whitehead S., Barrell B.G.; Suleton J.E., Taylor K., Whitehead S., Barrell B.G.; Tompthet genome sequence.";

T complete genome sequence.";

I complete genome sequence.";

Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 LGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGVNTPAIADLDAQYDQYRARNVAVAWNAYSWTRSALSDLPRWREPPQIYRG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 176;
                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; F70738, F70738.
Tuberculist; Rv3425; -
Interpro; IPR00030; Microbac_PPE.
Pfam; PF00823; PPE: 1.
Hypothetical protein; Complete proteome.
SEQUENCE 176 AA; 19855 MW; B8CEF2E9463B87B0 CRC64;
                                                                                                                                                                                                                                                                                                        Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.2%; Score 217.5; DB 1 33.5%; Pred. No. 2.5e-06;
                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1790thetical PPE-family protein RV3425.
RV3425 OR MTCY78.04C.
                                                                                                                                                                                 176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z77165; CAB01031.1; -.
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Best Local Similarity
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                                                                                 180
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STRAIN=H37Rv;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the buspean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics 23:125-131 (1994).

-!- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND

-!- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND

-!- SUBJUIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER

INTO AN EXTENSIBLE 3D NETWORK.

-!- SUBGELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.

-!- PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGIPGVGGPGIGGPGIVGGPGAVSPAAAAAAAAAA--YGARGGVGIPTYGVGAGGFPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --IGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          492 ALGGLVPGAVPGALPGAVPAVPGAGGVPGAGTPAAAAAAAAAAXAAKAALGPGVGGVPGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 GALP----PEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSW--
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human
                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131;
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                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRUE=Lung;
STRAATN=BABAC: TISSUE=Lung;
MEDLINE=9130069; PubWed=7229060;
Wydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
"Use of an intron polymorphism to localize the tropoelastin genues chromosome 5 in a region of linkage conservation with phromosome 7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OCOBESAAE1EDD7F1 CRC64;
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PIR; A55721; EAMS.
MGD; MGI-95317; Eln.
InterPro; IPR0013979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
Structural protein; Repeat; Signal; Connective tissue.
SIGNAL. 1 27 POTENITAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.9%; Score 153.5; DB
                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Elastin precursor (Tropoelastin).
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BY SIMILARITY.
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855 BY
71955 MW;
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   STANDARD;
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860 AA;
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nes 115; Conserv
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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                                                                                                                                                                                                                   Mus musculus
ELS MOUSE
P54320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29
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us-09-688-672a-26.rsp

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(Rel.
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01-OCT-1996
                                                                                                                                                                                                     15-SEP-2003
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                                                                                                               ELS RAT
                                                                RESULT 15
ELS_RAT
                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch.
                                             731
                                                                                          346
                                                                                                                                  784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=H37RV;

MEDILINE=9829897; PubMed=9634230;

MEDILINE=9829897; PubMed=9634230;

A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

B Adordon S.V., Basham D., Brown D., Chillingworth T., Connor R.,

B Adordon S.V., Hamin N., Feltwell T., Gentles S., Hamin N., Holroyd S.,

A Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd S.,

A Hornsby T., Jagels K., Krelton S., Squares S., Squares R.,

A Rutter S., Seeger K., Kselton S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the

T complete genome Sequence.";

I Nature 393:537-544(1998).
----SGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRA
                                             672 YGAAGGLGGGPGGLGGPGGLGGAGVPGRVAGAAPPAAAAAAAAAAAKAAAKAAQYGLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 IPABYIŚNVIÝEGPRADŚLYAADQRLRQLADSVRTTAESLNTTLDELH-ENWKGSSSEWM
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                                                                                          289 MSSLGS-SLGSSGLG-GGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSA
                                                                                                                                7 LPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSAGLM
                                                                                                                                                                               347 AERGP---GOMLGG--LPVGOMGARAGGGLS------GVLRVPPRPY 382
                                                                                                                                                                                                                        785 AKYGAAGLGGVLGARPFÞGGGVAÁRÞGFGLSÞIYÞGGGAGGLGVGGKPÞKÞÝ 836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein, Complete proteome.
32 AA; 25872 MW; D76512D49EB272C6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                        232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation updat
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01-NOV-1997 (Rel. 35, Last sequence upd,
16-OCT-2001 (Rel. 40, Last annotation upypothetical PPE-family protein Rv3426.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z77165; CAB01030.1; -.
PIR; G70738; G70738.
Tuberculizer; Rv426; -.
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
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                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
    248 HMSMTN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 LG 128
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SEQUENCE 23
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                                                                                                                                                                                                                                                                                                                                        MYCTU
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND
-!- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTEFELY.
-!- SUBUNIT: LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY.
-!- SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER
INTO AN EXTRANSIBLE 3D NETWORK.
-!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                             Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 264-533 AND 558-864 FROM N.A., AND ALTERNATIVE SPLICING. MEDILTB=92941859; PubMed=157537; Pierce R.A., Alatawi A. Deak S. B., Boyd C.D.; "Elements of the rat tropoelastin gene associated with alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-91104868; PubMed=1702999;
Blerce R.A., Deak S.B., Stolle C.A., Boyd C.D.;
"Heterogeneity of rat tropoelastin.mRNA revealed by cDNA cloning.";
Blochemistry 29:9677-9683(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=8;
Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 781-864 FROM N.A.
MEDLINE=88330866; PubMed=2971041;
Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.;
"Rat tropoelastin is synthesized from a 3.5-kilobase mRWA.";
J. Biol. Chem. 263:13504-13507(1988).
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                                                                                                                 Last sequence update)
Last annotation update)
864 AA.
                                                                                                                                                                                15-SEP-2003 (Rel. 42, Last annotation updat
Elastin precursor (Tropoelastin) (Fragment)
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                                                                        34, Created)
34, Last seq
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EMBL, J04035; AAA42268.1; -.
EMBL, M86372; AAA42271.1; -.
STANDARD;
                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
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233 PHRSPISNMVSMANNHMSMTNSGVSM-TNTLSSMLKGF-APAAAAQAVQTAAQNGVRAMS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.

ELASTIN.

BY SIMILARITY.

Missing (in isoform 2, isoform 5, isoform 7 and isoform 8).

/FITG=VSP 004244.

Missing (in isoform 3, isoform 5, isoform 6 and isoform 8).

/FITG=VSP 004245.

Missing (in-isoform 4, isoform 6, isoform 7 and isoform 8).

/FITG=VSP 004246.

/FITG=VSP 004246.

/FITG=VSP 004246.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 -- IGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       457 YGVGAGAĞL------GGASQAAAA----AAAAKAAKYGAG------ 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 ELMILIATNLIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 SAGGLL---EQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSS-KLGGLWKTVS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   528 GTGGVPGAGTPAAAAAAAAAAAA------KAGOYGLGPGVGGVPGGVGGLPGGVG 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        487 -----GAGTLGGLVPG------AVPGALPGAVPGALPGAVPGALP-GAVPGVP 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 GALP----PEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSW-- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.7%; Score 150; DB 1; Length 864;
Best Local Similarity 25.9%; Pred. No. 0.11;
Matches 102; Conservative 31; Mismatches 153; Indels 108; Gaps
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3.8
/label= Histidine tag
/lote= "Nickel chelating region used for purifying
the fusion protein"
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/label= MtB81_region
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AAR40846
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Misc-difference
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                                                                                           November 21, 2003, 15:50:31 ; Search time 70.9578 Seconds (without alignments) 2621.664 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                             A Geneseq 19Jun03;*

1. SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2. SIDS1/gcgdata/geneseq/geneseqg-embl/AA1981.DAT:*
3: SIDS1/gcgdata/geneseqg-embseqp-embl/AA1982.DAT:*
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28: SIDS1/gcgdata/geneseqg/geneseqg-embl/AA2003.DAT:*
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6061
1 MQHHHHHHTDRVSVGNLRIA......SAATRRPRCTRGRDGRWACQ 1172
         GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                   1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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AAU08233
AAR63567
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Score

Result No.

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Bifidobacterium lo
M. tuberculosis an
M. tuberculosis re
Novel human diagno

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                             IREEVDNNCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVI
                                                                                               TSADVRASLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPI
                                                                                                                                LHRRRREFKARAAEKPAPSDRAGDDAARVQKYGGSSVADAERIRRVAERIVATKKQGNDV
                                                                                                                                                                                                VVVVSAMGDTTDDLLDLAQQVCPAPPPRELDMLLTAGERISNALVAMAIESLGAHARSFT
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IREEVDNNCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATIRISSQLLANWIRHGVI
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99US-0158425
 10-OCT-2000; 2000WO-US28095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 1172; Conservative
                                                                                                                                                  WPI; 2001-290576/30
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Novel Mycobacterium tuberculosis polypeptide comprising an immunogenic portion of M. tuberculosis antigens Mtb-81 and Mtb-67.2, useful for diagnosis, treatment and monitoring therapy of tuberculosis Polypeptides comprising an immunogenic portion of Mycobacterium tuberculosis antigens Mtb-81 or Mtb-67.2 or variants that differ by substitutions, additions, insertions and/or deletions but which still react with antigen specific antisera or T-cells are described. 'note= "Encoded by TAA stop codon" note= "Encoded by TGA stop codon" note= "Encoded by TGA stop codon" codon" codon" note= "Encoded by TAG stop codon" note= "Encoded by TGA stop codon" codon" note= "Encoded by TGA stop codon" by TAA stop codon" "Encoded by TAA stop codon' stop note= "Encoded by TAA stop stop "Encoded by TAA stop note= "Encoded by TAA stop TGA stop note= "Encoded by TGA stop note= "Encoded by TAA stop note= "Encoded by TGA stop note= "Encoded by TAA stop 'note= "Encoded by TGA stop note= "Encoded by TAA stop note= "Encoded by TAA stop "Encoded by TGA stop note = "Encoded by TAA stop 1691..2438 /label= Mtb-81 polypeptide TGA Houghton RL; TGA ρχ "Encoded by note= "Encoded by "Encoded Claim 1; Fig 1a-f; 91pp; English. "Encoded 17-MAR-2000; 2000WO-US07196. 99US-0272975 Lodes MJ, note= note≕ note= note= note= /note= 2000-638180/61. (CORI-) CORIXA CORP Hendrickson RC, N-PSDB; AAA53971 Misc-difference WO200055194-A2 18-MAR-1999; 21-SEP-2000 Protein 

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Also described are polynucleotides encoding the polypeptides. The polypeptides, expression vectors expressing the polypeptides or comprising an antisense polynucleotide, or an antigen presenting cell comprising a sequence encoding the polypeptides are useful for determining the presence or absence of M.tuberculosis in whole blood, serum, sputum, plasma, saliva, cerebrospinal fluid or urine in a patient infected with human immunodeficiency virus (HIV).
                                                                                                                                                                                                                                     DB 21; Length 2502;
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                                                                                                                                                                                                                                   63.8%; Score 3866.5; DB 21
88.3%; Pred. No. 3.8e-286;
iive 8; Mismatches 27;
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Best Local Similarity
Matches 768; Conserv
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The present invention relates to a method for early detection of active mycobacterial disease or infection comprises assaying a biological fluid sample for the presence of early antibodies specific for an 88-kDa Mycobacterium tuberculosis (Mt) protein or immune complexes consisting of an 88-kDa M. tuberculosis protein antigen complexed with an antibody specific for the antigen. The method is useful for the early and rapid distection of mycobacterial disease, particularly tuberculosis, in individuals at heightened risk of developing tuberculosis. This individuals include human immunodeficiency virus (HIV)-infected subjects or other immunocompromised individuals. This method is a rapid and inexpensive screening procedure for detecting mycobacterial disease. The present sequence is a Mt 88 kDa secreted protein early antigen, used in the exemplification of the invention.
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                                                                                                                                                               Mycobacterial disease, infection, 88-kDa protein, tuberculosis, TB, early antigen, human immunodeficiency virus, HIV, secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting a mycobacterial disease (tuberculosis) in individuals comprise assaying a biological sample for the presence of anti-Mycobacterium tuberculosis antibodies or M. tuberculosis antiben antiben complex
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                                                                                                                                  Mycobacterium tuberculosis 88 kDa secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 3810; DB 22;
Pred. No. 1.3e-282;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Belisle JT;
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                              741 AA.
                                AAE05665 standard; peptide;
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                                                                                                                                                                                                                     Aycobacterium tuberculosis
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Page 7-8; 12pp; German.
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                                                                                                    IMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKWHGPAEVAFTCELFSRVEDVLG 421
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                                                                                                                                  TMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAW 548
                                                                                                                                                                      TMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAW 541
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LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI
                             LIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA
                                                                                    IMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKWHGPAEVAFTCELFSRVEDVLG
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AAR77501 is encoded by an approx. 3 kb BfrI-PvuI fragment contg. the aceB gene from Cornyeform glutemicum (see AA705501). Nucleorides 1 to 574 can be isolated and used to regulate the expression of a protein-encoding structural gene placed downstream of it, after incorporation into a vector and transfer into a Cornyeform bacterium. Induction of protein expression occurs even when the culture medium contains carbon sources other than acetate.
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Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; discopportate; aromatic compound; vitemain; cofactor; polyketide; diagnosis; Corynebacterium diphtheriae; evolutionary study.
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VPSPTGATLHATHYHLVDVFKVQDELRAAGRRDSLRNILTIPTAPNTNWSEEEKKEEMDN
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                                                               ENSKNGRIFTRELNKDRVYIGRNGTELVLHGRSLLFVRNVGHLMQNPSIL-IDGEEIFEG
                                                                                                 IMDALFTGLIALHGLKASDVNGPLINSRTGSIYIVKPKMHGPAEVAFTCELFSRVEDVLG
                                                                                                                                                         LPQNTMKIGIMDEERRTTVMLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQIDXWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 29; SEQ ID NO: 6988; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                   Ochiai K,
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; Pred. No. 3.6e-166;
90; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                   Ando S, Hayashi M,
da M, Ozaki A;
                                                             C glutamicum protein fragment SEQ ID NO: 6988.
                                                                                                                                                                                                                                                                                                                                    H, Ando
Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.8%;
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2000JP-0159162.
2000JP-0280988.
                                                                                                                                                                                                                                                                                                         (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                   18-DEC-2000; 2000EP-0127688
                                                                                                                                    Corynebacterium glutamicum.
                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             444; Conservative
                                                                                                       organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                    Nakagawa S, Mizoguchi
Tateishi N, Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           European Patent Office.
                                                                                        Coryneform bacterium;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH68453
                                                                                                                                                                                                                                                16-DEC-1999;
07-APR-2000;
                                                                                                                                                             EP1108790-A2
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                                    26-SEP-2001
                                                                                                                                                                                          20-JUN-2001
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       AAG93234;
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IMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKMHGPAEVAFTCELFSRVEDVLG 428
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                                                                                                                                                                                                                                                                                                                                                 LPRHTLKVGVMDEERRTSVNLDASIMEVADRLAFINTGFLDRTGDEIHTSMEAGAMVRKA 494
                                                                                                                                                                                                                                                                                                          LPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG 488
      LDGASHADVEKYNITDGKLAAHIGDSVYRLKNRESYRGFTGNFLDPEAILLETNGLHIEL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum; carbon metabolism and energy production; SMP Protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; carbohydrate; aromatic compound; vitemin; cofactor; polyketide; diadgnosis; Corynebacterium diphtheriae; evolutionary study.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                615 NCQSILGYVVRWVEHGVGCSKVPDIHDIDLMEDRATLRISSQMLANWIRHDVVSKEQVLE
                                                LIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA
                                                                         259 QIDPVHPIGKADKTGLKDIVLESAITTIMDFEDSVAAVDAEDKTLGYSNWFGLNTGELKE
                                                                                                                                  309 AVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEG
                                                                                                                                                            319 EMSKNGRIFTRELNKDRVYIGRNGTELVLHGRSLLFVRNVGHLMQNPSIL-IDGEEIFEG
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                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum SMP protein sequence SEQ ID NO:596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB79540 standard; Protein; 712 AA.
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99DE-1031412.
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FKAK 738
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08-JUL-1999;
08-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metabolism and oxidative phosphorylation (SMP) proteins given in AAB72243 to AAB 79633 which are involved in carbon metabolism and central control of the control of the capression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a miclocide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (II) encoded by them are used for diagnosing the presence or activity of cortaining them are used for diagnosing the presence or activity of cortaining them are used to map genomes of organisms related to containing them are used to map genomes of organisms related to containing them are used to map genomes of organisms related to containing them are used to map genomes of organisms related to containing them are used to map genomes of organisms related to containing them are used to map genomes of organisms related to containing the sugars, and in modulating sMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production and the containing and protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated Corynebacterium glutamicum nucleic acid encoding a metabolism and oxidative phosphorylation protein for production modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haberhauer
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61.0%; Pred. No. 4.2e-165;
ive 90; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 992-995; 1246pp; English
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99DE-1031562.
99DE-1031634.
99DE-1031230.
99DE-1032230.
99DE-1032924.
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99DE-1042123.
99DE-1042125.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAF71656
                                                                                                                                                                                                                31-AUG-1999;
03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
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03-SEP-1999;
03-SEP-1999;
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03-SEP-1999
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                                                                                                                                                                                                                                                                                     FTRELNKDRVYIGRNGTELVLHGRSLLFVRNVGHLMQNPSIL-IDGEEIFBGIMDAVLTT
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                                                                                                                                                                                                                                                    FLRVLNRDRNYTAPGGGOFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEGIMDALFTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    497 LAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAWVPSPTAAT
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immunostimulant, MO-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200162893-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metabolism and oxidative phosphorylation (SMP) proteins given in AAB7943 to AAB 7963 which are involved in carbon metabolism and oxidative phosphorylation (SMP) proteins given in AAB7943 to AAB 79633 which are involved in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a mucleoside, a uncleotide, a seturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a coffactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (II) encoded by them are used for diagnosing the presence or activity of corpuspactorium diphtheriae in a subject. (I), (II), (III) or host cells containing them are used to map genomes of corganisms related to c. glutamicum, identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determining SMP protein regions required for the clon, in modulating SMP protein regions required metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Corynebacterium glutamicum nucleic acid encoding a sugar metabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NN-SGTIDQEAYEDFLKEIGYLVEEPEAAEIRTQNVDTEISSTAGPQLVVPILNARFALN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
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; Pred. No. 1.9e-163;
89; Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Page 998-1000; 1246pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAE---- 1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tuberculosis antigen polypeptides (e.g. TD224) and the nucleic acids encoding them. The invention describes compounds and methods for the encoding them. The invention describes compounds and methods for the flagnosis of tuberculosis of tuberculosis of for inducing protective immunity against tuberculosis. The compounds comprise at least one immunogenic portion of one or more Mycobacterium proteins and nucleic acid molecules encoding such polypeptides. The Mycobacterium proteins and nucleic acid molecules encoding them can be used in diagnostic kits for the detection of Mycobacterium infection in patients and biological samples. The compounds of the invention and antibodies directed against the Mycobacterium infections. The nucleic acids encoding the Mycobacterium proteins may be used in vaccines for immunisation against proteins may be used in gene therapy. The present sequence represents Mycobacterium polypeptide for MO-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ELDMLLTAGERISNALVAMAIESLGAHARSFIGSQAGVITTGTHGNAKIIDVTPGRLQTA 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEEGRVVLVAGFQGVSQDTKDVTTLGRGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKDVPMEDPILIGVAHDRSEAKVIIVGLPDIPGYAAKVFRAVA------DADVNIDM 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEEGRIVILVAGFOGVSODTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 VLONVSKVEKGKTDITFTCSRDVGPAAVEKLDSLRNEIGFSQLLYDDHIGKVSLIGAGMR 355
                                                                                                                                                                                                                                                                                                                                                                                                                       64
                           An isolated polypeptide comprising a Mycobacterium antigen, e.g., from Mycobacterium tuberculosis, useful in a vaccine for enhancing an immune response to and inhibiting development of a Mycobacterium infection -
                                                                                                                                                                                                                                                                                                                                                                                           749 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
                                                                                                                                                                                                                                                                                                                                                                                                              Feedback inhibition release aspartokinase, Brevibacterium flavum;
Corynebacterium; L-lysine production.
                                                                                                                                                                                                                                                                                                                                       / Match 26.7%; Score 1619.5; DB 22; Length 421; Local Similarity 85.1%; Pred. No. 2.7e-115; les 338; Conservative 8; Mismatches 34; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHPGVTATFCEALAAVGVNIELISTSEDQRSRCCAAT 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHPGVTATFCEALAAVGVNIELISTSEIRISVLCRDT 392
                                                                                                         present invention relates to the isolation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feedback inhibition release aspartokinase 279Ala,
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                                                                              Fig 17; 161pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                        AAQ72693 encodes AAR63567 Brevibacterium flavum feedback inhibition release aspartokinase, it was used in the construction of a plasmid. The plasmid was used to transform Corynebacterium cells, where the expression of AAQ72693 resulted in incresed L-lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             579 RATIEQLLTIP------LAKELAWAPDEIREEVDNNCQSILGYVVRWVDQ--
                                                                                                                                                                                                                                                              encoding feedback inhibition release asparto-kinase - used the production of L-Lysine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 842;
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llarity 36.9%; Pred. No. 1e-86;
Conservative 128; Mismatches 240;
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93JP-0055451
                                                     93JP-0055451
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Best Local Similarity
Matches 346; Conserv
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16-MAR-1993;
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DD 60	Qy         623 GVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRASLERMAPLVDRQNAG 682           Db         351 GAGMKSHPGV-TAEFMEALEDVNVNIELISTSEIRISVLIREDDL 394           Qy         683 DVAYRPAMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRREFKARAAEKPAPSDRA 742           Db         1   1   1   1   1   1   1   1   1   1	Oy 863 GRLQTALEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAALGADVCEIYTDVDG 922	Qy 1033 RRRQHRHGAAERLQGRGRQD-RHHLHLLPQTSGPPPWGWTRSETRSASTQLLYDDH1 1089  720 NFSSVEDGTTDITFTCPRSDGRRAMEILKKLQVQGNWTNVLYDDQV 765  Qy 1090 GKVSLIGAGMRSHPGVTAFFCEALAAVGVNIELISTSE 1127  Db 766 GKVSLIGAGMRSHPGVTAFFEALADVNVNIELISTSE 803  RESULT 11  AAG64046  ID AAG64046,  XX  AC XX  DF 11-SEP-2001 (first entry)  XX  Corynebacterium thermoaminogenes lysin biosynthetic enzyme lysC.  XX  KW Heat-resistant; lysin biosynthesis; enzyme; coryneform;  KW aspartate-semialdehyde dehydrogenase; lysC.  XX  Corynebacterium thermoaminogenes.
Qy         863 GRLQTALEEGRVVLVAGFOGVSODTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDG         922           Db         540 GRVREALDEGKICTVAGFOGVSONKETRDVTTLGRGGSDTTAVALAAALANDVCEIYSDVDG         599           Qy         923 IFSADPRIVENARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPG         892           CO         VYTADPRIVPNAQKLEKLSFEEMLELAAVGSKILVLRSVEYARAFRNVPLRVRSSYSDRPG         659           Qy         983 TVVVGSIKDVPWBDPILTGVAHDRSEAKVTIVGLPDIPGYAARVFRAVA	R63	XX XX YE	YX FT DNA encoding feedback inhibition release asparto-kinase - used FT for the production of L-Lysine.  XX SX Claim 4; p21; 28pp; Japanese.  XX C AAQ72696 encodes AAR63570 Brevibacterium flavum feedback inhibition C release aspartokinase, it was used in the construction of a plasmid. The plasmid was used to transform Corynebacterium cells, CC plasmid. The plasmid was used to transform Corynebacterium cells, CC plasmid. The plasmid was used in the construction of a plasmid. The plasmid was used in the construction of a plasmid. The plasmid was used to transform Corynebacterium cells, CC production.  XX SQ Sequence 842 AA; Query Match Best Local Similarity 36.9%; Pred. No. 1e-86; Matches 346; Conservative 128; Mismatches 240; Indels 224; Gaps 31; Author SS QVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGINKGDLAAAVDKO 314  ZS RIVATKKAGNNVVVCSAMG

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Brevibacterium
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                                                                                                                                                                                                                                                                               749 VQKYGGSSVADAERIRRVAERIVATKKOGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
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                                                                                                                                                                                                                                                                                                                                                                      RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                        The invention relates to a gene from a high temperature-resistant coryneform microbe that encodes a heat-resistant lysin biosynthetic enzyme. The enzyme asspartate-semialdehyde dehydrogenase activity and can be used for growing amino acid-producing microbes. The present amino acid sequence corresponds to an enzyme of the
                                                                                                                                                                                                                                                     Gaps
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65.2%; Pred. No. 6.9e-87;
iive 58; Mismatches 63; Indels
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                                                                                                                A heat-resistant lysin biosynthetic system enzyme temperature-resistant coryneform microbe
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                                                                                                                                        Claim 6; Page 21-22; 27pp; Japanese.
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                                                                                                                                                                                                                                           al Similarity 65.2
251; Conservative
                                                                        (AJIN ) AJINOMOTO KK.
                                                                                        WPI; 2001-364760/38.
N-PSDB; AAH45374.
                                                                                                                                                                                                                   421 AA;
        JP2001120270-A
                                        01-NOV-1999;
                                                        01-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAVDKDG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BEAV--LTGVATDKSEAKVTV--LGISDK--PGEVAKVFRALADAEINIDMVLQNVSSVE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
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                                                                                                                                                                                                                                                                                                                                                                                                                            release asparto-kinase - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 842;
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ilarity 36.8%; Pred. No. 2.1e-86;
Conservative 128; Mismatches 241;
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                                                                                                                                                                                                                                                                                 CO LID
                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding feedback inhibition for the production of L-Lysine.
                                                                                                                                                                                                                                                                              (MITP ) MITSUBISHI PETROCHEMICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; p18; 28pp; Japanese
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flavum
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Best Local Similarity<sup>.</sup>
Matches 345; Conserv
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1033 RRROHRHGAAERLOGRGROD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHI 1089
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         TAFLEVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEGIMDALF 374
                                                                                                                                                                                                                                                                                         251 EEAV--LIGVATDKSEAKVTV--LGISDK--PGEVAKVFRALADAEINIDMVLQNVSSVE 304
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                                                                                                                                                                                                LDRTGDEIHTSMEA-GPMVRKGTMKSQPWILAY-----EDHNVDAG-LAAGFSGRAQV
                                                                                                                                                                                                                                                                                                                                                      DGTTDITFTCPRSDGRRAMEILKKL-----OVQGNWTNVL----YDDQVGKVSLV
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                                                                                          82 AMAIESLGAEAQSFIG----SQAG---VLTTERHGNARIVDVTP--GRVREALDEGKICI
                                                                                                                                                                                                                                                           GKGMWIMTELMADMVETKIAQPRAGASTAWVPSPTAATLHALHYHQVDVAAVQQGLAGKR
                                                                        TGLIAIHGLKASDVNGPLINSRIGSIYIVKPKMHGPAEVAFICELFSRVEDVL-----
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                                                                                       GRVREALDEGKICIVAGFOGVNKETRDVTTLGRGGSDTTAVALAAALNADVCEIXSDVDG
                                                                                                                        IFSADPRIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPG
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                                                           GRLQTALEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ72695 encodes AAR63569 Brevibacterium flavum feedback inhibition release aspartokinase, it was used in the construction of a plasmid. The plasmid was used to transform Corynebacterium cells, where the expression of AAQ72695 resulted in incresed Liysine production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feedback inhibition release aspartokinase, Brevibacterium flavum,
Corynebacterium, L-lysine production.
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                                                                                                                                                                                                                                                                                                            GKVSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSE 1127
                                                                                                                                                                                                                                                                                                                             766 GKVSLVGAGMKSHPGVTAEFMEALRDVNVNIELISTSE 803
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larity 36.8%; Pred. No. 2.1e-86;
Conservative 128; Mismatches 241;
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Matches 345; Conserv
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                                                      GAGMKSHPGVTAEFMEALRDVNVNIELISTSE
                                  GAGMRSHPGVTATFCEALAAVGVNIELISTSE
 305 DGTTDIIFTCPRSDGRRAMEILKKLQVQG--
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                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                          ABP97764 standard; Protein; 421
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                                                                                                                                                                                                                                                                                                                                                         Synthetic.
Corynebacterium glutamicum.
                                                                                                                                                                                                                                (first entry)
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N-PSDB; ABZ77392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 AA;
                                                                                                                                                                                                                                                                                                      Coryneform bacter:
aspartate kinase.
                                                                                                                                                                                                                                                                                                                                                                                                              Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003014330-A2
                                                                                                                                                                                                                                28-MAY-2003
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                                  1096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 929 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a modified aspartokinase from Corynebacterium glutamicum (e.g., AAB25607) and to DNA encoding the modified aspartokinase (e.g., AAAC64119). The aspartokinase of the invention is modified to remove its sensitivity to feedback inhibition by L-threonine or L-lysine. This is achieved by substituting the wild-type Thr 311 with any other amino acid; for example, in AAB29607 Thr 311 is substituted by Ile. The invention also relates to expression vectors and host coryneform bacteria containing the modified DNA, and to the preparation of L-lysine using coryneform bacteria transformed with the modified aspartokinase-encoding DNA. Culturing coryneform bacteria transformed with the modified aspartokinase DNA culturing coryneform bacteria transformed with the modified aspartokinase DNA of the invention provides efficient production of L-lysine. The present sequence represents a modified Corynebacterium glutamicum aspartokinase of the invention, T3111.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 VQKYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLELALAAVNPVPPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        809 BLDMLITAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEBGRVVLVAGFOGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding modified aspartokinase without synergistic feedback inhibition by L-lysine and L-threonine for efficient production of L-lysine by coryneform bacterium fermentation -
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                                                                                                      Key
    Location/Qualifiers
Misc-difference 311
    /note= "Wild-type Thr replaced with Ile"
L-lysine; L-threonine; insensitive; product inhibition; coryneform bacterium; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                         Yonetani Y, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 29-30; 33pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                         Ochiai K,
                                                                                                                                                                                                                                                                                                                     (KYOW ) KYOWA HAKKO KOGYO KK
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                                                   Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                       Ohnishi J,
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N-PSDB; AAC64119.
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                                                                                                                                                                           WO200063388-A1
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                                                                                                                                                                                                             26-OCT-2000
                                                                     Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   809 ELDMLLTAGERISNALVAMAIESLGAHARSFIGSQAGVITIGTHGNAKIIDVTPGRLQTA 868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coryneform bacteria to produce chemical compounds e.g. L-lysine, has at least two copies of open reading frame, gene or allele in question at a particular desired site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           749 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
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                                                                                      bacteria; chemical compound; L-amino acid; vitamin; lysC;
Amino acid sequence of a aspartate kinase carrying T3111 mutation.
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1096 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 1127
                                                                               351 GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
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AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 AVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDALVDTDGSEVFEG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQPAGYTGAAESPTSVLLINHGLHIEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVDKDGTAFLRVLNRDRNYTAPGGGFTLPGRSLMFVRNVGHLMTNDALVDTDGSEVFEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 LIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA
                                                                                                                                                                                                                                                                                                                                                                     Sequence 106, Application US/09001984C
| Sequence 106, Application US/09001984C
| Patent No. 624531
| GarberAL Information:
| APPLICANT: Lail, Suman |
| APPLICANT: Lail, Suman |
| APPLICANT: Belisle, John T |
| TILE OF INVENTION: BEALY DETECTION OF WYCOBACTERIAL DISEASE |
| TILE OF INVENTION: BEALY DETECTION OF WYCOBACTERIAL DISEASE |
| TILE OF INVENTION: BALLY DETECTION OF WYCOBACTERIAL DISEASE |
| TILE OF INVENTION: BALLY DETECTION OF WYCOBACTERIAL DISEASE |
| TURRENT APPLICATION NUMBER: US/09/001,984C |
| CURRENT APPLICATION NUMBER: 60/034,003 |
| PRIOR FILING DATE: 1996-12-31 |
| PRIOR FILING DATE: 1996-12-31 |
| MUMBER OF SEQ 1D NOS: 106 |
| LENGTH: 741 |
| TYPE: PRT |
| TYPE: PRT |
| ORGANISM: Mycobacterium tuberculosis |
| US-09-001-9845-106
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Matches 740, Conservative
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-08-956-36-6
US-08-912-91A-29720
US-08-512-91A-29720
US-09-075-595-22
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Sequence 7, Appli
Sequence 6, Appli
Sequence 8, Appli
Sequence 1124, Appli
Sequence 6090, Ap
Sequence 5503, Ap
Sequence 5609, Ap
Sequence 14, Appli
Sequence 2, Appli
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242 LIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA 301
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Matches 502; Conserv
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| Sequence 106 Application US/09396347F
| Patent No. 6506384
| GENERAL INFORMATION:
| APPLICANT: Laal, Suman
| APPLICANT: Laal, Suman
| APPLICANT: Colla-baner, Susan
| APPLICANT: Belisle, John T
| TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
| FILE REFERENCE: 32004-169276
| CURRENT FILING DATE: 1999-09-14
| PRIOR APPLICATION NUMBER: 09/001,984
| PRIOR FILING DATE: 1997-12-31
| NUMBER OF SEQ ID NOS: 106
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 106
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62.9%; Score 3810; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 740; Conservative 0; Mismatches
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US-09-396-347F-106
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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

IIILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERGUAINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERGUAINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/22-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22524
                                                               428
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                                                                                                        362 IMDALFIGLIAIHGLKASDVMGPLINSRIGSIYIVKPWHGPAEVAFICELFSRVEDVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      542 VPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIREEVDNN
302 AVDKDGTAFLRVLNRDRNYTAPGGGQFTLPFGRSLMFVRNVGHLMTNDAIVDTDGSEVFEG
                                                                                                                                                                                    LPONTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG
                                                                                                                                                                                                                         LPQNTWKIGIMDEERRTTVNLKACIKAAAADRVVFINTGFLDRTGDEIHTSMEAGBWVRKG
                                                                                                                                                                                                                                                                                                     TMKSQPWILLAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAW
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                                                               369 IMDALFIGLIAIHGLKASDVNGPLINSRIGSIYIVKPKWHGPAEVAFICELFSRVEDVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRAS
                                                                                                                                                                                                                                                                                                                                                           TMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAW
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69.1%; Pred. No. 9.6e-222;
live 77; Mismatches 139;
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US-09-282-991A-22524
; Sequence 22524, Application US/09252991A
; Patent No. 651795
; GENERAL INFORMATION:
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259 QIDPVHPIGKADKTGLKDIVLESAITTIMDFEDSVAAVDAEDKTLGYSNWFCLNTGELKE
                                                                                                                                                                                                                                                                                        69 AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV
                                                                                                                                                                                                                                                                                                                                                                                                            LNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP
                                                                                                                                                                                                                                                                                                                                                                                                                              139 INARFALNAANARWGSLYDALYGTNAIPETDGAEKGKEYNPVRGQKVIEWGREFLDSVVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DMQTAPWKQAYENNNVDAGIQRGLPGKAQIGKGMWAMTELMAEMLEKKIGQPREGANTAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPSPTAATLHALHYHQVDVAAVQQGL-AGKRRATIEQLLTIPLAKELAWAPDEIREEVDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           615 NCQSILGYVVRWVEHGVGCSKVPDIHDIDLMEDRATLRISSQMLANWIRHDVVSKEQVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 MLIDDYHRNN-SGTIDQEAYEDFLKEIGYLVEEPEAAEIRTQNVDTEISSTAGPQLVVPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLERMAPLVDRONAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRRE
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                                                                                                                                                                                                                                9
                                                                                                                                                                                              Length 739;
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                                                                                                                                                                                                                                90; Mismatches 184;
                                                                                                                                                                                            37.8%; Score 2289; DB 2; 61.3%; Pred. No. 1.7e-196;
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 (718) 884-6600
                                                      2
                                                                                                                                                                                       Query Match
Best Local Similarity 61.3°
Matches 444; Conservative
                                 TELEX: 620428
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 739 amino acids
TYPE: amino acid
                  718/601-1099
                                                                                                                                          ; MOLECULE TYPE: protein US-08-836-943-2
                                                                                                                           linear
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US-09-328-352-7603
 TELEPHONE:
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                                                                     /KDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLA 307
                                                                                     248 IQIDPSSPVGQTDAAGVKDVLMBAALTTIMDCEDSVAAVDADDKVVIYRNWLGLMKGDLA 307
                                                                                                                                      AAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFE 367
                                                                                                                                                              BEVSKGGSTFTRIMNPDRVYTRADGSELTLHGRSLLFVRNVGHLMTNDAILDKDGNEVPE 367
                                                                                                                                                                                                           GIMDALFIGLIAIHGLKASDVNGPLI--NSRIGSIYIVKPKMHGPAEVAFICELFSRVED 425
                                                                                                                                                                                                                                VLGLPQNTMKIGIMDEERRITVNLKACIKAAADRVVFINTGFLDRIGDEIHTSMEAGPMV 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        663 VESLKRWAVVUDRQNASDPSYRPMAPNFDDNVARQAALELVVEGTRQPNGYTEPVLHRRR 722
LSSGSFGDATGFTVQDGQLVVALPDKS-TGLANPGQFAGYTGAAESPTSVLLINHGLHIE 247
                  EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,943
FILING DATE: 08-MAY-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Myers, Jonathan
REFERENCZ/DOCKET NUMBER: 26,963
REFERENCZ/DOCKET NUMBER: 20357
TELECOMMUNICATION INFORMATION:
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APPLICANT: Reinscheid, Dieter
APPLICANT: Rikmanns, Bernhard
APPLICANT: Eikmann, Hermann
TITLE OF INVENTION: DNA WHICH REGULATES
TITLE OF INVENTION: CORYNEFORM BACTERIA
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: The Firm of Karl F. Ross, STREET: 5676 Riverdale Ave. CITY: Bronx STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08836943
Patent No. 5965391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFKAR 731
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US-08-836-943-2
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368 377 428 434 488 494 548 554 607 614 667

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INFORMATION FOR SEQ ID NO: 30:
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LENGTH: 421 amino acids
TYPE: amino acid
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Best Local Similarity 80.4<sup>3</sup>
Matches 319; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    617/720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
ORGANISM: MYC
                                                                                                                                                                                                             ZIP: 02210
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TELEFAX: 6
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                                                                                                                                                                                                                                                                           10 TARIQKGKLAIAKELYDFIENEALPGSGLDSETYWKNFEQVVVDLSPKNKALLAKRDELQ
                                                                                                                                                                                                                                                                                                                                                                                               RNARYCLNAANARWGSLYDALYGFDVISEEGGAEKGKGYNPVRGAKVIEFAKNFLNEIFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 AAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 GIMDALVTPLLSIADIRSENENK---NSRKGSMYIVKPKWHGPEEVAFAVELFERAEQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               423 GLPAKSLKIGIMDEBRRTSVNLKNCIAAAKDRTIFINTGFMDRTGDEIHTSMEAAPVVRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           543 WVPSPTGAVIHAMHYHQVNVKARQDQLKAEEMLSLDDLLTPPFATDTNWSAEEINNELEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV
                                                                                                                                                                                                                                                                                                                                   LSSGSFGDATGFTVQDGQLVVALPD-KSTGLANPGQFAGYTGAAESPTSVLLINHGLHIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKWHGPAEVAFTCELFSRVEDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 GTMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTA
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                                                                                                                                                                                                                                                         9 TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ
APPLICANT: Gary L. Breton et al.

TITE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: BAUMANNI POR DIAGNOSTICS AND THERAPEUTICS
FILE REPREBLOCE: GTC99-03PA CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 729
                                                                                                                                                                                                                              Gaps
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8
                                                                                                                                                                                               Length 729;
                                                                                                                                                                                             36.7%; Score 2225; DB 4; Length 7 59.8%; Pred. No. 9.5e-191; ive 97; Mismatches 185; Indels
                                                                                                                                                  ORGANISM: Acinetobacter baumannii
US-09-328-352-7603
                                                                                                                                                                                                                           Matches 432; Conservative
                                                                                                                                                                                               Query Match
Best Local Similarity
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US-08-311-731A-30
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; Sequence 30, Application US/08311731A

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Patent No. 6583266

GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 VQKYGGSSVADADRIRRVAERIVQIKKQGNDIVVVVSAMGDTTDDLLDLAQQVCPEPPAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 VLONVSKVEDGKTDITFTCSRDSGPIAVAKLGSLRDEIGFTÖLLYDDHIGKVSLIGAGMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            749 VOKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
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                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/POCKET NUMBER: 31,616
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 61/720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHPGVTATFCEALAAVGVNIELISTSEIRISVLCRDT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
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80.4%; Pred. No. 4.2e-130;
tive 18; Mismatches 43;
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1039 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 1095
    ----RRRRQHR 1038
                                                                                                                 305 DGTTDITFTCPRADGRRAMEILKKLQVQG-----NW------TNVLYDDQVGKVSLV 350
                           869 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59; Indels
989 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA--
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SUGIMOTO, MASAKAZU
APPLICANT: SUGIMOTO, WASAKAZU
APPLICANT: USUDA, YOSHTHIRO
APPLICANT: TANAKA, TOMOKO
APPLICANT: TANAKA, AKIKO
APPLICANT: MATSUI, HIROSHI
TILLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.2%; Score 1223.5; DB ]
64.0%; Pred. No. 3.6e-101;
ive 55; Mismatches 59;
                                                                                                                                                                     1096 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 1127
                                                                                                                                                                                                           351 GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS TEXT EDITOR
CURRENT APPLICATION NUMBER: US/08/700,359
FLING DATE: 08-OCT-1996
CLASSIPICATION: 435
PROOR APPLICATION NUMBER: US/08/700,359
FILING DATE: 04-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 10-819-0 PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/08700359
Patent No. 5766925
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 251; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-08-700-359-9
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Best Local Similarity
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                                                                                                                                                                                                                                                                             RESULT 8
US-08-700-359-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          809 ELDMILTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 VQXXGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLELALALAVNPVPPAR 64
                                                                      Sequence 3. Application US/08532828B
Patent No. 568671
GENERAL INFORMATION:
APPLICANT: GCGNM, Yuri
APPLICANT: GCGNM, Yuri
APPLICANT: TANAKA, Akiko
APPLICANT: TANAKA, Akiko
APPLICANT: TANAKA, Akiko
APPLICANT: MATSUI, Hiroshi
TITLE OF INVENTION: MUTANT ASPARTOKINASE GENE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.2%; Score 1223.5; DB 1; Length 421; 64.0%; Pred. No. 3.6e-101; tive 55; Mismatches 59; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Flappy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS TEXT EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,828B
FILING DATE: 27-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24,618
ER: 10-764-0 PCT
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ATCC13869
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CLAING DATE: 27-COI-1295

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-101450
FILING DATE: 27-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-764-0
TELEPHONE: 703-413-2200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                 STREET: 1755
CITY: ARLING
STATE: VA
COUNTRY: US/
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251;
                                 RESULT 7
US-08-532-828B-3
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US-08-532-828B-3
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us-09-688-672a-52.rai

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989 IKDVPMEDPILIGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA-------RRRROHR 1038
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                                                                                                                                                                                               65 EMDMLLITAGERISNALVAWAIESLGAEAQSFTGSQAGVLTTERHGNARIVDVTPGRVREA 124
                                                                                                                                                                                                                                                                                                                                                                    -----TNVLYDDQVGKVSLV 350
                                                                                                                                                                       809 ELDMLITAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 868
                                                                                                                                                                                                                                                                                     749 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVSAMGDTTDDLLDLAQQVCPAPPPR
                                                                                                                     5 VQKYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLELAAAVNPVPPAR
                                                                                                                                                                                                                                                          869 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
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                                               Gaps
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    Length 421;
tch
al Similarity 64.0%; Pred. No. 3.6e-101;
251; Conservative 55; Mismatches 59; Indels.
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STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400
STREET: YES JEFFERSON DAVIS HIGHWAY, SUITE # 400
STATE: VIRGINIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305 DGTTDITFTCPRADGRRAMEILKKLOVOG-----NW----
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APPLICATION NUMBER: US/08/967,104 FILING DATE: CASASTECATION DATA:
APPLICATION NUMBER: US 08/596,366 FILING DATE: 29-ARF.1996
APPLICATION NUMBER: US 5-209775 FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 5-209776 FILING DATE: 24-AUG-1993
PROR APPLICATION NUMBER: US 6-153876 FILING DATE: 05-UUL-1994
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    Query Match
Best Local S
Matches 251
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                                                                                                                                                                                                                      1039 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 1095
                                                                                                                                                              245 MEDIPVEERAVLTGVATDKSEAKVTVLGISDKPGBAAKVFRALADABINIDMVLQNVSSVE 304
                                                                                                                                                                                                                                               ---TNVLYDDQVGKVSLV 350
                                                 929 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 988
                                                                        125 LDEGKICIVAGFQGVNKETRDVTTLGRGGSDTTAVALAAALNADVCEIYSDVDGVYTADP 184
                                                                                                                                                                                                                                                                                                                                           Sequence, Application US/08596366;
Patent No. 587683
GENERAL INFORMATION:
APPLICANT: SUGIMOTO, Masakazu
APPLICANT: SUZUKI, Tomoko
APPLICANT: MATSUI, Hiroshi
APPLICANT: MATSUI, Hiroshi
APPLICANT: MATSUI, Hiroshi
APPLICANT: MATSUI, RESILA
ITILE OF INVENTION: ITS GENE, AND PRODUCTION METHOD OF AMINO ACID
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPANING SYSTEM: PC-DOS/MN-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/596,366
FILING DATE: 24-ANG-1996
CLASSIFICATION NUMBER: US/08/596,366
FILING DATE: 24-ANG-1993
PROOR APPLICATION NUMBER: 195-209776
FILING DATE: 24-ANG-1993
PROOR APPLICATION NUMBER: 195-19376
FILING DATE: 24-ANG-1993
PROOR APPLICATION NUMBER: 24-ANG-1993
ATPONEY/AGENT INPOMMATION:
NAME: OBLOW, NORMAN F.
REGISTRATION NUMBER: 24,618
RESTERENCE/DOCKET NUMBER: 10-784-0 PCT
TELEDENOMICATION INFORMATION:
TELEDENOMICATION INFORMATION:
TELEDENOMICATION INFORMATION:
TELEDENOMICATION INFORMATION:
TELEDENOMICATION INFORMATION:
TELEDENOMICATION INFORMATION:
TELEDENOMICATION NUMBER: 10-784-0 PCT
TELEDENOMICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 421 aminotonic
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Sequence 14, Application US/08852730

Patent No. 6090597

GENERAL INFORMATION:
APPLICANT: SEIKO HIRANO, MASAKAZU SUGIMOTO, EIICHI NAKANO,
APPLICANT: NARAMATSU
APPLICANT: NARAMATSU
APPLICANT: NARAMATSU
APPLICANT: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER AND NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CIIY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 989 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA-------RRRRQHR 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEEGRVVLVAGFOGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
                                                                                                                                                                                                                                                                                                                                                                                    ; Score 1223.5; DB 3; Length 421;
; Pred. No. 3.6e-101;
55; Mismatches 59; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORMITER: IBM PC compatible
COERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/852,730
FILING DATE: 05-07-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 DGTTDITFTCPRADGRRAMEILKKLOVOG----NW----
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         APPLICATION NUMBER: JP 8-32565
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-300
TELEPHONE: 703-413-300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 mmino acids
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 64.0%;
Matches 251; Conservative 55
                                                                                                                                                                                                                                                : 421 amino acids
amino acid
                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-908-5
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Patent No. 6004773

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            989 IKDVPMEDPILIGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA------RRRRQHR 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 039 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKWWTRSETRSASTQLLYDDHIGKVSLI 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            809 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEEGRVVLVAGFOGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 MEDIPVEEAVLTGVATDKSEAKVTVLGISDKPGEAAKVFRALADAEINIDMVLQNVSSVE 304
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEATHING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralease #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/985,908
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION: DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            3.6e-101;
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ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-784-0 PCT
TELEPHONE: (703) 413-2220
TELEPHONE: (703) 413-2220
TELEPHONE: (703) 413-2220
TELEPHONE: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
LENGTH: 421 amino acids
                                                                                                                                                                                                                                                                                                                                                                          Query Match
20.2%; Score 1223.5;
Best Local Similarity 64.0%; Pred. No. 3.6e
Matches 251; Conservative 55; Mismatches
                                                                                                                                                                                                                                           : 421 amino acids
amino acid
                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
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US-08-985-908-5
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989 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA-------RRRRQHR 1038
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----TNVLYDDQVGKVSLV 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 EMDMLLTAGERISNALVAMAIBSLGABAQ§FTGSQAGVLTTERHGNARIVDVTPGRVREA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              749 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
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F: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27;
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 20.2%; Score 1223.5; DB 3; Length Best Local Similarity 64.0%; Pred. No. 3.6e-101; Matches 251; Conservative 55; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08532828B
; Sequence 4, Application US/08532828B
; Patent No. 5688671
; GENERAL INFORMATION:
; APPLICANT: SUZUMOTO, Masakazu
; APPLICANT: SUZUMOTO, Wasakazu
; APPLICANT: TANAKA, Yuxi
; APPLICANT: TANAKA, Hixosh
; TILLE OF INVENTION: MUTANT ASPARTOKINASE GENE
; TULE OF INVENTION: MUTANT ASPARTOKINASE GENE
; NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK
; STREE: 1755 s
CITV.
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-325658
FILING DATE: O5-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                          TELECOMMUN.
TELEPHONE: 703-1.220
TELEFAX: 703-413-2220
INPORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 421 amino acids
TOPE: amino acids
TOPE: amino acids
                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
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COUNTRY:
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APPLICANT: ATSUSHI HAYAKAWA, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
COUNTRY: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA-------RRRRQHR 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                               20.2%; Score 1223.5; DB 3; Length 64.0%; Pred. No. 3.6e-101; tive 55; Mismatches 59; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,916
FILING DATE: 05-DEC-1997
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                CLASSIPICATION: 435
PRIOR APPLICATION DATA:
PPELICATION NUMBER: JP 8-142812
FILING DATE: 05-UUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-985-916-5; Sequence 5, Application US/08985916; Patent No. 6221636
                                                                                                                               NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,616
TELECOMMUNICATION INFORMATION
TELECHHONE: 703-413-3000
                                                                                                                                                                                                                    TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                               : 421 amino acids
amino acid
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Best Local Similarity 64.0
Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                          linear
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Best Lócal Similarity 38.69
Matches 187; Conservative
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US-09-252-991A-29720
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Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGAAERLQGRGROD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 1095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 VQKYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLELAAAVNPVPPAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60; Indels
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63.8%; Pred. No. 8.3e-101;
iive 55; Mismatches 60;
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US-08-532-828B-4
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS-DOS TEXT EDITOR CURRENT APPLICATION DATA:
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Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
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ORIGINAL SOURCE
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US-09-252-991A-29720
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TYPE: amin
TOPOLOGY:
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963 YARRHNIPVHVRSSYSDRPGTVVVGSIKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGY 1022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 VALAAALKADECQIYTDVDGVYTTDPRVVPQARRLDKITFEEMLEMASLGSKVLQIRAVE
                                                                                                                                                                                                                                                                                                                                                                          663 ADVRASLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAOOPNGYTEPILH
                                                                                                                                                                                                                                                                                                                                                                                                                               -----GSERMWQVQKGALH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1023 AAKVFRAVARRRQ--------HTHGAABRLQGRGRQDRHHLHLLPQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 AFKILGPISAANVEVDMIVQNVAHDNTTDFTFTVHRNDYLNALE------ILKQT
                                                                                                                                                                                                                                                                            Length 461,
                                                                                                                                                                                                                                                                         13.6%; Score 827; DB 4; L
38.6%; Pred. No. 1.8e-65;
ive 86; Mismatches 130;
PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FLILMG DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 29720 LENGTH: 461
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:	November 21, 2003, 16:08:22 ; Search time 45.7107 Seconds (without alignments) 4680.740 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-688-672A-52 6061 1 MQHHHHHHTDRVSVGNLRIASAATRRPRCTRGRDGRWACQ 1172
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	666188 segs, 182559486 residues
Total number of	Total number of hits satisfying chosen parameters: 666188
Minimum DB seq length: 0 Maximum DB seq length: 20	Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
3: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
6: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
7: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
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9: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
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17: /cgn2\_6/ptodata/1/pubpaa/US108\_PUBCOMB.pep:\*
18: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

201111111111111111111111111111111111111	Query	re Match Length DB ID	63.8	63.8 753 11 US-09-272-975-58 Sequence 58,	37.8 739 10 US-09-738-626-6988 Sequence	26.7 421 9 US-09-793-306-163 S	20.2 421 10 US-09-738-626-3781	20.2 421 11 US-09-746-660A-24	20.2 421 15 US-10-226-136-5 Sequence	20.1 421 15 US-10-067-974-2 Sequence	20.0 421 15 US-10-067-974-16	18.9 430 15 US-10-156-761-12093 Secuence		12.7 156 12 US-10-084-843-227 Sequence	12.7 156 12 US-10-084-843-227 Sequence 12.7 156 12 US-10-193-002-222 Sequence	12.7 156 12 US-10-084-843-227 Sequence 12.7 156 12 US-10-193-002-222 Sequence 11.1 394 12 US-09-882-227-290 Sequence	12.7 156 12 US-10-084-843-227 12.7 156 12 US-10-193-002-222 11.1 394 12 US-09-882-227-290 6.2 564 10 US-09-890-813-17
o\**	Query	Match Ler	63.8	63.8	37.8	26.7	20.2	20.2	20.2	20.1	20.0	18.9		12.7	12.7	12.7 12.7 11.1	12.7 112.7 11.1 6.2
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US-09-8	US-10-301-997-2	US-09-989-33	US-09-890-813-1	US-10-226-136-	US-09-890-813-1	US-10-02	US-09-976-059-1	US-10-156-761-958	US-10-156-761-1	US-10-32	US-1	US-10-156-761-104	US-10-156-761-7	US-09-940-316B-7	US-10-329-0	US-10-156-761-796	US-10-156-761-1	US-09-861-289-	US-09-860-846-	US-09-836-	US-10-271-88	US-09-988-384B-	US-10-156-761-104	US-10-156-761-	US-10-01	US-10-156-761-95	US-10-080-17	US-10-132-134-3	-50
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## ALIGNMENTS

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	48;	VADLTP	SGVDAE	VRGDKV         VRGDKV	AAESPT
	Length 748; Indels 0	AGVDKV        AGVDKV	DFTITT        FTITT	GPTYNK 	FAGYTG
AND METHODS		DPDSFW 	CLPEPD	TDGAEK        TDGAEK	LANPGQ
AND M	DB 1	PGTDII	TEIGY	CDVIPE	PDKSTG:
ANTIGENS OR 272,975 sion 4.0	Score 3868; Pred. No. 0; ; Mismatches	VNNEAL	AYRQFI         AYRQFI	OBLYG        OBLYG	) LVVAL!
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LT 1  9-272-975-2  quence 2, Application US/09272975  duration No. US20030027774A1  WERAL INFORMATION:  PPLICANT: Hendrickson, Rohald C.  PPLICANT: Hodge, Michael J.  ILLE OF INVENTION: TUBERCULOSIS ANTIGEN  ILLE REFERENCE: 210121.474  UNERN APPLICATION OF USE THEREFOR  LERENT APPLICATION UNDRER: US/09/27,975  URRENT PILING DATE: 1999-03-18  UNDER OF SEQ ID NOS: 63  Q ID NO 2  LENGTH: 748  TYPE: PRT  ORGANISM: Mycobacterium tuberculosis  9-272-975-2	% . % . %	MQHHHHHHTDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGYDKVVADLTPQNQAL 	LNARDELQAQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTA 	GPOLVVBVINAR FALKAANARWGSLYDALYGTDVI PETDGAEKGPTYNKVRGDKVIAYAR 	KFLDDSVPLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLI
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1975-2 trion No. US2030027774, INFORMATION: ANT: Lodgs, Michael J. ANT: Lodgs, Michael J. ANT: Houghton, Raymon OF INVENTION: TUBERCO OF INVENTION: TUBERCO OF INVENTION: UMBER: THE APPLICATION WUMBER: THE APPLICATION WUMBER: THE FILING DATE: 1999-0 TO SEQ ID NOS: 63 MRS: FastSEQ for Windo NO. 2 HS: 748 HS 174	nilarit Conse	ZHHHHH ZHHHHH	VARDELO         VARDELO	OLWP!	LDDSVI
975-2 100 No. 110 N	ttch sal Sim 748;	ц ц Ж <u>ж</u>	61 EN	121 GE 121 GE	181 KE
RESULT 1 US-09-272-975-2 US-09-272-975-2 Sequence 2, Application US/0927 Publication No. US20030027774A1 GENERAL INFORMATION: APPLICANT: Hendrickson, Royand APPLICANT: Houghton, Raymond TITLE OF INVENTION: OF USE TH FILE REFRENCE: 210121.474 CURRENT APPLICATION NUMBER OF SEQ ID NOS: 63 NUMBER OF SEQ ID NOS: 63 SOFTWARE: FastSEQ for Windows; SOFTWARE: FastSEQ for Mindows; SOFTWARE: FastSEQ for Mindows; SOFTWARE: PastSEQ for Mindows; US-09-272-975-2.	Query Match Best Local Similarity Matches 748; Conser				
RESULT US-09- SOBOL PUDDI GENE APPP TITT TITT TITT TITT TITT TITT TITT	ō m ž	9 Q	සි හි	상 음	à

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GPQLVVPVLNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYAR 180
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                                                                                        KFLDDSVPLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLI
                                                                                                                        KFLDDSVPLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLI
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APPLICANT: NAKAGANA, SATOSHI
APPLICANT: NAICOGUCHI, HIROSHI
APPLICANT: HAZAGHI, MIKIRO
APPLICANT: HAZAGHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: SENOH, AKHHIRO
APPLICANT: SENOH, AKHHIRO
APPLICANT: SENOH, AKHHIRO
APPLICANT: SENOH, AKASTO
APPLICANT: OZAKI, AKIO
ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFRENCE: 249-125
CURRENT APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER: OF SEQ ID NOS: 7059
SEQ ID NO 6988
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                                                                 NHGLHIBILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLG
                                                                                                                                                         LNKGDLAAAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDT
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Publication No. US20030027774A1
GENERAL INFORMATION:
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: TUBERCULOSIS ANTIGENS AND METHODS
TITLE OF INVENTION: OF USE THEREFOR
FILE REFERENCE: 210121.474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 748; Conservative 0; Mismatches
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CURRENT FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT , ORGANISM: Mycobacterium tuberculosis US-09-272-975-58
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US-09-272-975-58
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989 IKDVPMEDPILIGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRQHRHGAAE---- 1043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 VLONVSKVEDGKTDITFTCSRDVGPAAVEKLDSLRNEIGFSQLLYDDHIGKVSLIGAGMR 355
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TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy TITLE OF INVENTION: of Tuberculosis FILE REFERENCE: 014058-008740US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         809 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
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                                                                                                                                                                                                                                                                                                                                                                                                                 35;
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Best Local Similarity 85.1%; Pred. No. 1.3e-130;
Matches 338; Conservative 7; Mismatches 35;
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APPLICANT: ANDO, SETKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TYOKOI, HARUHIKO
APPLICANT: TATRISHI, NAOKO
APPLICANT: TATRISHI, NAOKO
APPLICANT: TKEDA, MIHIRO
APPLICANT: TKEDA, MSATO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                      CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR FILING DATE: 2000-02-25
PRIOR FILING DATE: 2000-08-08
PRIOR FILING DATE: 2000-08-08
NUMBER: O'S SEQ ID NOS: 164
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 163
LENGTH: 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: MO-2 (aspartokinase)
US-09-793-306-163
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                                                                                                  Length 739;
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                                                                                                Query Match 37.8%; Score 2289; DB 10; Best Local Similarity 61.3%; Pred. No. 2.2e-188; Matches 444; Conservative 90; Mismatches 184;
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Patent No. US20020098200A1
GENERAL INFORMATION:
APPLICANT: Campos-Neto, Antonio
APPLICANT: Skeiky, Yasir
APPLICANT: Ovendale, Pamela
APPLICANT: Jen, Shyjan
APPLICANT: Lodes, Michael
APPLICANT: Corixa Corporation
                   TYPE: PRT
ORGANISM: Corynebacterium glutamicum
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Lodes, Michael
Corixa Corporation
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                                             ; ORGANISM: COLY;
US-09-738-626-6988
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US-09-793-306-163
LENGTH: 739
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989 IKDVPMEDPILIGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA------RRRRQHR 1038
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                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                              27;
                                                                                                                                                                                                                                                                   59; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/226,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IZUI, Masako
HAYAKAWA, Atsushi
NAKANO, Eiichi
KOBAYASHI, Masaki
YOSHIHARA, Yasuhiko
NAKANATSU, Tsuyoshi
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                          DB 11;
                                                                                                                                                                                                                          Score 1224.5; DB Pred. No. 7.7e-97;
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                                                                                                                                                                                                           20.2%; Scc. No. /...
64.0%; Pred. No. /...
'**e 55; Mismatches
PRIOR FILING DATE: 2000-03-09
PRIOR PEDLICATION NUMBER: DE 19931420.9
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 125
SOFTWARE: Patentin Vers. 2.0
SEQ ID NO 24
LENGTH: 421
                                                                                                                                         TYPE: PRT ORGANISM: Corynebacterium glutamicum
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Publication No. US20030054506Al

GENERAL INFORMATION;

APPLICANT: OTSUNA, Seiko
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COMPUTER READABLE FORM:
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Best Local Similarity
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APPLICANT: Schroder, Oskar
APPLICANT: Schroder, Gregor
APPLICANT: Harberhauer, Gregor
APPLICANT: Hee, Heung-Schick
APPLICANT: Lee, Heung-Schick
APPLICANT: Lee, Heung-Schick
APPLICANT: Hamay, BYUNG-Uoon
TITLE OF INVENTION: OCKNEBEGTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
TITLE OF INVENTION: WHERE: 09/606740
TITLE OF INVENTION NUMBER: 09/606740
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141031
PRIOR APPLICATION NUMBER: 60/141031
PRIOR PILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/14201
PRIOR APPLICATION NUMBER: 60/14201
PRIOR APPLICATION NUMBER: 60/148613
PRIOR APPLICATION NUMBER: 60/148613
PRIOR APPLICATION NUMBER: 60/148613
PRIOR PILING DATE: 1999-06-12
PRIOR APPLICATION NUMBER: 60/148613
                                                                                                                                                                                                                              Length 421;
                                                                                                                                                                                                                                                                   59; Indels
                                                                                                                                                                                                                            DB 10;
                                                                                                                                                                                                                          Score 1224.5; DB Pred. No. 7.7e-97
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                                                                                                                                                                                                                                                                     55; Mismatches
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 3781
LENGTH: 421
                                                                                                                                                   , ORGANISM: Corynebacterium glutamicum
US-09-738-626-3781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/09746660A Publication No. US20030049804A1 GENERAL INFORMATION:
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APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
APPLICANT: Kim, Unn-Won
APPLICANT: Lee, Heung-Schick
                                                                                                                                                                                                                            20.2%;
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Best Local Similarity 64.0°
Matches 251; Conservative
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US-09-746-660A-24
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ORGANISM: Corynebacterium glutamicum
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OTHER INFORMATION: May
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US-10-067-974-2
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Publication No. US20300055232A1
GENERAL INFORMATION:
APPLICANT: Li, Lhing-Yew
TITLE OF INVENTION: Polymucleotide Constructs for Increased Lysine Production
FILE REFERENCE: 1533.2640001
CURRENT APPLICANTON NUMBER: US/10/067,974
CURRENT PILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,183
PRIOR FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO: 25
TYPE: PRI
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Best Local Similarity 64.0%; Pred. No. 9.4e-97;
Matches 251; Conservative 55; Mismatches 59; In
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                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/952,976
FILING DATE: 8-DEC-1997
APPLICATION NUMBER: US 7-140614
FILING DATE: 0-UUL-1995
ATTORNEY-AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEPAX: 703-413-3200
TELEPAX: 703-413-220
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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*** MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-226-136-5
                                                                                                                                                                                                                                                       LENGTH: 421 amino acids TYPE: amino acid
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US-10-067-974-2
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US-10-067-974-16
| Sequence 16, Application US/10067974
| Sequence 16, Application No. US20030055232A1
| Publication No. US20030055232A1
| GENERAL INFORMATION:
| APPLICANT: Li, Lhing-Yew
| APPLICANT: Li, Lhing-Yew
| TILL OF INVENTION: Polynucleotide Constructs for Increased Lysine Production
| FILE REFERENCE: LS3.2.646001
| FILE REFERENCE: LS3.2.646001
| CURRENT APPLICATION NUMBER: US/10/067,974
| CURRENT FILING DATE: 2002-02-08
| PRIOR FILING DATE: 2001-02-08
| NUMBER OF SEQ ID NOS: 25
| SEQFWARE: Patentin Version 3.1
| LENGTH: 421
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-----TNVLYDDQVGKVSLV 350
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                                                  27;
  DB 15; Length 421;
                                                  60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 20.1%; Score 1217.5; DB Best Local Similarity 63.8%; Pred. No. 3.1e-96; Matches 250; Conservative 55; Mismatches 60
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NAME/KEX: MISC FEATURE
LOCATION: (317)..(317)
OTHER INFORMATION: May be either Ser or Ala
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NAMEN SECTIONS
NAMEN (40)
OTHER INFORMATION: May be either Cys
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LOCATION: (380).
OTHER INFORMATION: May be either Thr
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 227:
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ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-084-843-227

Sequence 227, Application US/10084843

Publication No. US20030143243A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
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TYPE: amino acid
STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS:
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STATE: Washington
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(206) 68
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                                                                              Gaps
                                                                            27;
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                                   20.0%; Score 1211.5; DB 15; Lengt. 63.5%; Pred. No. 1e-95; ive 55; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1096 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 1127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAMA, JUN
APPLICANT: ISHIKAMA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIVKI
APPLICANT: HATORI, MASHIKA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: J002-05-09 PRIOR APPLICATION NUMBER: JP 2001-204089 PRIOR FILING DATE: 2001-05-30 PRIOR FILING DATE: 2001-05-30 PRIOR PELICATION NUMBER: JP 2001-272697 NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Sequence 12093, Application US/10156761
, Publication No. US20030119018A1
, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CRGANISM: Streptomyces avermitilis
US-10-156-761-12093
                                                                            Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                       Best Local Similarity
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Matches 239; Conserv
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US-10-156-761-12093
US-10-067-974-16
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989 IKDVPM-------EDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRR-- 1034
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                                                                                                                                                                                                                                                                                  125 LDEGNIAIVAGFOGVSODKKDITTLGRGGSDTTAVALAAALDAEVCEIYTDVDGVFTADP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                   301 IDMVVQNVSAASTGLTDIS-----FTLPKTEGRKAIDALEKAKSVIGFDSLRYDDQIG 353
                                                                                                                       RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVVGS
                                                                                                                                                           LEEGRVVLVAGFOGVSODTKDVTTLGRGGSDTTAVAMAAALGADVCELYTDVDGIFSADP
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Skeiky, Yasir A.W.
Campos.Neto. Antonio
Houghton, Raymond
Yedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Romald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNO.
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <unhalber <unhalber <unhalber <unhalber <unhalber <unhalber <unhalber <unhalber <unhalber <ul>abplication Number: US/09/072,967abplication Number: US/09/072,967artoner/Agent Information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSE 1127
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us-09-688-672a-52.rapb

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APPLICANT: Al-Garawi, Amal Applicant: APPLICANT: Miler, Charles APPLICANT: Miler, Charles APPLICANT: Miler, Charles APPLICANT: Tomb, Jean-Francois APPLICANT: Tomb, Jean-Francois APPLICANT: Ocomen, Raymond P. TITLE OF INVENTION: Encoding No. US20030158396A1el Helicobacter Polypeptides in the 1 TITLE OF INVENTION: Genome FILE REFERENCE: 06132/047002 CURRENT APPLICATION NUMBER: US/09/882,227 CURRENT FILING DATE: 2001-06-15 PRIOR APPLICATION NUMBER: US 08/902,615 PRIOR APPLICATION NUMBER: US 08/902,615 NUMBER OF SEQ ID NOS: 638 SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1059 -LPQTSGPPPWKNWTRSETRSASTQLL-----YDDHIGKVSLIGAGMRSHPGVTATFC 1110
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                                                                                                                                                                           61 LDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTAL 120
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SSAALSMALERYGHRAISLSGKEAGILTSSHFQNAVIQSIDTKRITELLEKNYIVVIAGF
                                                           750 QKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                761 ERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPRELDMLLTAGERI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 VSGIALDKNQARVSMEGVEDRPGIAAEIFGALA----EYRINVDMIVQTIGRDGKTDLDF
                                                                                              1 OKYGGSSVADAERIRRVAERIVATKKOGNDVVVVVSAMGDTTDDLLDLAQOVCPAPPPRE
                                                                                                                                             810 LDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTFGRLQTAL
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11.1%; Score 673; DB 12;
Best Local Similarity 40.1%; Pred. No. 3e-49;
Matches 151; Conservative 83; Mismatches 119;
100.0%; Pred. No. 2.7e-58; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 290, Application US/09882227; Publication No. US20030158396A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-882-227-290
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kleanthous, Harold
Best Local Similarity 100.
Matches 156; Conservative
                                                                                                                                                                                                                              870
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                                                                                 Gaps
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Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Micheal J.
Hendrickson, Ronald C.
INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
                                       Length 156;
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
STATE: Washington
COUNTY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCEZ DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                            EEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAM 905
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0
                                       Score 770; DB 12;
Pred. No. 2.7e-58;
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                          12.7%; Scc...
100.0%; Pred. No. ...
0; Mismatches
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RAPPLICATION NUMBER: US/10/193,002
FILING DATE: 10-011-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: protein
DESCRIPTION: SEQ ID NO: 222:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                            Jour 193.002-222
Sequence 222, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MATION FOR SEQ ID NO: 222
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.7%;
                                                                                 Matches 156; Conservative
                                       Query Match
Best Local Similarity
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  US-10-084-843-227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    818 ERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVT----PGRLQ-TALEEG 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      933 NARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDR-PGTVVVGSIKD 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325 KAEPVPYLIFDEAAELAYFGAQVLHPQSMRPARESDIPVRVKNSYNPKAPGTLII---KA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 RDMSKAVLTSIVLKRNVTMLDIASTRMLGQYGFLAKVFSIFEELGISVDVVATSEVSVSL 441
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.2%; Score 377; DB 10; Length 564; Best Local Similarity 27.0%; Pred. No. 2e-23; Matches 128; Conservative 71; Mismatches 165; Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         749 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLL-
                               Sequence 17, Application US/09890813
Publication No. US20020183486A1
GENERAL INFORMATION:
TITLE OF INVENTION: Aspartate Kinase
TITLE OF INVENTION: Aspartate Kinase
FILE REFERENCE: BB1430 PCP.
CURRENT APPLICATION NUMBER: US/09/890,813
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/172944
PRIOR APPLICATION NUMBER: 60/172944
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
SEQ ID NO 17
LENGTH: 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Publication No. US20020183486A1

Publication No. US20020183486A1

GENERAL INFORMATION

APPLICANT: E.I. du Pont de Nemours and Company

TITLE OF INVENTION: Aspartate Kinase

FILE REPERENCE: BB1430 PCT

CURRENT APPLICATION NUMBER: US/09/890,813

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 60/172944

PRIOR FILING DATE: 1999-12-21
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CORGANISM: Glycine max

US-09-890-813-17
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RESULT 14
US-09-890-813-17
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                                                                                                                                                                                                       743 GDDAARVQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTD--
                                                                                                                          Length 555;
                                                                                                                      Query Match 6.0%; Score 365; DB 10; Length 5:
Best Local Similarity 29.9%; Pred. No. 2.1e-22;
Matches 103; Conservative 58; Mismatches 119; Indels
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:

November 21, 2003, 15:57:31; Search time 24.4499 Seconds
(without alignments)
4609.825 Million cell updates/sec

Title:

US-09-688-672A-52

Perfect score: 6061
Sequence: 1 MQHHHHHTDRVSVGNLRIA......SAATRRPRCTRGRDGRWACQ 1172
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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir2:\*
4: pir4:\*

283308

Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

REGULT F70022 pr0022 C;Speci C;Speci C;Date: C;Acces R;COLO, ; COLO Rajandr Naturbo A;Autbo A;Autbo A;Acces A;	RESULT 1  FYO7022  FYO702  FYO7022  FYOY022  FYO
Query Ma Best Loc Matches	Query Match 62.9%; Score 3810; DB 2; Length 741; Best Local Similarity 100.0%; Pred. No. 7.1e-221; Matches 740; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
yo, Ob	9 TDRVSVGNLRIARVLYDFVNNBALPGTDIDEDSFWAGVDKVVADLTPONOALLNARDELQ 68 
λζ Op	69 AQIDKWHRRIVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTGGVDAEITTTAGPQLVVPV 128
λ Dp	129 INARFALNAANARWGSLYDALYGTDVIPETDGAEKGFTYNKVRGDKVIAYARKELDDSVP 188 
oy Op	189 LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFACYTGAAESPTSVLLINHGLHIEI 248 
ò q	249 LIDBESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA 308 
\$ A	309 AVDKDGTAFLRVLARDRNYTAPGGGGFTLPGRSLMFVRNVGHLMTNDALVDTDGSEVFBG 368 
ò	369 IMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKWHGPAEVAFTCELFSRVEDVLG 428

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LNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP 188
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                                                                              LPQNTMKIGIMDEERRITVNLKACIKAAADRVVFINIGFLDRIGDEIHTSMEAGPMVRKG 481
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A;Cross-references: EMBL:AL008609; PIDN:CAA15459.1
A;Cross-references: cosmid B1788
C;Genetics:
A;Note: glcB
C;Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase
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Best Local Similarity 82.0%
Matches 597; Conservative
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RESULT 3
H83586
malate synthase G PA0482 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000
C;Accesion: H83586
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Briadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J., I. Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A;Accession: H83586
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-72 <STO>
A;Residues: 1-72 <STO>
A;Residues: 1-72 <STO>
A;Gross-reference: GB:AE004485; GB:AE004091; NID:g9946332; PIDN:AAG03871.1; GSPDB:GN001: A;Genetics:
A;Genetics:
A;Genetics:
423
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                                                                                                                                                                                                                                               DVRASLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHR
                                                                                                                                                                                                                     484 MVRKGTMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAG
                                                                                                                                                                                                                                                                                                                              544 ASTAWVPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIRE
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                                                                                                                                                          EDVLGLPQGTLKVGIMDEERRTTLNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGP
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247

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malate synthase G (PA0482) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)

G.Species: Agrobacterium tumefaciens
C.Species: Agrobacterium tumefaciens
C.Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C.Accession: F97364
A.; Liu, F: Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A.; Liu, F: Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2333-2328, 2001
A.; Liu, F: Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2333-2328, 2001
A.; Recence number: A97359; WUID:21608551; PMID:11743194
A.; Accession: F97364
A.; Accession: P97364
A.; Accession: P97364
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A;Residues: 1-744 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK85871.1; PID:g15154912; GSPDB:GN00169
C;Genetics:
A;Gene: AGR C 78
A;Map position: circular chromosome
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                                       PLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIE
                                                           ILIDPESOVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLA
                                                                                                                                                                                       AAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFE
                                                                                                                                                                                                                         321 EAVSKGGNTFTRRLNPDRYYTAPDGSALTLPGRSLMLVRNVGHLMTNPAILDRDGRDVPE
                                                                                                                                                                                                                                                              GIMDALFIGLIAIHGLKASDVNGPLINSRIGSIYIVKPKMHGPAEVAFTCELFSRVEDVL
                                                                                                                                                                                                                                                                                      GLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRK
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39.3%; Score 2380; DB 2;
Best Local Similarity 63.5%; Pred. No. 5.3e-135;
Matches 461; Conservative 91; Mismatches 170;
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     141
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malate synthase G [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C, Species: Agrobacterium tumefaciens
C, Species: Agrobacterium tumefaciens
C, Species: Agrobacterium tumefaciens
C, Species: Agrobacterium tumefaciens
C, Species: Agrobacterium tumefaciens
C, Accession: AH3582
R, Wood, D. W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Strile: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Accession: AH3582
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AH3582
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-744 <KUR>A;Residues: 1-744 <KUR>A;Residues: 1-744 <KUR>A;Residues: 1-745 <KUR>A;Coss-references: GB:AE008688; PIDN:AAL41078.1; PID:g17738367; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | VLNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSV 187
                                                                                                               425
                                                                                                                                   GIQDGLFTSLIAIH-----DLNGNTSRKNSRTGSVXIVKPKWHGPERAAFTNELFGRVED 416
                                                                                                                                                                                                             417 VLGLPRNTLKVGIMDEERRTTVNLKACIKAAKDRVVFINTGFLDRTGDEIHTSMEAGAVV 476
                                                                                                                                                                                                                                                                RKGTMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGAS 545
                                                                                                                                                                                                                                                                                                                                        TAWVPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIREEV 605
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                                   308 AAVDKDGTAFLRVLNRDRNYTAPGGGOFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFE 367
IQIDPSSPVGQTDAAGVKDVLMEAALTTIMDCEDSVAAVDADDKVVIYRNWLGLMKGDLA 301
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                                                           EEVSKGGSTFTRTMMPDRVYTRADGSELTLHGRSLLFVRNVGHLMTNDALLDKDGNEVPE
                                                                                                                                                                                                                                                                                    GIMDALFIGLIAIHGLKASDVNGPLI--NSRTGSIYIVKPKMHGPAEVAFTCELFSRVED
                                                                                                                                                                                       VLGLPQNTMKIGIMDEERRITVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMV
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.larity 63.5%; Pred. No. 5.3e-135;
Conservative 91; Mismatches 170;
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A;Map position: circular chromosome
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461; Conserv
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Best Local S:
Matches 461
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Nalate synthase (BC 4.1.3.2) - Corynebacterium glutamicum
C; Species: Corynebacterium glutamicum
C; Species: Corynebacterium glutamicum
C; Species: Corynebacterium glutamicum
C; Date: 16-Aug-1996 #sequence revision 16-Aug-1996 #text_change 05-May-2000
C; Accession: 140715; 140836
R; Reinscheid, D. 17; Eikmanns, B. 3 ahm, H.
M; Richology 140, 3099-3108, 1994
A; Reference number: 140715; MUID:95111631; PMID:7812449
A; Reference number: 140715
A; Reference number: 140715
A; Residues: preliminary, translated from GB/EMBL/DDBJ
A; Residues: 1-739 aRES
A; Residues: Bible:X78491; NID:9530011; PIDN:CAA55243.1; PID:9530012
R; Lee, M:
M; Microbiol. Biotechnol. 4, 256-263, 1994
A; Reference number: 140836
A; Recession: 140836
A; Recession: 140836
A; Recession: 140836
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-739 aRE2
A; Cross-references: GB:L27123; NID:9853573; PIDN:AAA68074.1; PID:9853574
A; Cross-references: GB:L27123; NID:9853573; PIDN:AAA68074.1; PID:9853574
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EKNGKQMTRRLNGDRTYTAPDGSTLTLKGRSLMLVRNVGHLMTNPAILDAEGNEVPEGIM
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                    DKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPVLNA
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AF2299
malate synthase (EC 4.1.3.2) [imported] - Brucella melitensis (strain 16M)
C.Species: Brucella melitensis
C.Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
C.Accession: AF3299
R.DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R.DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A.fitle: The genome sequence of the facultative intracellular pathogen Brucella melitens A; Reference number: AD3252; PMID:11756688
A; Reference number: AD3252; PMID:11756688
A; Accession: AF3299
A; Actuals: preliminary
A; Residences: GB:AD08917; PIDN:AAL51561.1; PID:g17982281; GSPDB:GN00190
A; Experimental source: strain 16M
C; Genetion: I
C; Reywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase
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                                 VLNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSV 187
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                                                         PLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIE
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PIDN:BAB05852.1; GSPDB:GN001
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851789
malate synthase (EC 4.1.3.2) isoenzyme G - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: 23-Aug-1995 #sequence_revision 13-Mar-1997 #text_change 01-Mar-2002
C;Accession: S51788; F65083
R;Molina, I.; Pellicer, M.T.; Baddia, J.; Aguilar, J.; Baldoma, L.
Bur. J. Blochem. 224, 541-548, 1994
A;Title: Molecular characterization of Escherichia coli malate synthase G. I
                                                                                                                                                                                                                                                                     GPQLVVPVNNARYAINAANARWGSLYDALYGSNVISEEDGCEKTGTYNPKRGTKVIQFAK
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|METYEH-----VGNLQVATKLITFIEQRALPGTGIKKDDFWSGVQQIITELMPENKML
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                                                                                                                                             1 MOHHHHHHTDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQAL
                                                                                            Length 727
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A,Molecule type: DNA
A,Residues: 1-727 <STO>
A,Cross-references: GB:AP001514; GB:BA000004; NID:g10174613;
A,Experimental source: strain C-125
C,Genetics:
A,Gene: BH2133
                                                                                         37.3%; Score 2258; DB 2;
59.9%; Pred. No. 1.1e-127;
iive 97; Mismatches 186;
                                                                                                       Best Local Similarity 59.9%;
Matches 441; Conservative
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C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: B83916
R;Takani, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F.;
Mucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A;Reference number: A89550; MUD:20512582; PMID:11058132
A;Accession: B83916
A;Status: preliminary
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                                                                                                                    AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV
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                          oxo-acid-lyase
                                                  Query Match 37.8%; Score 2289; DB 2; Best Local Similarity 61.3%; Pred. No. 1.5e-129; Matches 444; Conservative 90; Mismatches 184;
                           ď
                           coenzyme
             ;Gene: aceB
;Keywords: carbon-carbon lyase;
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probable ask protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Dacession: F70794
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Hamris, D.; Gordon, S.; Colnor, R.; Davish, K.; Peltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 333, 537-544, 1998
A;Authors: Sagares, R.; Sultson, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome farecession: F70794
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Status: Leferences: GB:AL02121; GB:AL123456; NID:g3261559; PIDN:CAA18031.1; PID:g296013: A;Experimental source: strain H37RV
C;Genetics:
A;Gene: ask
C;Superfamily: aspartate kinase, aspartate kinase homology oblis
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C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20.Apr-2001 #sequence_revision 20.Apr-2001 #text_change 14-Dec-2001
C;Accession: 687199
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor R:, Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squ
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7; Mismatches 35;
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A; Reference number: S51788, MUID:95010032; PMID:7925370
A; Accession: S51788
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-723 <MOL>
A; Cross-references: EMBL:X74547; NID:9517246; PIDN:CDA52639.1; PID:9517247
A; Cross-references: EMBL:X74547; NID:9517246; PIDN:CDA52639.1; PID:9517247
B; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Rose, D.J.; Mau, B.; Shao, Y.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: P65083
A; Accession: P65083
A; Accession: P65083
A; Residues: 1723 <BLAT>
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A; Residues: 1723 <BLAT>
A; Residues: 1723 <BLAT>
A; Cross-references: GB: MEXO0380; GB: U00096; NID:91789344; PIDN:AAC76012.1; PID:91789348; A; Cross-references: GB: Accession: Rose-references: Strain K-12, substrain MG1655
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Best Local Similarity
Matches 419; Conserva
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Aspartate kinase (EC 2.7.2.4) alpha chain - Corynebacterium glutamicum
N.Alternate names: aspartokinase alpha chain
C.Species: Corynebacterium glutamicum
C.Species: Corynebacterium glutamicum
C.Species: To-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Jun-1999
C.Accession: S15276; S49977
R.Alinowski, J., Cremer. J.; Bachmann, B.; Eggeling, L.; Sahm, H.; Puehler, A.
R.A.Itle: Genetic and biochemical analysis of the aspartokinase from Corynebacterium glut
A; Reference number: S15276; MUID:92065816; PMID:1956296
A; Accession: S15276
A; Molecule type: DNA
A; Residues: 1421 < PUES
A; Accession: S15276
A; Molecule type: DNA
A; Residues: BEL:X57226; NID:g40509; PIDN:CAA40502.1; PID:g580983
A; Experimental source: ATCC 13032
R; Serebrijski, I.; Wojcik, F.; Reyes, O.; Leblon, G.
Submitted to the EMBL Data Library, November 1994
A; Description: Two loci of Corynebacterium glutamicum ATCC17965 that complement Escheric
A; Reference number: S49977
A; Accession: S49977
A; Accession: S49977
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A; Residues: 329-421 <SER>
A; Residues: 329-421 <SER>
A; Residues: 329-421 <SER>
A; Cross-references: BmBi.K82928; NID:g599716; PIDN:CAAS8100.1; PID:g599717
A; Cross-references: Bachmann, B.; Thierbach, G.; Puehler, A.
Mol. Gen. Genet. 224, 317-324, 1990
A; Title: Aspartokinase genes lysC-alpha and lysC-beta overlap and are adjacent the Aspartokinase genes lysC-alpha and lysC-beta overlap and are adjacent the Contents: annotation
C; Genetics:
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        5 VQXYGGSSVADAERIRRVAERIVETXKAGNDVVVVVSAMGDTTDDLLDLARQVSPAPPPR
                                                                                              ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
                                                                                                                                                                                                          LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
                                                                                                                                                                                                                                                                                                                    929 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
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A)Start codon: GTG
C;Superfamily: aspartate kinase; aspartate kinase homology
C;Superfamily: aspartate hintiators; phosphotransferase
F;3-406/Domain: aspartate kinase homology <DKI>
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Best Local Similarity 64.3%
Matches 252; Conservative
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NyAlternate names: aspartokinase alpha chain
C;Specias: Mycobacterium smegmatis
C;Date: 07-May-1998 #sequence_revision 15-May-1998 #text_change 18-Jun-1999
C;Accession: 542422; S31801
E;Cirillo, J., D.; Weisbrod, T. R.; Pascopella, L.; Bloom, B.R.; Jacobs Jr., W.R.
Mol. Microbiol. 11, 629-639, 1994
A;Title: Isolation and characterization of the aspartokinase and aspartate semialdehyde
A;Reference number: 542421; MUID:94254720; PMID:7910936
A;Recession: 542421; MUID:94254720; PMID:7910936
A;Recession: S42421; MUID:94254720; PMID:7910936
A;Recession: S42421
A;Recession: S42421
A;Recession: S42421; MUID:944506; PIDN:CAA78984.1; PID:9581352
A;Note: the authors translated the initiation codon GTG for residue 1 as Val
C;Genetics:
A;Start codon: GTG
C;Superfamily: aspartate kinase; aspartate kinase homology
C;Keywords: alternative initiators; phosphorransferase
F;1-421/Product: aspartate kinase alpha chain #status predicted <ASA>
F;3-406/Domain: aspartate kinase beta chain #status predicted <ASA>
F;250-421/Product: aspartate kinase beta chain #status predicted <ASA>
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                                                                                                                                                                                                                                                                                                              Query Match 25.5%; Score 1545.5; DB 2; Length 421; Best Local Similarity 80.4%; Pred. No. 2.9e-85; Matches 319; Conservative 18; Mismatches 43; Indels 17;
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A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A66909; MUD:21128732; PMID:11234002
A;Accession: G87199
A;Status: Pariminary
A;Nolecule type: DNA
A;Residues: 1-421 <STO>
A;Cross-references: GB:AL450380; NID:g13093941; PIDN:CAC31839.1; C;Genetics:
A;Cene: ask
C;Superfamily: aspartate kinase; aspartate kinase homology
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CSpecies: Pseudomonas alpha and beta chain PA0904 [imported] - Pseudomonas aeruginosa (strain c) Species: Pseudomonas aeruginosa C; Species: Pseudomonas aeruginosa C; Species: Pseudomonas aeruginosa C; Species: Pseudomonas aeruginosa C; Species: Sep-2000 #sequence_revision 15-Sep-2000 #text_change 14-Dec-2001 C; Accession: C33531 R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bridan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000 A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A; Accession: C33331 A; Status: preliminary A; Molecule type: DMA A; Residues: 1-412 c420> A; Cross-references: GB:AE004525; GB:AE004091; NID:g9946805; PIDN:AAG04293.1; GSPDB:GN001: A; Residues: 1-412 c420> A; Cross-reference: strain PA01 C; Genetics: A; Genetics: A; Genetics: A; Gene: Lycc, PA0904 C; Superfamily: aspartate kinase; aspartate kinase homology .
    358 KSNPGVTADFFTALSDAGVNIELISTSE 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: November 21, 2003, 16:09:56 Job time : 26.4499 secs
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Best Local Similarity 42.6%;
Matches 170; Conservative 8
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probable aspartokinase - Streptomyces coelicolor
(Species: Streptomyces coelicolor
C;bate: O5-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 31-Jan-2000
C;Accession: T35383
R;Murphy, L: Harris, D: James, K.D.; Parkhill, J: Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, June 1999
A;Reference number: Z21576
A;Reference number: Z21576
A;Retaus: preliminary; translated from GB/EMBL/DDBJ
A;Gtatus: preliminary;
A;Molecule type: DNA
A;Retaus: preliminary;
A;Molecule type: DNA
A;Retaus: preliminary
A;Retaus: Brail-AL079348; PIDN:CAB45482.1; GSPDB:GN00070; SCOEDB:SC66T3.26c
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                      1039 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 1095
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                                                                                                                                                                                                                                   989 IKDVPMEDPILTGVAHDRSBAKVTIVGLPDIPGYAAKVFRAVA----
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C;Superfamily: aspartate kinase; aspartate kinase homology
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  Length 412;
Score 823; DB 2; Length 41; Pred. No. 6.8e-42; 80; Mismatches 105; Indels
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081878 pseudomonas
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3988.226 Million cell updates/sec
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1 MQHHHHHHHDRVSVGNLRIA......SAATRRFRCTRGRDGRWACQ 1172
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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## ALIGNMENTS

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턴	Creat
ΕĮ	(Rel. 35, Last
F i	15-SEP-2003 (Rel. 42, Last annotation update)
ų Ķ	Maiate synthase G (EC 2.3.3.9). GLCB OR RV1837C OR MT1885 OR MTCY1A11.06.
S	Mycobacterium tuberculosis.
ပ္င	Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Ν×	Corynebacterineae; Mycobacteriaceae; Mycobacterium. NCBT Taxin=1773;
8	(1)
Q,	SEQUENCE FROM N.A.
Ų,	STRAIN=H37RV;
55	rcher
S	Barry C.E. III, Tekaia F.,
<b>S</b> 5	nillingworth T., Connor R.,
<b>S</b> 5	Davies K., Devill K., Feitweir T., Gentles S., Hamiln N., Holroyd S.,
ţ a	Diver S. Osborne T. Onail M.A. Reheam C., Mouse S., Murphy L.,
: s	Sutter S. Seeder K. Skelton S. Squares S. Squares R.
Ą	Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
E۱	"Deciphering the biology of Mycobacterium tuberculosis from the
E E	complete genome sequence.";
33	Macule 353:337-314(1550).
ď	SEQUENCE FROM N.A.
Ų,	
⊴ :	J.A., Carpenter L.,
<b>5</b> 5	Gwinn M.L., Hait D., Hickey E.,
5 5	NOTOHIAY U.F., NETSOH W.C., UMBYAM D.A., ELMOTAEVA M.D., SAIZDELG S.D., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
5	
Ħ	"Whole genome comparison of Mycobacterium tuberculosis clinical and
E:	laboratory strains.";
3 5	databases.
ع ڊ	CAIALIIL ACIIVIII: ACELYI-COA + B(Z)O + GIYOXYIACE = S-MAIACE +
رې پ	-!- PATHWAY: Glyoxylate bypass; second step.
Ŋ	SUBUNIT: Monomer (By Similarity).
ပ္ပ	(By similarity).
ប្ត	SIMILARITY: Belongs to the malate synthase family. GlcB subfamily
بع ڊ	This SWISS-PROT entry is convright. It is produced through a collaboration
ņ	en the Swiss Institute of Bioinformatics and the EMBI
Ŋ	Bioinformatics Inst
0	non-profit institutions as long as its content i
ပ္က	statement is not rem
ין ני	entitles requires a license agreement (see nttp://www.isb-sib.cn/announce or send an email to license@isb-sib.ch).
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SEQUENCE 741 AA, 80403 MW, A92F54E0FE8B7C64 CRC64.
                            TIGR; MIN 1885; --
Tuberculist; Rv1837c; --
Tuberculist; Rv1837c; --
HAMAP; MF 00641; -; 1.
InterPro: IPR001465; Malate_synthase.
InterPro: IPR006253; Malate_synthG.
Pfam; PF01274; Malate_synthase; 1.
TIGRFAMs; TIGR01345; malate_syn G; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
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100.0%; Pred. No. 1.5e-205;
ive 0; Mismatches 0;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- PATHWAY: Glyoxylate bypass; second step.
-i- SUBDNIT: Monomer (By similarity).
-i- SUBCELULAR LOCATION: Cytoplasmic (By similarity).
-i- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21128732; PubMed=11234002;
Cole S.T., Edilmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Duthoy S., Fellwell T., Fraser A., Hamlin N.,
Murphy L., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                        Sacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
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CATALYTIC ACID (BY SIMILARITY)
3878CADA45DB416C CRC64;
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Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
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NCBI_TaxID=1769;
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82.0%; Pred. No. 7.4e-167;
M.cmatches 72;
                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9)
GLOB OR ML2069 OR MLCB1788.27.
Mycobacterium leprae.
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731
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InterPro; IPR001465; Malate_synthase.
InterPro; IPR00523; Malate_synthG.
Pfam, PF01274; Malate_synthase; 1.
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EMBL; AL583924; CAC31024.1; -.
PIR; T44752; T44752.
HSSP; P37330; ID8C.
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nes 597; Conservative
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                        724;
                                                                                                                                              HAMAP, MF_00641; -; 1.

InterPro; IPR001465; Malate_synthase.

InterPro; IPR006253; Malate_synthG.

Pfam; PF01274; Malate_synthG.

IGRPAMs; TIGR01345; malate_syn G; 1.

ITARDEFARS; TIGR01345; malate_syn G; 1.

ACT SITE 340 340 CATALYTIC BASE (BY SIMILARITY)

ACT SITE 631 631 CATALYTIC ACID (BY SIMILARITY)

SEQÜENCE 724 AA; 78609 MW; F889FE883890995E CRC64;
                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                      43.5%; Score 2634; DB 1;
69.0%; Pred. No. 7.5e-140;
tive 82; Mismatches 138;
                                                                                            EMBL; AJ301559; CAC35701.1; -. HSSP; P37330; 1D8C.
                                                                                                                                                                                                                                                                                                                                                                           499; Conservative
                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            721
                                                                                                            ILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLA 307
                                                                                                                                  421
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SUBUNIT: Monomer: (By similarity).
SUBCELULAR LOCATION: CYtoplasmic (By similarity).
SINILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                                                                                                                                                                                                                                                                                                                                                EDVLGLPQGTLKVGIMDEERRTTLNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVDNDCQSILGYVVRWVDQGIGCSKVPDIHNVALMEDRATLRISSQLLANWLRHGVITSE
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                                                           MIRKGAMKNSTWIKAYEDANVDIGLAAGFKGKAQIGKGMWAMTELMADMVEQKIGQPKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASTAWVPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIRE
                                                                                                                                                                                     AAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIV----DTDGS
                                                                                                                                                                                                                                                                                              EVFEGIIDAVFTGLAAIHGLKTGEANGPLTNSRTGSIYIVKPKWHGPAEVAFTCELFSRV
                                                                                                                                                                                                                                                                                                                                        EDVLGLPQNTMKIGIMDEERRITVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGP
                                                                                                                                                                                                                                                                                                                                                                                                               MVRKGTMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVRASLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTBPILHR
   LNARFALNAANARWGSLYDALYGTDTI PETEGAEKGSEYNKI RGDKVI AYARKFMDQAVP
                                     LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPT-SVLLINHGLHIE
                                                                                                                                                                                                                                                               EVFEGIMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKWHGPAEVAFTCELFSRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of a chromosomal locus that affects pathogenicity Abodococcus fascians."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=D188;
Vereecke D.M., Cornelis K., Van Montagu M., El Jaziri M., Holsters
Goethals K.;
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9).
Rhodococcus fascians,
Rhodococcus, Actinobacteria, Actinobacteridae,
Corynebacterineae, Nocardiaceae, Rhodococcus.
[1]
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Q9AE55;
15-SEP-2003
15-SEP-2003
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between
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242 igidėsspyggidaagykdylmeaaltiimpcedsyaavdaddkyviyknwigimkgdla
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                                                                                                                                                                                                                                                       362 GIQDGLFTSLIAIH-----DLNGNTSRKMSRTGSVYIVKPKWHGPEEAAFTNELFGRVED
                                                                                                                                                                                                                                                                                                                                                                                                                                              VLGLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 VLGLPRNTLKVGIMDEERRTTVNLKACIKAAKDRVVFINTGFLDRTGDEIHTSMEAGAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RKGTMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RKGAMKSEKWIGAYENNNVDVGLATGLOGKAQIGKGWWAMPDLMAAMLEQKIGHPLAGAN
LSSGSFGDATGFTVQDGQLVVALPDKS-TGLANPGQFAGYTGAAESPTSVLLINHGLHIE
                                                                                                          ILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       597 DNNAQGILGYVVRWIDQGVGCSKVPDINDVGLMEDRATLRISSQLLANWLRHGVISQEQV
                                                                                                                                                                                                                                                                                                                                 GIMDALFIGLIAIHGLKASDVNGPLI - - NSRIGSIYIVKPKWHGPAEVAFICELFSRVED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE=22423060; PubMed=12534463;
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Berinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Eauber J., Stiepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440.";
Environ. Microbiol. 4:799-808(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MASZ PSEPK STANDARD; PRT; 725 AA. Q88QX8;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9)
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-!- SUBUNIT: Monomer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gamma
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its wes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-aib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: Monomer (By Similarity).
-!- SUBCELLUTAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          opportunistic pathogen.";
Nature 406:959-964(2000).
-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN=ATCC 15692 / PAO1;

MEDLINE=20437; PubMed=10984043;

Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Bilckey M.J., Brinkman F.S.L., Huffnagle W.O., Kowalik D.J., Lagrou P Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y. Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Shancer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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CATALYTIC ACID (BY SIMILARITY).
3669670A9E38D391 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 725;
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TIGRFAMs; TIGR01345; malate syn G; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.4%; Score 2569; DB 1; Length 7 69.1%; Pred. No. 3.2e-136; ive 77; Mismatches 139; Indels
                                                                                                                                                               [5-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
115-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATHWAY: Glyoxylate bypass; second step
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InterPro; IPR001465; Malate synthase.
InterPro; IPR006253; Malate_synthG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE004485; AAG03871.1; -. PIR; H83586; H83586.
HSSP; P37330; 1D8C.
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                                                                                                                                                                                                                                                                                                                                                                 Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa.
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ACT_SITE 340
ACT_SITE 631
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502; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                  GLCB OR PA0482.
                                                                            MASZ PSEAE
AC 09452 PSEAE
AC 09452 PSEAE
AC 15-SEP-2003
DT 15-SEP-2003
DT 15-SEP-2003
DT 15-SEP-2003
DE Malate synth
GLGB OR PRO4
OS Bacteria; Pr
OC Bacteria; Pr
OC Bacteria; Pr
OC STRAIN=ATCC
RA HICKEY M.J.,
RA HICKEY M.J.,
RA HICKEY M.J.,
RA HICKEY M.J.,
RA Garber R.L.,
RA HICKEY M.J.,
RA Garber R.L.,
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                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL cutstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                  Length 725;
                                                                                                                                                                     340 CATALYTIC BASE (BY SIMILARITY)
631 CATALYTIC ACID (BY SIMILARITY)
78346 MW, 8363F218E6116AE1 CRC64;
                                                                                                                                      HAMAÞ; MF_00641; -; 1.
Transferase; Glyoxylate bypase; Tricarboxylic acid cycle;
                                                                                                                                                                                                                                     95; Mismatches 139; Indels
                                                                                                                                                                                                                 41.9%; Score 2541; DB 1; 67.1%; Pred. No. 1.2e-134;
                                                                                                                  EMBL; AE016775; AAN65987.1; -. TIGR; PP0356; -.
                                                                                                                                                                                                                                     486; Conservative
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-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Artiguenave F.M., Delecu M., Vilagines R., Danglot C.;
"A functional glyoxylate bypass is mandatory for utilization of
alkanes by Pseudomonas fluorescens."
Submitted (MAR-1997) to the BMBL/GenBank/DDBU databases.
-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.
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HAMAP; MF 00641; -; 1.

Interbro; IPR001465; Malate_synthase.

Interbro; IPR001273; Malate_synthase; 1.

Ffam; PF01274; Malate_synthase; 1.

TIGRFAMs; TIGR01345; malate_syn G; 1.

Transferase; Glyoxylate bypass; Tricarboxylic acid cycle.

Transferase; Glyoxylate bypass; Tricarboxylic acid cycle.

ACT SITE 340 CATALYTIC BASE (BY SIMILARITY).

ACT SITE 731 CATALYTIC ACID (BY SIMILARITY).
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Local Similarity 66.7%; Pred. No. 3.4e-132;
tes 483; Conservative 85; Mismatches 152;
                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9).
                                                                                                                                                              725 AA
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Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                    fluorescens.
722
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(Rel. 42, (Rel. 42, 1)
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                    PSPT00480; -.; MF_00641; -;
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                                                                              Complete proteome.
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242 IQIDASTPVGQTDAAGVKDVLMEAALTTIMDCEDSVAAVDADDKVVIYRNWLGLMKGDLA 301
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-:- SUBDATT: Monomer (By similarity).
-:- SUBCELLULAR LOCATION: Cytoplemnic (By similarity).
-:- SUBCELLULAR Belongs to the malate synthase family. GlcB subfamily.
                                                              WVPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIREEVDN
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                                                                                                                                                                 GILDGLLTSLAAIHSLNG---NSSRKNSRTGSVYIVKPKMHGPEEAAFTNELFGRIEDVL
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                                            308 AAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
Dodson R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
White O., Fraser C., Collmer A.;
"Complete sequence of Fseudomonas syringae.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G 1 (EC 2.3.3.9).
GLCB1 OR GLCB-1 OR PSPTO0480.
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                                                                                                                           Length 725;
                                   CATALYTIC BASE (BY SIMILARITY)
CATALYTIC ACID (BY SIMILARITY)
F1993264E8083660 CRC64;
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
                                                                                                                                                                Indels
                                                                                                                       Query Match
41.1%; Score 2489; DB 1;
Best Local Similarity 65.3%; Pred. No. 9.6e-132;
Matches 473; Conservative 97; Mismatches 150;
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IMDALFTGLIAIHGLKASDV--NGPLINSRTGSIYIVKFKMHGPAEVAFTCELFSRVEDV
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                                                                                                                                                                                                                                                        COA..
PATHWAY: Glyoxylate bypass; second step.
SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                                                                                             MEDLINE-21082930; PubMed=11214968; MEDLINE-21082930; PubMed=11214968; MEDLINE-21082930; PubMed=11214968; MEDLINE-21082930; PubMed=11214968; Maranabo A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Moorizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ
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                                  Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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CATALYTIC ACID (BY SIMILARITY)
65376311A7E1BFDF CRC64;
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InterPro; IPR001465; Malate_synthase.
InterPro; IPR006253; Malate_synthG.
FPGMP, PF01274, Malate_synthase; 1.
TIGRN 1945; Malate_syn G; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
or Mirate G (EC 2... OR Mirate64.
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP003004; BAB51267.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78058 MW;
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467; Conservative
                                                                                                                                                                                                                    Mesorhizobium loti.";
DNA Res. 7:331-338(2000)
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629
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629 6
721 AA;
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ACT_SITE 338
ACT_SITE 629
SEQUENCE 721 AA;
                                                                                                    FROM N.A
                                                                          NCBI TaxID=381;
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Best Local S:
Matches 467
                                                                                                   SEQUENCE
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                                                                                                                                                     416 LGMPRNTIKMGIMDEBRRTTVNLKEAIRARERVVFINTGFLDRTGDEIHTSMEAGPMIR
                                                                                                                                                                                                                                                                                                                                                                                                                             AWVPSPTAATLHALHYHQVDVAAVQQGLAGKRAATIEQLLTIPLAKELAWAPDEIREEVD
                                                                                                                                                                                                                                                                    KGTMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGWWTMTELMADMVETKIAQPRAGAST
                                                                                                                                                                                                                                                                                                                                                KGDMKQAAWISAYEAWNVDTGLECGLAGHAQIGKGMWAMPDLMAAMLEQKIAHPKAGANT
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NNCOSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVR
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MEDLINE-2160551; PubMed=11743194;

Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,

Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,

Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,

Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,

Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,

Cielo C., Slater S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   596 NNAQGILGYVVRWIDQGVGCSKVPDINDVGLMEDRATLRISSQHIANWLRHKVCSEIQVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE_ZI60856; PubMed=11743193; Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okuta V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McCelland E., Palmieri A., Saymond C., Rouse G., Saemphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the plant pathogen and biotechnology agent Agrobacementium tumefaciens CS8";
Science 294:3232-2328(2001).
-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agrobacterium tumefaciens (Strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
date synthase G (EC 2.3.3.9)
GLCB OR ATU0047 OR AGR_C_78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 ARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVPLS 190
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NAQGILGYVVRWVDQGVGCSKVPDINNIGLMEDRATLRISAQHMANWLRHGVVTEAQIIK 664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATHWAY: Glyoxylate bypass; second step.
SUBUNIT: Monomer. (By similarity).
SUBCELDULAR LOCATION: CYtoplasmic (By similarity).
SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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R EMBL, AYOS9637; AA117965.1; -.

R HAMAP; MF 00641; -; 1.

R InterPror; IPR006253; Malate_synthase.

R InterPror; IPR006253; Malate_synthG.

R ITGRRAMS; TIGR01345; Malate_synthG.

R TIGRRAMS; TIGR01345; Malate_synthG.

R Transferase; Glyoxylate bypass; Tricarboxylic acid cycle.

FT ACT_SITE 338

CATALYTIC BASE (BY SIMILARITY).

FT ACT_SITE 629 629 CATALYTIC ACID (BY SIMILARITY).

FT ACT_SITE 629 629 CATALYTIC ACID (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobium leguminosarum (biovar viciae).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ate synthase gene from Rhizobium leguminosarum.", nitted (OCT-2001) to the BMBL/GenBank/DDBJ databases. CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-2003 (Rel. 42, Last sequence update)
Malate synthase G (EC 2.3.3.9).
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                                                                                                                                                                                                                                                                                                                                                                                                              723
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LKAKQA 730
                                                                                                                                                                                          FKARAA 733
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SEQUENCE FROM N.A.
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                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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PMR1; ABC07947; AAK85871.1; ALT_INIT.
PMR1; AH2582.
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IDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAA 309
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-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                                                                                                                                         VAKGGTSFIRTLNPDLOYAGPDGAAFEVHRRSLMLVRNVGHLMTNPAILDRDGNEVPEGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
"Analysis of the chromosome sequence of the legume symbiont
sinorhizobium meliloti strain 1021.",
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthas G (EC. 2.3.3.9)
GLCB OR R0062 OR SMC02581.
Rhizobium meliloti (Sinorhizobium meliloti).
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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MEDLINE=21396507; PubMed=11481430;
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NCBI_TaxID=382;
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InterPro; IPR006253; Malate_synthG.
Pfam; PF01074; Dece Synthase; 1
TIGRPAMS; TIGR01345; malate_syn G; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- PATHWAY: Glyoxylate bypass; second step.
-i- SUBUNIT: Monomer (By Similarity)
-i- SUBCINIT: CATOPLEMENT (CATOPLEMENT (By Similarity).
-i- SUBCELLULAR LOCATION: CYTOPLEMENT (By Similarity).
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MEDIINE=22247741; PubMed=12271122;
Paulien I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
Read T.D., Dodon R.J., Umayam L., Brinkac L.M., Beanan M.J.,
Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.
Riedmuller S., Tettellin H., Gill S.R., White O., Salzberg S.L.,
Hoover D.L., Lindlar L.E., Halling S.M., Boyle S.M., Fraser C.M.;
"The Brucella suis genome reveals fundamental similarities between
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. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9).
GLCB OR BR1648.
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Q8FZ50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=16M / ATCC 21456 / Biotype 1;
MEDLINE=20020109; PubMed=1175668;
DelVecchio V.G., Kaparral V., Redkar R.J., Patra G., Mujer C., Los T.,
Loanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Cellaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
"The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
Droc. Natl. Acad. Sci., U.S.A. 99:443-448(2002).
--- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 VEIEGLAVAPELVEFLAKEAAPGTGVEPEKFWKGFAAIIRDLAPKNRALLAKRDELQARI
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36 CATALYTIC ACID (BY SIMILARITY).
79985 MW; E1313A617979270D CRC64;
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Brucellaceae; Brucella.
NCBI_TaxID=29459;
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HAWAP; MF 00641; -; 1.

HAWAP; MF 006641; -; 1.

InterPro; IPR001465; Malate_synthg.

Pfam; PF01274; Malate_synthase, 1.

TIGRFAMS; TIGR01345; malate_syn_G; 1.

Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
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(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
hase G (EC 2.3.3.9).

    -!- PATHWAY: Glyoxylate bypass; second step.

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                                                                                                                                             STANDARD;
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ACT_SITE 345
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GLCB OR BMEI0380
                                                                                                                                       MASZ BRUME
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"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., SEQUENCE OF 1-10, AND CHARACTERIZATION.
STRAIN=ATC 13032 / DSM 20300 / NCIB 10025;
MEDLINE=55111631; PubMed=7812449;
Reinscheid D.J., Eikmanns B.J., Sahm H.;
"Malate synthase from Cozynebacternum glutamicum: sequence ans of the gene and blochemical characterization of the enzyme.";
Microbiology 140:3099-3108(1994).
                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
Malate synthase G (EC 2.3.9)
GLCB OR ACEB OR CGL2329.
Corphabbacterium glutamicum (Brevibacterium flavum).
Bacteria, Actinobacteria, Actinobacterides, Corphabacterinese, Corphabacterinese, Corphabacterinese, Corphabacterium flavum).
NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=ATCC 13059 / AS019;
Lee H.S., Sinskey A.J.;
"Molecular characterization of aceB, a gene
in Corynebacterium glutamicum.";
J. Microbiol. Biotechnol. 4:256-263(1994).
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                         38.2%; Score 2313; DB 1; Length 728; 61.6%; Pred. No. 6.6e-122; cive 97; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                          CATALYTIC BASE (BY SIMILARITY)
CATALYTIC ACID (BY SIMILARITY)
F95669D002A14EDE CRC64;
                                                                                                                      TIGR; BR1648; -. 1.
HAWAP; MF 00641; -.; 1.
HAMAP; MF 00641; -.; 1.
InterPro; IPR001465; Malate_synthase.
InterPro; IRR006523; Malate_synthG.
Pfam; PF01274; Malate_synthase; 1.
TIGRFAMs; TIGR01345; malate_syn G; 1.
Transferase; Glyoxylate_bypass; Tricarboxylic acid cycle;
                                                                                                                                                                                                                                                                                                                          345 345 CJ
636 636 CJ
728 AA; 79966 MW;
                                                                                                      EMBL; AE014458; AAN30550.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                443; Conservative
                                                                                                                                                                                                                                                                                                   Complete proteome.
ACT_SITE 345
ACT_SITE 636
SEQUENCE 728 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Matches 44
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encoding malate synthase

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- ENZYME REGULATION: Inhibited by oxalate, glycolate and ATP.
-!- PATHWAY: Glyoxylate bypass; second step.
-!- SUBUNIT: Monomer.
-!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQIDKWHRRRVIBPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP, MF 00641; -; 1.
InterPro; IPR01465; Malate_synthase.
InterPro; IPR06253; Malate_synthG.
Pfam; Pf2174; Pf2174; Malate_synthG.
TIGRRPMS; TIGR01345; malate_syn_G; 1.
Transferase; Glyoxylate_bypass; Tricarboxylic acid cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC BASE (BY SIMILAI CATALYTIC ACID (BY SIMILAI 72AA0663AE7C87F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP005281; BAB99722.1; -. PIR; 140715; I40715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82231 MW;
                                                                                                                                                                                                                                                                                                                                               EMBL; X78491; CAA55243.1; -. EMBL; L27123; AAA68074.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity ._
...hes 444; Conservative
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646
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646 6
738 AA;
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ACT_SITE
SEQUENCE
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Α̈́ 738

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 LIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA 308
   SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to the malate synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKWHGPAEVAFTCELFSRVEDVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLERWAPLVDRQNAGDVAYRPWAPNFDDSTAFLAAQELILSGAQQPNGYTEPILHRRRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQLDEYYRENPGKP-DPEKYEAFLREIGYLVDEPAPAEIRTQNIDSEIATTAGPQLVVPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 QIDPTHPIGKEDKTGLKDIILESAITTIMDFEDSVAAVDAEDKTLGYRNWFLLNTGELTE
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                                                                                                                                                                                                                                                                                                                                                                                                             9 IDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEG
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                                                                                                                                                                                                                                                                                                                                                   Length 748;
                                                                                                                                                                                                                                                                                       CATALYTIC BASE (BY SIMILARITY)
CATALYTIC ACID (BY SIMILARITY)
F9550473EC4E9A09 CRC64;
                                                                                                                                                                             HAMAR, MF 00641, -; 1.
InterPro; IPR001465; Malate_synthase.
InterPro; IPR001465; Malate_synthG.
Ffan; PF01274; Malate synthase; 1.
TIGRPAMs; TIGR01345; malate_syn_G; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
                                                                                                                                                                                                                                                                                                                                                  37.5%; Score 2273; DB 1;
61.5%; Pred. No. 1.2e-119;
tive 90; Mismatches 182;
                                                                                                                                                                    EMBL; AP005221; BAC19041.1; -.
                                                                                                                                                                                                                                                                                                                     83491 MW;
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ACT_SITE 362 3
ACT_SITE 653 6
SEQUENCE 748 AA;
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Matches 44
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197
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                                                                                                          LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI
                                                                                                                          258 QIDPVHPIGKADKTGLKDIVLESAITTIMDFEDSVAAVDAEDKTLGYSNWFGLNTGELKE
                                                                                                                                                                                                                                                                                                        |:: || |||::||||| ||:||||| DMQTAPWKQAYENNNVDAGIQRGLPGKAQIGKGWWAMTELMAEMLEKKIGQPREGANTAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LNARFALNAANARWGSLYDALYGTDVI PETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP
                                                                          LNARFALNAANARWGSLYDALYGTNAIPETDGAEKGKEYNPVRGQKVIEWGREFLDSVVP
                                                                                                                                                                                                                            AVDKDGTAFLRVLNRDRNYTAPGGGOFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEG
                                                                                                                                                                                                                                                        EMSKNGRIFTRELNKDRVYIGRNGTELVLHGRSLLFVRNVGHLMQNPSIL-IDGEEIFEG
                                                                                                                                                                                                                                                                                        IMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKMHGPAEVAFTCELFSRVEDVLG
                                                                                                                                                                                                                                                                                                                                                                             LPRHTLKVGVMDEERRISVNLDASIMEVADRLAFINTGFLDRTGDEIHTSMEAGAMVRKA
                                                                                                                                                                                                                                                                                                                                                                                                           TMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPSPTAATLHALHYHQVDVAAVQQGL-AGKRRATIBQLLTIPLAKELAWAPDEIREEVDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1] —
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
IKeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
USuda Y., Sugimoro S.; acquence of Corynebacterium efficiens YS-314.";
"The entire genomic sequence of Corynebacterium efficiens YS-314.";
submitted (WAY-2002) to the EMBL/GenBank/DDBJ databases.
--- CATALYTIC ACTIVITY: Acetyl-COA + H(2)O + glyoxylate = S-malate +
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NCBI_TaxID=152794;
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
14-SEP-2003 (Rel. 42, Last annotation update)
GLCB OR MASZ OR CE2231.
Corynebacterium efficiens.
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Vereecke D.M., Cornelis K., Van Montagu M., El Jaziri M., Holsters M.,
Goethals K.,
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43.5%; Score 2634; DB 2; Length 724;
Best Local Similarity 69.0%; Pred. No. 3.2e-144;
Matches 499; Conservative 82; Mismatches 138; Indels 4
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Nocardiaceae, Rhodococcus.
NCBI_TaxID=1828,
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Q92ta4 rhizobium m
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STRAIN=ATCC 15692 / PAO1;

MEDLINE=20437377; PubMed=10984043;

Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou N. Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou N. Hickey M.J., Golltry L., Tolentino E., Westbrock-wadnan S., Yuan Y., Brody L.L., Coulter S.N., Tolger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen.";

Nature 406:959-964(2000).
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Pseudomonadaceae; Pseudomonas.
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69.1%; Pred. No. 1.9e-140;
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HSSP; P37330; IDBC.
InterPro; IPR001465; Malate synthase.
InterPro; IPR006253; Malate_synthG.
Pfam; PF01274; Malate synthase; 1.
TIGRFAMS; TIGR01345; malate_syn_G; 1.
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Matches 502; Conservative
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                                                                                                                  ASLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRR
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01-UTN-2002 (TrEMBLrel. 21, Created)
01-UTN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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InterPro; IPR006253; Malate_synthG.
Pfam; PF01274; Malate_synthase; 1.
TIGRFAMs; TIGR01345; malate_syn_G; 1.
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                          Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
'NCBL_TaxID=381;
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64.4%; Pred. No. 1.4e-131;
live 86; Mismatches 164;
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Best Local Similarity 64.4%;
Matches 467; Conservative 8
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SEQUENCE 721 AA;
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Malate synthase G.
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ILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLA
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01-DEC-2001 (TrEMBirel. 19, Last sequence update)
01-MAR-2003 (TrEMBirel. 23, Last annotation update)
MASG.
Rhizobium leguminosarum (biovar viciae).
Rhizobiaceae; Rhizobium.
Rhizobiaceae; Rhizobium.
Rhizobiaceae; Rhizobium.
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Garcia de los Santos A., Hynes M.F.;
Garcia de los Santos A., Hynes M.F.;
whalate synthase gene from Rhizobium leguminosarum.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AX059637; AAL17965.1;
InterPro; IPR0046253; Malate synthase.
InterPro; IPR006253; Malate synthas.
FFGU, PFC01244; Malate synthas.
IGREMMS; ITGR01345; malate synthas.
TIGREMMS; ITGR01345; malate synthas.
TIGREMMS; TIGR01345; malate synthas.
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RVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQ
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MEDLINE=21396507; PubMed=11481430;
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MRA-2003 (TrEMBLrel. 23, Last annotation update)
01-MRA-2003 (TrEMBLrel. 23, Last annotation update)
Probable malate synthase G protein (EC 4.1.3.2).
GLCB OR R00062 OR SMC02581.
GLCB OR R00062 OR SMC02581.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiacea; Sinorhizobium.
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Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.", Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
BMBL, ALS9182; CAC41449.1; -...
InterPro; IPR01465; Malate_synthase.
InterPro; IPR006253; Malate_synthase.
Pfam: PF01274; Malate_synthase; 1.
TIGRFAMS; IIGR01445; malate_syntG;
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38.8%; Score 2351.5; DB 16; Lengt
Best Local Similarity 62.9%; Pred. No. 7.6e-128;
Matches 455; Conservative 94; Mismatches 169; Indels
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SEQUENCE 723 AA; 78853
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STRAIN=16M (A ATCC 23456 / Biotype 1;
MEDLINE=20020109; PubMed=11756689;
MEDLINE=20020109; PubMed=11756689;
MEDLINE=20020109; PubMed=11756689;
Ivanova N., Raparral V., Ref8tar R.J., Patra G., Mujer C., Los T Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jashova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jashova N., Danova N., Bernal A., Mazur M., Goltsman Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.;
"The genome sequence of the facultative intracellular pathogen Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
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Brucellaceae; Brucella.
NCBI_TaxID=29459;
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61.8%; Pred. No. 6.8e-126;
cive 97; Mismatches 174;
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InterPro; IPR006253; Malate synthG.
Pfam; PF01274; Malate synthase; 1.
TIGREAMS; TIGR01345; malate syn_G; 1.
                                          01-MAR-2002 (TrEMBLrel, 20, 01-MAR-2002 (TrEMBLrel, 20, 01-MAR-2003 (TrEMBLrel, 23, Malate synthase G (EC 4.1.3.
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Best Local Similarity 61.8%
Matches 444; Conservative
                                                                                                                                                     Brucella melitensis.
Q8YIR3
Q8YIR3;
01-MAR-2002
01-MAR-2002
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SPIAATLHATHYHKIDVAAVQEKLKSRPRAKLDDILSVPVAVRPNWTPDDIQHEIDNNAQ 606
                                     SILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRASLE 670
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MEDLINE=2247741; PubWed=12271122;

Rad T.D., Sephadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,

Rad T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,

Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,

Nelson W.C., Ayodelj B., Kraul M., Shetty J., Malek J., Van Aken S.E.

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BMBL, AEGH458; AAN30550.1; -. 99:13148-13153(2002).
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; Pred. No. 1.3e-125;
97; Mismatches 175; Indels 4
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NCBL_TaxID=29461;
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GLCB OR BR1648.
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                          427 PNTLKIGIMDEERRTTVNLKEAIRAAKDRVVFINTGFLDRTGDEIHTSMEAGPMIRKGDM
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                                                                                     KSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAWVP
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Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005221; BAC19041.1;
Lyase; Complete proteome.
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Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TAXID=152794;
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61.5%; Pred. No. 2.9e-123;
iive 90; Mismatches 182;
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01-MAR-2003 (TrEMBLrel. 23, L.
Malate synthase (EC 4.1.3.2).
MASZ OR CE2231.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
EMBL. AE016766, AAN82151.1;
Lyass; Complete protecme.
SEQUENCE 723 AA; 80440 MW; AAF740E5FE038F6F CRC64;
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SEQUENCE FROM N.A.

SEQUENCE TROM N.A.

SEQUENCE 125 / JCM 9153;

MEDLINE=20512582; PubMed=11058132;

A Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,

D. Fuji F., Hitama C., Nakamura Y., Ogasawara N., Kuhara S.,

R. Fuji F., Hitama C., Nakamura Y., Ogasawara N., Kuhara S.,

D. Fuji F., Hitama C., Nakamura Y., Ogasawara N., Kuhara S.,

T. Complete genome sequence of the alkaliphilic bacterium Bacillus

T. Complete genome sequence comparison with Bacillus subtilis.";

Nucleic Acids Res. 28:4317,4331(2000).

R. Nucleic Acids Res. 28:4317,4331(2000).

R. RNBL, APOOLISI4; Babcs6822.1;

R. SSP; P37330, 1DBC.

R. InterPro; IPRO06523; Malate_Synthase.

DR InterPro; IPRO06523; Malate_Synthase; 1.

Pfam; PF01274; Malate_Synthase; 1.

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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Malate synthase.
BH1213. Alphodurans.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Q8KQ29
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                                                                                                                       64
                                                                                                                                                                                                                                                        DANGRIGKDDSAHINDVIVEAAISTILDCEDSVAAVDAEDKILLYRNLLGLMQGTLQEKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSTPWIKAYERNNVLSGLFCGLRGKAQIGKGWAMPDLMADMYSQKGDQLRAGANTAWVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPVLNA
                                                                                                                                                                                           DEWHRSNPGPVKDKAAYKSFLRELGYLVPQPDHVTVETTGIDSEITSQAGPQLVVPAMMA
                                                                                                                                                                                                                                 RFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVPLSS
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                                                                                       12 VSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQI
                                                                                                                                                                                                                                                                                                       GSFGDATGFTVQDGQLVVALPD-KSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEILI
                                                   Gaps
                                                   15;
               DB 16; Length 723;
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                   Indels
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Last annotation update)
                                  Best Local Similarity 58.4%; Pred. No. 3.1e-117;
Matches 422; Conservative 113; Mismatches 173;
               35.8%; Score 2168.5; DB 1658.4%; Pred. No. 3.1e-117;
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ASK OR ML2323.
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AC 09087
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DD ASPAR
GN MYCOD
OC COTYN
OX NCBI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEEGRVVLVAGFOGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
MEDLINE=21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Bavies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Aspartete kinase alpha subunit (EC 2.7.2.4) (Aspartokinase)
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                                                                                                                                                                                                                                                                                                      "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL; AL683925, CAC31839.1; -.
Leproma, ML2323; -.
InterPro; IPR001048; Aa kinase.
InterPro; IPR001341; Aspartate_kinase.
Pfam; PF00656; aakinase; 1.
Pfam; PF00482; ACT; 2.
TIGRPAMS; TIGR00657; asp kinases; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 25.5%; Score 1545.5; DB Best Local Similarity 80.4%; Pred. No. 1.7e-81; Matches 319; Conservative 18; Mismatches 43
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IKDVPMEDPILIGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRROHRHGAAE---- 1043
WEDLINE=99453302; PubMed=10521665;
Zhang W., Jiang W., Zhao G., Yang Y., Chiao J.;
The Sequence analysts and expression of the aspartckinase and aspartate
T semialdehyde dehydrogenase operon from rifamycin SV-producing /
T mycolatopsis mediterranel.";
T mycolatopsis mediterranel.";
T amycolatopsis mediterranel.";
T c-CATALYHIC ACTIVITY: ATP + L-ASPARTATE = ADP + 4-PHOSPHO-L-
ASPARTATE.

-1 SIMILARIYI' BELONGS TO THE ASPARTOKINASE FAMILY.

EMBL, AF134837; AAD49557.1; -.
THEFPRO, IPRO01941; ASPARTATE & Kinase.

NR INTERPRO, IPRO01941; ASPARTATE & Kinase.

NR INTERPRO, IPRO01057; Glu_5kinase.

NR INTERPRO, IPRO01057; Glu_5kinase.

Pram; PF01842; ACT; 2.

PRINTS; PR00474; GLU5KINASE.

TIGRRAMS; TIGRO0557; asp Kinases; 1.

TIGRRAMS; TIGRO0557; asp Kinases; 1.

TIGRRAMS; TIGRO0557; asp Kinases; 1.

TIGRRAMS; TIGRO0557; asp Kinases; 1.

TIGRRAMS; TIGRO0557; asp Kinases; 1.

TIGRRAMS; TIGRO0557; asp Kinases; 1.

KW Kinase; Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.9%; Score 1267.5; DB 2; Length 421; llarity 65.3%; Pred. No. 2.2e-65; Conservative 53; Mismatches 61; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EC 2.7.2.
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Corynebacterium crenatum.

Corynebacterium crenatum.

Corynebacterinobacteria, Actinobacteridae, Actinomycetales,

Corynebacterinese. Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 AA; 44393 MW; 633D9C2D023145E9 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Feedback-resistant aspartokinase LysC alpha subunit
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STRAIN=CD945;
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les 254;
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SEQUENCE
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                          "Isolation and characterization of the aspartokinase and aspartate semilalebyke dehydrogenase genes from cephamycin C-producer Streptomyces clavuligents.";

**Treptomyces clavuligents.";

**Treptomyces (2002), University of Middle Bast Technical University, Ank:
                                                                                                                              1. CATALYTIC ACTIVITY: ATP + L-ASPARTATE = ADP + 4-PHOSPHO-L-ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASPARTATE = ASSARTATE = ASSARTATE = ASSARTATE = ASSARTATE = ASSARTATE = ASSARTATE = ASSARTATE = ASSARTATE = ASSARTATE = ASSARTATE = ASSAR
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
21.0%; Score 1272.5; DB 2; Length
Best Local Similarity 66.1%; Pred. No. 1.1e-65;
Matches 257; Conservative 51; Mismatches 60; Indels
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Aspartokinase subunit A (BC 2.7.2.4) (Aspartate kinase)
ASKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44399 MW; 08262D81045735C1 CRC64;
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124 928 184 988 244

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1039 HGAAERLQGRGRQD-RHHLHLL--PQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 1095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            27; Gaps
Liu Y., Ding J., Wang J.;

T "Cloning and sequence analysis of aspartokinase genes from "Corynabacterium creatum.";

Submitted (AUG-2001) to the BMBL/GenBank/DDBJ databases.

-:- CATALYTIC ACTIVITY: ATP + L-ASPARTATE = ADP + 4-PHOSPHO-L-ASPARTATE

-:- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.

REL; AF414084; AAL07807.1; -..

R InterPro; IPR001341; Aspartate kinase.

InterPro; IPR001341; Aspartate kinase.

InterPro; IPR001341; Aspartate kinase.

R InterPro; IPR00556; Asp_kin_monofn.

R Pfam; PF01842; ACT; 2.

R TIGRFAMS; TIGR00657; asp_kin_monofn; 1.

R TIGRFAMS; TIGR00656; asp_kin_monofn; 1.

R PROSITE; PS00324; ASPARTÖKINASE; 1.

Kinase; Transferase.

O SEQUENCE 421 AA; 44738 MW; 473A19409C0215E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 421;
                                                                                                                                                                                                                                                                                                                                                               20.3%; Score 1232.5; DB 2; Length 64.3%; Pred. No. 2.3e-63; tive 55; Mismatches 58; Indels
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Best Local Similarity 64.34
Matches 252; Conservative
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Search completed: November 21, 2003, 16:08:15 Job time : 60.6698 secs

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Title: Perfect score:

Sequence:

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OM protein

Run on:

Scoring table:

Searched:

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Database

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3..8
/label= Histidine tag
/note= "Nickel chelating region used for purifying
the fusion protein"
9..74
/label= Ra3_region
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525..983
/label= FL_TbH4_region
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AAW32377
AAW81681
                AAW64367
AAY39164
AAY39021
AAY39225
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AAW64339
AAY39136
AAY38993
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AAR30090
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/label= 38kD_region
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Mycobacterium tuberculosis.
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WO200124820-A1
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Binding-site
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                                                                             AKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDSSAELTDTPRVATAGEPNFMDLKEAA
                                                   AKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDSSABLTDTPRVATAGEPNFMDLKEAA
                                                                                                                         RKLETGDOGASLAHFADGWNTFNLTLOGDVKRFRGFDNWEGDAATACEASLDQORQWILH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the fusion protein TbF-2 which is composed immunogenic polypeptides from Mycobacterium tuberculosis (MT). This
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Twardzik DR, Vedvick TS;
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96US-0730510.
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Reed SG, Skeiky YAW,
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N-PSDB; AAV64567.
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                                                                                                                                                                                                                                                                                                                                 The sequence represents Mycobacterium fusion protein antigen TbF15 consisting of a His tag for purification, antigens Ra3, 38kD, 38-1 and RL-TbH4 (full-length TbH4). Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammal (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease figequently affecting patients with acquired immunodeficiency disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLEVSFKMRPAQPRCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLWG
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                                                                                                                                                             PD,
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                                                                                                                                                             McNeill
                                                                                                                                                             RL,
                                                                                                                                                                                                                                                  Vaccinating against Mycobacteria proteins comprising combinations
                                                                                                                                                                                                                                                                                                     Claim 6; Fig 4; 168pp; English
                                                                                                                                                              Houghton
                                                                        99US-0158338.
99US-0158425.
                                      2000WO-US28095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    983; Conservative
                                                                                                                                                                                                WPI; 2001-290576/30.
                                                                                                                           (CORI-) CORIXA CORP
                                                                                                                                                             Reed S,
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                                      10-OCT-2000;
                                                                        07-0CT-1999;
07-0CT-1999;
                                                                                                                                                              Skeiky Y,
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                                                                                                                                                     Gaps
protein is used in a method for inducing protective immunity againtuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of TB
                                                                                                                                                     116;
                                                                                                                    Length 802;
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                                                                                                                  53.2%; Score 2700; DB 19;
66.6%; Pred. No. 2.9e-158;
ive 27; Mismatches 153;
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KLEVSFKMRPAQPRCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLWG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This polypeptide comprises a fusion protein, designated TDF-2, composed of Mycobacterium tuberculosis antigens TDRa3 (see AAW64295), 38 kDa antigen (see AAW64321) and DDPF (see AAW64322). It was produced by PGCR amplification (see AAW44450-57) of the appropriate antigen DNA sequences, cloning into an expression vector, and expression in E. coli. TDF-2 can be used for serodiagnosis of tuberculosis. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising antigenic or immunogenic portions of M. tuberculosis antigens, or funion proteins, DNA sequences encoding such polypeptides, recombinant expression vectors and host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient.
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infection
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Twardzik DR, Vedvick TS;
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and diagnosis of tuberculosis
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96US-0729622.
                  standard; Protein;
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Tb38-1; TbF-2.
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         GDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIG
                                                                                                                                  ATISSAEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVV
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                                              ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGY
                                                               ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAGFASKTPANQAISMIDGPAPDGY
                                                                                                   PIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALI
                                                                                                                        ATI SSAEMKTDAATLAQEAGNFERI SGDLKTQI DOVESTAGSLOGOWRGAAGTAAQAAVV
                                                                                                                                                                                                                   PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVR-----
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                                                                                   PIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQFLPPAVVKLSDALI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fusion protein, TbF-2; TbRa3; 38kD; y; vaccine; immunogen.
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                                                                                                                                                                                                                                                                                            GOPPPVANDTRIVLGRLDOKLYASAEATDSKAAA-
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DPEP; diagnosi
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                                                                                                                                                                                                     This sequence represents a recombinant Mycobacterium tuberculosis tetra-antigen fusion protein, termed TbF-2, composed of the antigens TbRan, 39kD, TbS8-1 and DpBP. The fusion protein is expressed in host cells using a vector carrying a polymucleotide (see AAZ20198) comprising the 4 coding sequences. The invention provides fusion proteins (see AAX2059-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polymucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of effective immunogens than mixtures of the individual protein
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                                                                            New fusion proteins useful for diagnosis, prevention and tuberculosis -
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Pred. No. 2.9e-158;
27; Mismatches 153;
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66.6%;
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Best Local Similarity 66.6<sup>5</sup>
Matches 591; Conservative
WPI; 1999-601610/51
N-PSDB; AAZ20198.
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This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420 ATISSAEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVV
                                                                                                                                                                                541 ANEVEAPMADPPTDVPITPCELTAAKNAAQQLVLSADNMREYLAAGAKERQRLATSLRNA
                                                                                                                                                                                                                                                                                                     ------IDNPVGGFSFALPAGWVESDAAHFDYGSALLS-----KTTGDPPFP
                                                                                                                                                                                                                                                                                                                                                                                       -----YM
                                                                                                                                                                                                                                                                                                                                                                                                                            NWEGDAATACEASLDQQRQWILHMAKLSAAMAKQAQYVAQLHVWARREHPTYEDIVGLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           758 LYAENPSARDQILPVYAEYQQRSEKVLTEYNN------KAALEPVNP-PKPPPAIKIDP
                                                                                                                                     480 RFQEAANKOKOELDEISTNIRQAGVQYSRADEEQQQALSSOMGFV--PTTAASPPSTAAA
                                                                                                                                                                                                                                                                601 AKAYGEVDEBAATALDNDGEGTVQAESAGAVGGDS-----SAELTDTPRVATAGEPNF-
                                                                                                                                                                                                                                                                                                                                              654 -------MDLKEAARKLETGDOGASLAHFADGWNTFNLTLQGDVKRFRGFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  676 PYPGTRINQETVŠLĎ------ANGVSGSASÝŠEVKFSDPSKPNGQIWTGVIGSPA
                                                                                                                                                                                                                     538 PPAPATPVAPPPPAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  771 APAPAEPA-----PAPAPAGEVAP-----TPTTPTPORTLPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           810 PPPPQEQGLIPGFLMPPSDGSGVTPGTGMPAAPMVPPTGSPGGGLPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hendrickson RC, Ho
YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                       631 GOPPPVANDTRIVLGRLDQKLYASAEATDSKAAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; Page 316-318; 323pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M tuberculosis fusion protein TbF-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY39081 standard; Protein; 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campos-Neto A, Dillon DC,
Lodes MJ, Reed SG, Skeiky
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-527416/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ19245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY39081;
                                                                                                 481
                                                                                                                                                                                                                                                                                                     590
                                                                                                                                                                                                                                                                                                                                                                                                                            698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY3908.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 PIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALI 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag) Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion tuberculosis-immune subjects, AAX19499 to AAX19460 and AAX39083 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLEVSFKMRPAQPR-GSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QOVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGWGGWVTGCAETPGCVAYIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGHHHHHHVIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLEVSFKMRPAQPRCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLWG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAFHERYPNVTITAQGTGSGAGIAQAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 802;
!mmunotherapy; diagnosis; immunisation; vaccine; infection;
                                                                                                                                                                                                                                                                                                                                              Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.2%; Score 2700; DB 20; 66.6%; Pred. No. 2.9e-158; iive 27; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                              Hendrickson RC, Hc
YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 205-208; 299pp; English
                                                                                                                                                                                                                                                                                                                                          Campos-Neto A, Dillon DC,
Lodes MJ, Reed SG, Skeiky
                                                                                                                                                                                                    99WO-US03268
                                                                                                                                                                                                                                           98US-0072967
                                                                                                                                                                                                                                                            98US-0025197
                                                                             tuberculosis.
                   immune response; skin test.
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                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
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Best Local Similarity
Matches 591; Conserv
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                                                                             Mycobacterium
                                                                                                                                                                                                  17-FEB-1999;
                                                                                                                  WO9942076-A2
                                                                                                                                                                                                                                         05-MAY-1998;
18-FEB-1998;
                                                                                                                                                           26-AUG-1999
                                                        Synthetic
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KLEVSFKWRPAQPR-GSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLMG 119
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                                                                                                                                                                 MGHHHHHHVIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRI
                                                                                                                                                                                        MGHHHHHUIDIIGTSPISWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRI
                                                                                                                                    Gaps
                               as
biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed current vaccination strategies do not provide 100% immunity.
                                                                                                                                   Indels 116;
                                                                                                      Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPPPQEQGLIPGFLMPPSDGSGVTPGTGMPAAPMVPPTGSPGGGLPA 856
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; Pred. No. 2.9e-158;
27; Mismatches 153;
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al Similarity 66.6%;
591; Conservative 27
                                                                        802 AA
                                                                                                   Query Match
Best Local S
Matches 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel recombinant antigens and their encod mucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in biological sample by detecting antibodies which bind with the biological sample by detecting antibodies which bind with the Dylypeptidies, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                            detection; infection; antibody; immunisation;
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                                                                                                                                                                                                                                                                                                                                     o A, Dillon DC, Hendrickson RC, Ho
Reed SG, Skeiky YAW, Twardzik DR,
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98US-0024753
standard; Protein;
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66.6%;
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                                                                         541 ANEVEAPMADPPTDVPITPCELTAAKNAAQQLVLSADNMREYLAAGAKERQRLATSLRNA
                                                                                                                                             -----IDNPVGGFSFALPAGWVESDAAHFDYGSALLS----KTTGDPPFP
                                                                                                                                                              ------MDLKEAARKLETGDQGASLAHFADGWNTFNLTLQGDVKRFRGFD
                                                                                                                                                                            GOPPPVANDTRIVLGRLDOKLYASAEATDSKAAA-------RLGSDMGEF--YM
                                                                                                                                                                                              NWEGDAATACEASLDQQRQWILHMAKLSAAMAKQAQYVAQLHVWARREHPTYEDIVGLER
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                               ATISSAEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVV
                                                                                                                              AKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDS-----SAELTDTPRVATAGEPNF-
                                                                                                                                                                                                            PYPGTRINOETVSLD------ANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPA
                                                                                                              PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPOPVR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Campos-Neto A;
                                                                                                                                                                                                                                                                                                                                                                                  ubberculosis; Mycobacterium tuberculosis; immunogen; vaccine; TbRa3-38KD-Tb38-1-DPEP;
                                                                                                                                                                                                                                                                           APAPAEPA------PAPAPAGEVAP------TPTTPORTLPA 802
                                                                                                                                                                                                                                                            PPPPQEQGLIPGFLMPPSDGSGVTPGTGMPAAPMVPPTGSPGGGLPA
                                                                                                                                                                                                                                                                                                                                                                   Antigenic fusion protein TbRa3-38kD-Tb38-1-DPEP (TbF-2)
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                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric - Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                   AAU74592 standard; Protein; 802
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97US-0942578.
98US-0025197.
98US-0056556.
98US-0223040.
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SKEIKY Y A.
DILLON D C.
ALDERSON M.
CAMPOS-NETO A
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tuberculostatic;
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01-OCT-1997;
18-FEB-1998;
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The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protectin in animals against the development of tuberculosis. The protectin coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents an M. tuberculosis fusion protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------MDLKEAARKLETGDQGASLAHFADGWNTFNLTLQGDVKRFRGFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MCHHHHHHVIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDWAVDSAGKITYRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAFHERYPNVTITAGGTGSGAGTAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVNYYLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDIFLFIQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATISSAEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGGWRGAAGTAAQAAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RFQEAANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGFTQSQTVTVDQQEILNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFQEAANKOKOELDEISTNIRQAGVOYSRADEEQQQALSSOMGFV--PTTAASPPSTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------IDNPVGGFSFALPAGWVESDAAHFDYGSALLS-----KTTGDPPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601 AKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDS-----SAELTDTPRVATAGEPNF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGHHHHHHVIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
New fusion proteins of Mycobacterium tuberculosis antigens, usef
diagnosing, treating or preventing M. tuberculosis infection,
particularly as vaccine for treating or preventing tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPAPATPVÁPPPPAAANTPNAQPGDPNÁAPPPADPNAPPPPVIÁPNÁPQPVŘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        802;
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; Pred. No. 2.9e-158;
27; Mismatches 153;
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704 181

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ARDQILPVYAEYQQRSEKVLTEYNNKAALEPVNPPKPPPAIKIDPPPPPQEQGLIPGFLM 824
                                                                                                                                                           ARDQILPVYAEYQQRSEKVLTEYNNKAALEPVNPPKPPPAIKIDPPPPQEQGLIPGFLM 301
                                                                                                                                                                                                                         302 PPSDGSGVTPGTGMPAAPMVPPTGSPGGGLPADTAAQLTSAGREAALSGDVAVKAASLG 361
                                                                                                                                                                                                                                                                                      362 GGGGGVPSAPLGSAIGGAESVRPAGAGDIAGLGQGRAGGGAALGGGGMGMPMGAAHQGQ 421
                    122 VATAGEPNFMDLKEAARKLETGDQGASLAHFADGWNTFNLTLQGDVKRFRGFDNWEGDAA
                                                                                  PPSDGSGVTPGTGMPAAPMVPPTGSPGGGLPADTAAQLTSAGREAAALSGDVAVKAASLG
                                                                                                                                                                                                                                                           GGGGGGVPSAPLGSAIGGAESVRPAGAGDIAGLGQGRAGGGAALGGGGMGMPMGAAHQGQ
                                                               TACEASLDQQRQWILHMAKLSAAMAKQAQYVAQLHVWARREHPTYEDIVGLERLYAENPS
VATAGEPNFMDLKEAARKLETGDQGASLAHFADGWNTFNLTLQGDVKRFRGFDNWEGDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This polypeptide is the predicted amino acid sequence of Mycobacterium tuberculosis antigen TPH-XPI. The sequence was deduced from a composite sequence (see AAV44440) of overlapping DNA clones TbH4 and XPI. TbH4 (see also AAW64319) was isolated from a M. tuberculosis strain H37Rv expression library and XPI from a M. tuberculosis Exchan expression library. Recombinant XPI protein was prepared. It stimulates cell proliferation and interferongamma production in T cells isolated from M. tuberculosis-immune donors. The invention relates to methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuberculosis; infection; diagnosis; antigen; TbH-4; XP1
                                                                                                                                                                                                                                                                                                                                                  GGAKSKGSQQEDEALYTEDRAWTEAVIGNRRRQDSKESK 460
                                                                                                                                                                                                                                                                                                                          GGAKSKGSQQEDEALYTEDRAWTEAVIGNRRRQDSKESK 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R, Lodes MJ;
Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis antigen TbH-4-XP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis strain H37Rv. tuberculosis strain Erdman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 189-191; 250pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW64367 standard; Protein; 460 AA
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96US-0729622.
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Reed SG, Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-251292/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium
Mycobacterium
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                                                                                                   LYAENPSARDQILPVYAEYQQRSEKVLTEYNN-----KAALEPVNP-PKPPPAIKIDP 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                  NWEGDAATACEASLDQQRQWILHMAKLSAAMAKQAQYVAQLHVWARREHPTYEDIVGLER 757
                                              676 PYPGTRINQETVSLD------ANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPA 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method inducing protective immunity against tuberculosis (TB). This sequence be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOSOTVTVDQOEILNRANEVEAPMADPPTDVPITPCELTAARNAAQQLVLSADNMREYLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            525 TOSQIVIVDQOEILNRANEVBAPMADPPIDVPITPCELTAAKNAAQQLVLSADNMREYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Tuberculosis, immunogenic, soluble, antigen, protective immunity, TB; vaccine, pharmaceutical, infection, diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
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                                                                                                                                               810 PPPPQEQGLIPGFLMPPSDGSGVTPGTGMPAAPMVPPTGSPGGLPA 856
                                                                                                                                                                              771 APAPAEPA-----PAPAGEVAP------TPTTPTPQRTLPA 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                          M. tuberculosis immunogenic polypeptide TbH4-XP1 #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;
Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
46.8%; Score 2375; DB 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-138;
Matches 459; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3c; Page 178-179; 230pp; English.
                                                                                                                                                                                                                                                              Ā
                                                                                                                                                                                                                                                            AAW81737 standard; Protein; 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-US18293
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96US-0730510
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                          (first entry)
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11-OCT-1996;
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                                                                                                                                                        TOSQTVTVDQQEILNRANEVBAPMADPPTDVPITPCELTAARNAAQQLVLSADNMREYLA
                                                                                                                                                                                  AGAKERQRLATSLRNAAKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDSSAELTDTPR
                                                                                                                                                                                             AGAKERQRIATSLRNAAKAYGEVDEBAATALDNDGEGTVQAESAGAVGGDSSAELTDTPR
                                                                                                                                                                                                                           VATAGEPNFMDLKEAARKLETGDQGASLAHFADGWNTFNLTLQGDVKRFRGFDNWEGDAA
                                                                                                                                                                                                                                                                                                             ARDQILPVYABYQQRSEKVLTBYNNKAALEPVNPPKPPPAIKIDPPPPPQEQGLIPGFLM
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                                                                                                                                        525 TQSQTVTVDQQEILNRANEVEAPMADPPTDVPITPCELTAAKNAAQQLVLSADNMREYLA
                                                                                                                                                                                                                                                                   TACEASLDQQRQWILHMAKLSAAMAKQAQYVAQLHVWARREHPTYEDIVGLERLYAENPS
                                                                                                                                                                                                                                                                                       TACEASIDOQRQWILHWAKISAAMAKQAQYVAQLHVWARREHPTYEDIVGLERLYAENPS
                                                                                                                                                                                                                                                                                                                                 ARDQILPVYAEYQQRSEKVLTEYNNKAALEPVNPPKPPPAIKIDPPPPPQEGGLIPGFLM
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                                                                                                                                                                                                                                                                                                                                                                                               GGGGGGVPSAPLGSAIGGAESVRPAGAGDIAGLGQGRAGGGAALGGGGGMGMPMGAAHQGQ
                                                                                                                      Gaps
comprising antigenic or immunogenic portions of M. tuberculosis antigens, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tuberculosis, M. tuberculosis, antigen, immunogen, diagnosis, immunisation; vaccine; infection;
                                                                                                                    ;
0
                                                                                                460;
                                                                                                Length
                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAKSKGSQQEDEALYTEDRAWTEAVIGNRRRQDSKESK 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M. tuberculosis antigen TbH4-XPlamino acid seguence
                                                                                              Score 2375; DB 19;
Pred. No. 1.6e-138;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAKSKGSQQEDEALYTEDRAWTEAVIGNRRRQDSKESK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą
                                                                                                        Best Local Similarity 100.0%; P:
Matches 459; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY39164 standard, Protein, 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis; M.
                                                                                              46.8%;
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98US-0025197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                          460 AA;
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                                                                                                                                                                                                                                                                                             The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents is kin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion tuberculosis.—Immune subjects.—AZI29460 and AAX13963 to AAX139225 are used in the exemplification of the present invention.
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  Houghton R;
                                                                                                                                                             New antigens from Mycobacterium tuberculosis useful i
skin tests and protective or therapeutic vaccines or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAKSKGSQQEDEALYTEDRAWTEAVIGNRRRQDSKESK 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.8%; Score 2375; DB 20;
100.0%; Pred. No. 1.6e-138;
live 0; Mismatches 0;
Campos-Neto A, Dillon DC, Hendrickson RC, Ho
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                 Example 3; Page 174-175; 299pp; English
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                                                                              1999-527409/44
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tes 459; Conserv
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                                                                                                        N-PSDB; AAZ19350
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Antigen; diagnosis; detection; infection; antibody; immunisation;

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us-09-688-672a-54.rag

s; M. tuberculosis; antigen; immunogen; immunisation; vaccine; infection;

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Houghton R;

Hendrickson RC, Ho YAW, Twardzik DR,

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New antigens from Mycobacterium tuberculosis useful in diagnostic
skin tests and protective or therapeutic vaccines or compositions
                                                                                                                M. tuberculosis fusion protein TbF-8 amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 37; Page 274-276; 299pp; English.
                 AAY39225 standard; Protein; 652
                                                                                                                                                 Mycobacterium tuberculosis; M.
                                                                                                                                                                                                                                                                                                                                                              98US-0072967
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skeiky
                                                                                                                                                                                                                                                                                                                               99WO-US03268
                                                                                                                                                                                  immune response; skin test.
                                                                                                                                                                                                                  Synthetic.
Mycobacterium tuberculosis.
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Lodes MJ, Reed SG, Skeik
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                                                                                 05-NOV-1999
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                                                  AAY39225;
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                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 ARDQILPVYAEYQQRSEKVLTEYNNKAALEPVNPPKPPPAIKIDPPPPOEOGLIPGFLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 AGAKERQRIATSIRNAAKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDSSAELTDTPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 VATAGEPNEMDLKEAARKLETGDQGASLAHFADGWNTFNLTLQGDVKRFRGFDNWEGDAA
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                                                                                                                                                                                                                                                                                                                                               New polypeptide comprising antigenic portions of M. tuberculosis
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 460;
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                                                                                                                                                                                                                                                 Houghton R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
46.8%; Score 2375; DB 20;
Best Local Similarity 100.0%; Pred. No. 1.6e-138;
Matches 459; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                 on DC, Hendrickson RC, Ho
Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 219-220; 323pp; English.
                                                                                                                                99WO-US03265
                                                                                                                                                               98US-0072596
98US-0024753
                                 Mycobacterium tuberculosis
                                                                                                                                                                                                                                             Campos-Neto A, Dillon DC,
Lodes MJ, Reed SG, Skeik
                                                                                                                                                                                                                                                                                                WPI; 1999-527416/44.
                                                                                                                                                                                                                (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460 AA;
 vaccine; immunity
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                                                                WO9942118-A2
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                                                                                                                                                               05-MAY-1998;
18-FEB-1998;
                                                                                                 26-AUG-1999
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The present invention describes polypeptides comprising an immunogenic are vaccines and fusion tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion tuberculosis-immune subjects. AZI9249 to AAZI9460 and AAXI99083 to AAXI9225 are used in the exemplification of the present invention.
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                                                                                          ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAGFASKTPANQAISMIDGPAPDGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------GSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLWG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGHHHHHHHVIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAFHERYPNVT1TAQGTGSGAG1AQAAAGTVN1GASDAYLSEGDMAAHKGLMN1ALA1SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---RLATSLRNAAKAYGEVDEBAATALDND--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                    nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                 tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 310;
                                                                                                                                                                                                                                                                                                 This invention describes novel recombinant antigens and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 652;
                               TS;
   Houghton R;
                                                                                                                                                                                 Σ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.3%; Score 1839; DB 20; 48.5%; Pred. No. 3.2e-105; ive 26; Mismatches 132;
                                                                                                                                                                              New polypeptide comprising antigenic portions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 PPPPAA-----ANTPNAOPG------
                               DR,
Campos-Neto A, Dillon DC, Hendrickson RC,
Lodes MJ, Reed SG, Skeiky YAW, Twardzik
                                                                                                                                                                                                                                      Example 10; Page 320-321; 323pp; English.
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---KFSDPSKPNGOIWTGV

δ	668 QGASLAHFADGWNTFNLTLQGDVKRFRGFDNWFGDAATACEASLDQQRQWILHMAKLSAA 727	CEASLDQQRQWILHMAKLSAA 727
QQ	570 IGSPAANAPDAGPPQRWFVVWLGTANNPVDK	: /DK 600
δ,	728 MAKQAQYVAQLHVWARREHPTYEDIVGLERLYAENPSARDQILPVYAEYQQRSEKVLTEY 787	OQILPVYABYQQRSEKVLTEY 787
QQ	601GAAKALAE-SIRPLVAP	:   PLVAP 616
δ	788 NNKAALEPVNPPKPPPAIKIDPPPPQEQGLIPGFLMPPSDGSGVTPGTGMPAAPMVPPT 847	SDGSGVTPGTGMPAAPMVPPT 847
QQ	617PPAPAPA-PAEPAPAPAGEV	
δλ	848 GSPGGGLPA 856	
අධ	644 PIPQRILPA 652	

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Perfect score:

Sednence:

OM protein

Run on:

Scoring table:

Searched:

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Sequence 2, Appliance 2, Appliance 117, Appliance 112, Appliance 112, Appliance 112, Appliance 251, Appliance 251, Appliance 251, Appliance 251, Appliance 251, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 27, Appliance 
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Best Local Similarity 66.6%; Pred. No. Se-187;
Matches 591; Conservative 27; Mismatches 153; Indels 116; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 214, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Read, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUDKESSE: SEED and BERKI LLE
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
CITY: Seattle
COUNTRY: USA
ZATE: Washington
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOSDY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILNG DATE: 07-APR-1998
CLESSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKY, DAVIG J.
REGISTRATION NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 214:
SEQUIENCE CHARACTERIZICS:
SEQUIENCE CHARACTERIZICS:
LENGTH: 802 amino Acids
                     PCT-US93-11298-2
US-08-818-112-117
US-08-818-111-112
US-09-056-556-117
US-09-072-596-112
US-08-311-731A-251
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US-09-056-556-77
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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US-09-056-556-214
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US-09-056-556-214
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Appl
                                                                                                                                                                                                                                                                     November 21, 2003, 15:58:31 ; Search time 20.7299 Seconds (without alignments) 2006.354 Million cell updates/sec
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5072
1 MGHHHHHUIDIIGTSPTSW......RAWTEAVIGNRRQDSKESK 983
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1. /cgr2_6/ptodata/1/iaa/5A_COMB.pep:*

2. /cgr2_6/ptodata/1/iaa/6A_COMB.pep:*

3. /cgr2_6/ptodata/1/iaa/6A_COMB.pep:*

3. /cgr2_6/ptodata/1/iaa/6B_COMB.pep:*

5. /cgr2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

5. /cgr2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

5. /cgr2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                                  GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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US-09-076-556-184

US-09-072-596-370

US-08-018-111-148

US-08-018-111-148

US-09-076-556-155

US-09-076-556-155

US-09-072-596-148

US-09-072-596-148

US-09-0718-426-6

US-09-0718-426-6

US-09-078-586-150

US-08-118-112-89

US-08-118-111-90

US-08-118-111-90

US-08-118-111-90

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US-08-118-111-110
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Database :

Score

Result

TREATM

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KLEVSFKMRPAQPRCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLWG 120

1 MGHHHHHHVIDIIGTSPTSWEQAAABAVQRARDSVDDIRVARVIEQDWAVDSAGKITYRI 60

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Sequence Sequence

Sequence Sequence Sequence

5-09-116-492A-5 5-08-818-112-88 5-08-818-111-89 5-09-056-556-88

Sequence

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1 MGHHHHHHUIDIIGISPISWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRI

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KLEVSFKWRPAQPRCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLWG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 802;
                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
    1: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.2%; Score 2700; DB 4; 66.6%; Pred. No. 5e-187; iive 27; Mismatches 153;
                                                                                                                                                                                                                                                                     FILLING CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REPREMCEDOCKET NUMBER: 210121.417C9
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 209: SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
TYPE: amino acid
TYPE: amino acid
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      ADDRESSEE:
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Best Local Simil
Matches 591, C
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                                                              STATE: WA
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                                                                                                                                             QQVNYNLPGVSEHLKINGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGS
                                                                                          120 PAFHERYPINVIITAQGIGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISA
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APPLICANT: Reelly, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Campoon, Davin C.
APPLICANT: Campoon, Davin C.
APPLICANT: Houghton, Raymond
APPLICANT: Twardix, Thomas S.
APPLICANT: Twardix, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Compounds Ronal C.
APPLICANT: Compounds And METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
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US-09-072-596-209
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Oy 1 МGНННЯНVIDIIGTSPT	Oy 61 KLEVSFKMRPAQPRGSK	OY 121 PAFHERYPNVIITAQGTG	2y 181 QOVNYNLPGVSEHLKLNG 		2y 301 ISFLDQASQRGLGEAQLG	360 PIINYEYAL 421 ATISSAEMK	Db 420 AIISSAEMKIDAATLAQE		Db 538 PPAPATPVAPPPAAANT		Qy 654BD Db 631 GQPPPVANDTRIVLGRLD	Qy 698 NWEGDAATACEASLDQOR	Qy 758 LYAENPSARDQILPUYAE	810 PPPPQEQGLIPGFI	DD 7/1 AFAFAEFAFAFAF RESULT 4 US-09-056-556-184 ; Sequence 184, Application US/C ; Patent No. 5350456 ; GENERAL INFORMATION:	APPLICANT: Reed, Steven G. APPLICANT: Skeiky, Yasir A APPLICANT: Dillon, Davin C ITILE OF INVENTION: COMPOU CORRESPONDENCES: 241 CORRESPONDENCE ADDRESS:
QY 601 AKAYGEVDEEAATALDNDGEGTVQAESAGAYGGDSSAELTDTPRVATAGEPNF-653	QY 654	QY 698 NWBGDAATACEASLDQQRQWILHMAKLSAAMAKQAQYVAQLHVWARREHPTYEDIVGLER 757	QY 758 LYAENPSARDQILPVYAEYQQRSEKVLTEYNNKAALEPVNP-PKPPPAIKIDP 809   STATE	ا ق	RESULT 3 US-09-072-596-346 ; Sequence 346, Application US/09072596	GENERAL INFORMATION:  APPLICANT: Reed, Steven G.  APPLICANT: Skeiky, Yasir A.W.  APPLICANT: Dillon, Davin C.	; AFFLICANT: Campos-Neco, Antonia ; APPLICANT: Houghton, Raymond ; APPLICANT: Vedvick, Thomas S. ; APPLICANT: Twardzik hanjel R	APPLICANT: Lodes, Michael 1. APPLICANT: Lodes, Michael C. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS , NUMBER OF SEQUENCES: 350	CORRESPONDENCE ADDRESS:  ADDRESSEE: SEED and BERRY LLP STREET: 6300 Columbia Center, 701 Fifth Avenue	STATE: Sealington STATE: Washington ; COUNTRY: USA	) COMPUTER READING FORM: ) MEDIUM TYPE: Floppy disk ) COMPUTER: IBM PC compatible	; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: Patentin Release #1.0, Version #1.30 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/09/072,596	; FILING DAIE: US-MAY-1998 ; CLASSIFICATION: ; ATTORNEY AGENT INFORMATION: ; NAME: Maki, David J.	REGISTRATION NUMBER: 31,392 REFERENCE/DOCKET NUMBER: 210121.417C9 TELECOMMUNICATION INFORMATION:	TELEFAX: (206) 682-6930 	<pre>// MOLECULE TYPE: protein US-09-072-596-346 Query Match S3.2%; Score 2700; DB 4; Length 802; Best Local Similarity 66.6%; Pred. No. 5e-187; Matches 591; Conservative 27; Mismatches 153; Indels 116; Gaps 15;</pre>

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STNIROAGVOYSRADEBOOOALSSOMGFTQSQTVTVDQQEILNR 540
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                                         GNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGY
    TSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRI
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C.
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TREATM

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122 VATAGEPNEMDLKEAARKLETGDQGASLAHFADGWNTFNLTLQGDVKRFRGFDNWEGDAA 181
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APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and Purring
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CURRENT APPLICATION DATA:
APPLICATION NUMBER:
ELING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAK1, DAVIG J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.417C9
TELECOMMUNICATION:
TELEPHONE: (206) 622-4900
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al Similarity 100.0%; Pred. No. 7.3e-164;
459; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 179:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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amino acid
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Best Local Similarity
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US-09-072-596-179
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                                                                                                                      COUNTRY: USA
ZIP: 98104-7092
COMPUTER RELABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: U7-APR-1998
CLASSIFICATION NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION OF SEQ. 1D NO: 184:
SEQUENCE CHARACTERISTICS:
TENERGY FOR SEQ 1D NO: 184:
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                         3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 460 amino acids
TYPE: amino acid
STRANDEDNESS:
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Matches 459; Conservative
                                                                                               Washington
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                                                                      Seattle
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764 241 362 GGGGGGVPSAPLGSAIGGAESVRPAGAGDIAGLGQGRAGGGALGGGGMGMPMGAAHQGQ 421

PPSDGSGVTPGTGMPAAPMVPPTGSPGGGLPADTAAQLTSAGREAAALSGDVAVKAASLG GGGGGGVPSAPLGSAIGGAESVRPAGAGDIAGLGQGRAGGGAALGGGGMGMPMGAAHQGQ

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885

Sequence 179, Application US/09072596; Patent No. 6458366; GENERAL INFORMATION: APPLICANT: Reed, Steven G.

RESULT 5. US-09-072-596-179

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  241 GDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIG 300
                                                                                                                                                                      PIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 GDIFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIG
                                                                                      301 ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGY
                                                                                                                      234 ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASXTPANQAISMIDGPAPDGY
                                                                                                                                                                                                               294 PIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALI
                                                                                                                                                                                                                                                          ATISSAEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVV
                                                                                                                                                                                                                                                                                                                                              481 RFQEAANKOKQELDEISTNIRQAGVQYSRADBEQQQALSSQMGFTQSQTVTVDQQEILNR
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APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND FITTLE OF INVENTION: AND DIAGNOSIS OF NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
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; Sequence 153, Application US/08818112
; Patent No. 6290969
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6300 Columbia Center,
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: Washing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGS 240
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                                                                                                                                                                                                      APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Slilon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Thomas S.
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Gomboly Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 310;
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945 GGAKSKGSQOEDEALYTEDRAWTEAVIGNRRRQDSKESK 983
                         422 GGAKSKGSQGEDEALYTEDRAWTEAVIGNRRRQDSKESK 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.3%; Score 1839; DB 4;
48.5%; Pred. No. 7.7e-125;
iive 26; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
TATCAREY/AGBNT INFORMATION:
NAME: Maki, David J
REGISTRATION NUMBER: 31,392
REFERENCE/POCKET NUMBER: 210121.417C9
TELECOMUNICATION INFORMATION:
TELECHONE: (206) 622-4900
                                                                                                                                             Sequence 350, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 350:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: protein
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STREET: 6300
CITY: Seattle
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Washingto
COUNTRY: USA
ZIP: 98104-7092
                                                                                                                             US-09-072-596-350
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
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95.2%;
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Matches 355; Conservative
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     Washington
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US-09-056-556-153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLM 121
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/ Patent No. 6338852
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Unique. Naymond
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Twardatk, Daniel R.
/ APPLICANT: Twardatk, Daniel R.
/ TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF T
/ NUMBER OF SEQUENCES: 148
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
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9
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: FatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MRR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                             Score 1831; DB 3;
Pred. No. 1.3e-124;
3; Mismatches 9;
                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6931
INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
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95.2%;
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Best Local Similarity 95.2
Matches 355; Conservative
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US-08-818-111-148
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Patent No. 6350456
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Steiky, Yasir A.W.
APPLICANT: Steiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Steiky, Yasir A.W.
ADPRESSEE: 241
COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
COMPOUNDS ADDRESS:
ADDRESSEE: SEED ADBRESS:
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 374;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER. IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INPORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMULCATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEFAK: COSO 682-6031
TELEFAK: COSO 682-6031
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Pred. No. 1.3e-124;
3; Mismatches 9;
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59 RIKLEVSFKMRPAQP-----RCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLL 112
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6300 Columbia Center, 701 Fifth Avenue
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Pred. No. 1.3e-124;
3; Mismatches 9;
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Patent No. 645836
GENERAL INPOWATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonia APPLICANT: Houghton, Raymond;
APPLICANT: Houghton, Raymond;
APPLICANT: Wedvick, Thomas S.
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Best Local Similarity 95.2%;
Matches 355; Conservative
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                                                                                 Washington
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                                                                                                                       COUNTRY:
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US-09-056-556-155
Sequence 155, Application US/09056556
Sequence 155, Application US/09056556
Settle No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Compound C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                          ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
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TELEPHONE: (206) 622-6031
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Pred. No. 1.3e-124;
3; Mismatches 9;
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Best Local Similarity 95.2%;
Matches 355; Conservative
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                                      Washington
                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233
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113 YPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLM 172
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                                            APPLICANT: Reed, Steven G.
APPLICANT: Reed, Vasir A.W.
APPLICANT: Skekky, Yasir A.W.
APPLICANT: Olilon, Davin C.
APPLICANT: Campos-Netco, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Twardik, Thomas S.
APPLICANT: Twardik, Daniel R.
APPLICANT: Hendiickson, Ronald C.
APPLICANT: Lodes, Michael J.
APPLICANT: Compounds AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INPORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMOMICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/072,596 FILING DATE: 05-MAY-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98104-7092
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                              S: SEED and BERRY LLP 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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amino acid
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STATE: Washington
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US-09-072-596-150
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APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael C.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
                                                                                                                                                                                                 STREET: 6300 COLUMDIA CENTER, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
CONTRY: USA
ZIP: 98104-7092
COMPUTER: ERADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FLING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/POCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEFORM: (206) 682-4900
TELEFER (206) 682-6031
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LEMETH AND ASSIGNMENT OF SEQ ID NO: 148:
                                                                                                                                                                 B: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-09-072-596-150
; Sequence 150, Application US/09072596
; Patent No. 6458366
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Best Local Similarity 95.2
Matches 355; Conservative
                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and I
STREET: 6300 Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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FILING DATE: 1
CLASSIFICATION:
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US-08-818-112-89
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US-09-110-426-5

Sequence 5, Application US/09118426C

Sequence 5, Application US/09118426C

Retent No. 6517839

GENERAL INFORMATION:
APPLICANT: Modili, Robert L.
TITLE OF INVENTION: T-CELL RESPONSE

FILE REFERENCE: 30435,44001

CURRENT APPLICATION NUMBER: US/09/118,426C

CURRENT APPLICATION NUMBER: US/09/118,426C

CURRENT APPLICATION NUMBER: G0/052,970

EARLIER FILING DATE: 1998-07-17

BARLIER FILING DATE: 1998-07-17

CORRANISM: Mycobacterium tuberculosis

PUBLICATION INFORMATION:
JOURNAL: Infect. Immun.

VOLUME: 57

FARE SE 88

SECTION OF SECTION INFORMATION:
JOURNAL: Infect. Immun.

SECTION OF SECTION INFORMATION:
SECTION OF SECTION INFORMATION:
JOURNAL: Infect. Immun.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 KLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYLSKQD 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09118426C
Retent No. 6517839
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Modilin, Robert L.
APPLICANT: Libraty, Daniel H.
TITLE OF INVENTION: METHODS FOR INDUCING INTERLEUKING-12 AND A TYPE 1/TH1
TITLE OF INVENTION: T-CELL RESPONSE
FILE REFERENCE: 30435.4US01
CURRENT PELLING NUMBER: US/09/118,426C
CURRENT FILING DAME: 1998-07-17
EARLIER APPLICATION NUMBER: 60/052,970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 KINGKVLAAMYQGTIKIWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYLSKQD
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36.1%; Score 1829; DB 4; Length 3'
Best Local Similarity 100.0%; Pred. No. 1.8e-124;
Matches 351; Conservative 0; Mismatches 0; Indels
  362 VKLSDALIATISS 374
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; DATE: 1989
US-09-118-426-5
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US-09-118-426-6
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    376 DAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALIATISS 425
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35.9%; Score 1820; DB 4; Length 351;
Best Local Similarity 100.0%; Pred. No. 7.4e-124;
Matches 350; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                         NAME/KEY: LIPID
LOCATION: (1)
COTHER INVERMATION: Xaa is N_ACYL DIGLYCERIDE cysteine
US-09-IB-426-6
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STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: 6300 Columbia Center, 701 Fifth Avenue
STATE: Mashington
CONTEX: USA
ZIP: 98104-7092
COMPUTER: READABLE FORM:
MEDIUM: TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRY TOP MADER: US/08/818,112
RILING DATE: 13-MAR-1997
EARLIER FILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 31
TYPE: PAT
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 89, Application US/08818112; Patent No. 6290969; GENERAL INFORMATION:
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585 AGAKERQRIATSLRNAAKAYGEVDEBAATALDNDGGGTVQAESAGAVGGDSSAELTDTPR 644
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15.6%; Score 791; DB 3; Length 166;
Best Local Similarity 95.2%; Pred. No. 7.4e-50;
Matches 157; Conservative 0; Mismatches 8; Indels
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ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
RELECOMMUNICATION INFORMATION:
FELEPHONE: (206) 622-4900
FELEFAR: (206) 682-6031
FELEFAR: (206) 682-6031
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Search completed: November 21, 2003, 16:11:43 Job time: 22.7299 secs

Sequence 40, Appl Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 35, Appl Sequence 35, Appl Sequence 117, Appl Sequence 117, Appl Sequence 71, Appl Sequence 71, Appl Sequence 73, Appl Sequence 73, Appl Sequence 74, Appl Sequence 77, Appl Sequence 77, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 69, Appli Sequence 69, Appli Sequence 69, Appli Sequence 69, Appli Sequence 69, Appli Sequence 67, Appli Sequence 67, Appli Sequence 67, Appli Sequence 67, Appli Sequence 67, Appli Sequence 67, Appli Sequence 67, Appli Sequence 67, Appli

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General 10, Application US/09287849

Sequence 10, Application US/09287849

Sequence 10, Application US/09287849

GENERAL INFORMATION:

APPLICANT: Rede, Seeven G.

APPLICANT: Dillon, Davin C.

APPLICANT: Allon, Davin C.

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Autonio

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APPLICANT: Campos-Neto, Autonio

APPLICANT: Campos-Neto, Autonio

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APPLICANT: Campos-Neto, Autonio

APPLICANT: Campos-Neto, Autonio

APPLICANT: Overation

TILLE OF INVENTION: UNGER: US/09/287, 849

CURRENT FILING DATE: 1999-04-07

PRIOR APPLICATION NUMBER: US/09/287, 197

PRIOR FILING DATE: 1998-04-07

PRIOR FILING DATE: 1998-04-07

PRIOR PILING DATE: 1998-04-07

PRIOR PILING DATE: 1998-04-07

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

SEQ ID NO 10

LENGTH: 802

TYPE: PPRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: Description of Artificial Sequence:tetra-fusion US-09-287-849-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2700; DB 9; Length 802;
Pred. No. 6.1e-161;
2 US-10-193-002-150

US-10-359-460-6

US-10-359-460-6

US-10-098-732A-39

2 US-10-084-843-89

2 US-10-084-843-89

2 US-10-084-843-115

2 US-10-084-843-115

2 US-10-084-843-115

2 US-10-084-88

2 US-10-084-88

2 US-10-084-88

2 US-10-084-88

2 US-10-084-88

2 US-10-084-843-88

2 US-10-084-843-117

2 US-10-098-734-88

2 US-10-098-734-88

2 US-10-098-734-88

2 US-10-098-734-73

2 US-10-098-734-73

2 US-10-088-734-73

2 US-10-088-734-73

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2 US-10-088-734-73

2 US-10-088-734-74

2 US-10-088-734-74

2 US-10-088-738-69

2 US-10-088-738-69

2 US-10-186-74-73

2 US-10-186-74-73

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2 US-10-186-74-73
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     Query Match
Best Local Similarity
   324
324
324
313.5
276
217.5
202.5
192
       Sequence 10, Appl Sequence 214, App Sequence 351, App Sequence 346, App Sequence 10, Appl Sequence 179, App Sequence 179, App Sequence 355, App Sequence 6, Appl Sequence 6, Appl Sequence 151, App Sequence 153, App Sequence 153, App Sequence 153, App Sequence 153, App Sequence 153, App Sequence 153, App Sequence 153, App Sequence 155, App Sequence 155, App Sequence 155, App Sequence 155, App Sequence 155, App
                                                                                                                           November 21, 2003, 16:08:22 ; Search time 38.3392 Seconds (without alignments) 4680.740 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                             US-09-688-672A-54
5072
1 MGHHHHHHVUDIIGTSPTSW......RAWTEAVIGNRRRQDSKESK 983
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1: /cgm2_6/ptodata/1/pubpaa/NSC7_PUBCOMB.pep:*

2: /cgm2_6/ptodata/1/pubpaa/PCT_MBW_PUBL_pep:*

3: /cgm2_6/ptodata/1/pubpaa/NSC6_NBW_PUB.pep:*

4: /cgm2_6/ptodata/1/pubpaa/USC6_NBW_PUB.pep:*

5: /cgm2_6/ptodata/1/pubpaa/USC6_NBW_PUB.pep:*

6: /cgm2_6/ptodata/1/pubpaa/USC6_NBW_PUB.pep:*

7: /cgm2_6/ptodata/1/pubpaa/USC8_NBW_PUB.pep:*

8: /cgm2_6/ptodata/1/pubpaa/USC9_NBW_PUB.pep:*

9: /cgm2_6/ptodata/1/pubpaa/USC9_PUBCOMB.pep:*

10: /cgm2_6/ptodata/1/pubpaa/USC9_PUBCOMB.pep:*

11: /cgm2_6/ptodata/1/pubpaa/USC9_PUBCOMB.pep:*

12: /cgm2_6/ptodata/1/pubpaa/USC9_PUBCOMB.pep:*

13: /cgm2_6/ptodata/1/pubpaa/USC9_PUBCOMB.pep:*

14: /cgm2_6/ptodata/1/pubpaa/USC0_PUBCOMB.pep:*

15: /cgm2_6/ptodata/1/pubpaa/USC0_PUBCOMB.pep:*

16: /cgm2_6/ptodata/1/pubpaa/USC0_PUBCOMB.pep:*

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18: /cgm2_6/ptodata/1/pubpaa/USC0_NEW_PUB.pep:*
                      GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-10-084-843-351
US-10-193-002-209
US-10-193-002-209
US-10-193-002-346
US-10-084-843-184
US-10-084-843-184
US-10-084-843-355
US-10-084-843-355
US-10-084-843-356
US-10-084-843-356
US-10-084-843-356
US-09-287-849-40
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US-10-084-843-155
US-10-193-002-148
                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-287-849-10
                                                                                                                                                                                                                                                                                                                          666188 segs, 182559486 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                           1 MGHHHHHHVIDIIGTSPISWEQAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRI
  Gaps
 Indels 116;
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  153;
 Mismatches
 27;
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US-10-084-843-214
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Sequence 214, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
SPELICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond

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Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 116;
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                                                                                                                                                                                            701 Fifth Avenue
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%; Pred. No. 6.1e-161;
27; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREEDIIN Release #1.0, Ve
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/10/084,843
FLING DATE: 25-Feb-2002
CLASSIFICATION: «UNKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 214: US-10-084-843-214
                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 802 amino acids
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66.6%;
                                                                                                                             NUMBER OF SEQUENCES: 355
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 66.69
Matches 591, Conservative
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                                                                                     TITLE OF
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                                                                                                                                                                                                                                                                                                                                           Query Match 53.2%; Score 2700; DB 12; Best Local Similarity 66.6%; Pred. No. 6.1e-161; Matches 591; Conservative 27; Mismatches 153;
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REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                         INFORMATION FOR SEQ ID NO: 351:
SEQUENCE CHARACTERISTICS:
JENGTH: 802 amino acids
TYPE: amino acid
STRANDEDNESS: single
JOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 351:
US-10-084-843-351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----RIGSDMGEF -- YM 675
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                                                                                                                                                                                                                        541 ANEVEAPMADPPTDVPITPCELTAAKNAAQQLVLSADNMREYLAAGAKERQRLATSLRNA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- ANGVSGSASYYEVKFSDPSKPNGOIWTGVIGSPA 724
                                                                                                                                                                                                                                                                                                                      601 AKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDS----SAELTDTPRVATAGEPNF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              758 LYAENPSARDQILPVYAEYQQRSEKVLTEYNN-----KAALEPVNP-PKPPPAIKIDP
                                 ATISSAEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVV
                                                                                                                            RFQEAANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGFTQSQTVTVDQQEILNR
                                                                                                                                                                          RFORMANKOKOELDEISTNIRQAGVOYSRADERQQQALSSQMGFV--PTTAASPPSTAAA
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Skeiky, Yasir A.W.

Dillon, Davin C.

Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.

Twardzik, Daniel R.

Lodes, Michael J.

Hendrickson, Ronald C.

INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY

OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            810 PPPPQEQGLIPGFLMPPSDGSGVTPGTGMPAAPMVPPTGSPGGGLPA 856
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COUNTER READABLE FORM:

MEDIUW TYPE: PLOSPY disk

COMPUTER: IBM PC Compatible

CONFUTER: PATEM: PC-DOS/NS-DOS

SOFTWARE: PATEMIN Release #1.0, Version #1.30

CURRINT APPLICATION DATA:

APPLICATION NUMBER: US/10/084,843

FILING DATE: 25-Feb-2002

CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  631 GOPPPVANDTRIVLGRLDOKLYASABATDSKAAA-----
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APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-WAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APAPAEPA-----PAPAPAGEVAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 351, Application US/10084843 Publication No. US20030143243A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCES: 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           676 PYPGTRINQETVSLD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
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US-10-084-843-351
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GDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RFQEAANKOKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGFV--PTTAASPPSTAAA
                                 QQVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGS
                                                                                                                                                                                                                                                                                                                                                                                          ATISSAEMKTDAATLAOEAGNFERISGDLKTOIDOVESTAGSLOGOWRGAAGTAAOAAVV
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  QQVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGS
                                                                                                                                  GDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGWVTGCAETPGCVAYIG
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                                                                                                                                                                              ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGY
                                                                                                                                                                                                                                                                    PIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   771 APAPAEPA-----PAPAPAGEVAP-----TPTTPTPQRTLPA 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           810 PPPPQEQGLIPGFLMPPSDGSGVTPGTGMPAAPMVPPTGSPGGGLPA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: TUBERCULOSIS
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Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
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Publication No. US20030135026A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         725 ANAPDAGPPORWFVVW---
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STATE: Washington
COUNTRY: USA
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US-10-193-002-346
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Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 53.2%; Score 2700; DB 12; Length 802; Best Local Similarity 66.6%; Pred. No. 6.1e-161; Matches 591; Conservative 27; Mismatches 153; Indels 116
  856
                                        771 APAPAEPA------PAPAPAGEVAP------TPTTPTPQRTLPA 802
810 PPPPOEQGLIPGFLMPPSDGSGVTPGTGMPAAPMVPPTGSPGGGLPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 209:
US-10-193-002-209
                                                                                                                                                    Sequence 209, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206) 682-6031
N FOR SEQ ID NO: 209:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCES:
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STATE: Washing
                                                                                                            RESULT 4
US-10-193-002-209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER
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GENERAL INCOMENTION:
GENERAL INCOMENTION:
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Sheillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
ITILE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
ITILE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens
ITILE OF INVENTION: Baid Their Uses
FILE OF INVENTION: Baid Their Uses
FILE OF INVENTION: WHERE: US/09/287, 849
FRIOR PELLING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR PELING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR PELING DATE: 1998-02-10-01
PRIOR PELING DATE: 1998-02-10-01
PRIOR PELING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-02-130
PRIOR PELING DATE: 1998-02-130
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLEVSFKMRPAQPRCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLWG 120
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                                                                                                                                                                                                                                                                            676 PYPGTRINQETVSLD-----ANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPA 724
                           601 AKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDS-----SAELTDTPRVATAGEPNF- 653
                                                                                                                                  ------MDLKEAARKLETGDQGASLAHFADGWNTFNLTLQGDVKRFRGFD
                                                                                                                                                                                    ----RLGSDMGEF--YM
                                                                                                                                                                                                                                        NWEGDAATACEASLDQQRQWILHMAKLSAAMAKQAQYVAQLHVWARREHPTYEDIVGLER
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                                                                                ----KTTGDPPFP
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US-10-359-460-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116;
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                                                                                ---IDNPVGGFSFALPAGWVESDAAHFDYGSALLS-
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llarity 66.6%; Pred. No. 6.1e-161;
Conservative 27; Mismatches 153;
                                                                                                                                                                                 631 GOPPPVANDTRIVLGRLDQKLYÁSAEATDSKAÁA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-359-460-10; Sequence 10, Application US/10359460; Publication No. US20030147911A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
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Best Local Similarity
Matches 591; Conserva
                                                                                                                                                                                                                                        698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 802;
                COMPUTER EXADABLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compartible
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/072,596

FILING DATE: 05-MAY-1998

ATTORNEY/AGRYT INFORMATION:

NAME: MAKi, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.417C9

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-6031

INFORMATION FOR SEQ ID NO: 346:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 53.2%; Score 2700; DB 12; Best Local Similarity 66.6%; Pred. No. 6.1e-161; Matches 591; Conservative 27; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 TOPOLOGY: linear
7 MOLECULE TYPE: protein
7 SEQUENCE DESCRIPTION: SEQ ID NO: 346:
US-10-193-002-346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 802 amino acids
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STRANDEDNESS: single
ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGGGGVPSAPLGSAIGGAESVRPAGAGDIAGLGQGRAGGGAALGGGGMGMPMGAAHQGQ 421
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                                                                                                                                                           Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 46.8%; Score 2375; DB 12; al Similarity 100.0%; Pred. No. 6.9e-141; 459; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                               NAME: Maki, David J.
REGIESTRATION NUMBER: 31,392
REPERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                    APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                   COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; SEQUENCE DESCRIPTION: SEQ ID NO: 184: US-10-084-843-184
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 460 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 184:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                 CURRENT APPLICATION DATA:
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US-10-193-002-179
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Best Local S:
Matches 459
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PAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALALSA
                                                                                               QQVNYNLPGVSEHLKINGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGS
                                                                                                                                                                                                      GDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIG
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                                                                                                                                                                                                                                                    ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGY
                                                                                                                                                                                                                                                                              ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGY
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                                                                     QQVNYNLPGVSEHLKLNGKVLAAMYQGT1KTWDDPQ1AALNPGVNLPGTAVVPLHRSDGS
                                                                                                                                                                                                                                                                                                                                          PIINYEYAIVNNROKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601 AKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDS----SAELTDTPRVATAGEPNF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            538 PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPVIAPNAPQPVR-----
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Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
OF INVENTION: COMPONDES AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            771 APAPABPA-----PAPAPAGEVAP------TPTTPTPQRTLPA 802
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 184, Application US/10084843
Publication No. USZ0030143243A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
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US-10-084-843-184
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302 PPSDGSGVTPGTGMPAAPMVPPTGSPGGGLPADTAAQLTSAGREAAALSGDVAVKAASLG 361
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                                                        885 GGGGGGVPSAPLGSAIGGAESVRPAGAGDIAGLGQGRAGGGAALGGGGMGMPMGAAHQGQ
                                                                                                              362 GGGGGGVPSAPLGSAIGGAESVRPAGAGDIAGLGQGRAGGGAALGGGGMGMPMGAAHQGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardick, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
AND DIAGNOSIS OF TUBERCULOSES
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STRATE: Washington
COUNTR: Washington
COMPUTER: Washington
COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OOFRAATING SYSTEM: PC-DOS/MS-DOS
OOFRAATING SYSTEM: PC-DOS/MS-DOS
OOFRAATING SYSTEM: PC-DOS/MS-DOS
OOFRAATING NSYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 25-Feb-2002
CLASSIFICATION NUMBER: US/09/072,967
FILING DATE: OS-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
RETERRACE/DOCKET NUMBER: 210121.411C9
TELEFARE (206) 622-4900
TELEFARE: (206) 622-4900
                                                                                                                                                                                                           422 GGAKSKGSQQEDEALYTEDRAWTEAVIGNRRQDSKESK 460
                                                                                                                                                                       945 GGAKSKGSQQEDEALYTEDRAWTEAVIGNRRRQDSKESK 983
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48.5%; Pred. No. 4.4e-107;
tive 26; Mismatches 132;
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TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 355:
US-10-084-843-355
                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 355, Application US/10084843; Publication No. US20030143243A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 652 amino acids TYPE: amino acid
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Best Local Similarity
Matches 441; Conserv
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US-10-084-843-355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             765 ARDQILPVYAEYQQRSEKVLTEYNNKAALEPVNPPKPPPAIKIDPPPPPQEQGLIPGFLM 824
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CONTRY: USA...
CONTRY: USA

CONTRY: USA

CONTRY: USA

CONDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-7U1-2002

CLASSIFICATION NUMBER: US/09/072,596
FILING DATE: 0-7U1-2002

CRASSIFICATION NUMBER: US/09/072,596
FILING DATE: 0-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVIG 1

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELEPHORIS: (206) 622-4900

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                                                                                                           Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TILE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 46.8%; Score 2375; DB 12; Best Local Similarity 100.0%; Pred. No. 6.9e-141; Matches 459; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 179:
                             Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
  Reed, Steven G.
  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-193-002-179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 652;
                       DIAGNOSIS
                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-7ul-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                              ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                     METHODS FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 36.3%; Score 1839; DB 12; Best Local Similarity 48.5%; Pred. No. 4.4e-107; Matches 441; Conservative 26; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
                                                                                                                                                                   COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 350:
 Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND
TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5) 622-4900
682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 652 amino acids
IYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERISTICS
                                                         NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS:
                                                                                                                                                     STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206)
TELEFAX: (206) 68
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                       53
------GSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLKWG
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                                                           PAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISA
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Publication No. US20030135026A1
GENERAL INFORMATION:
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia Houghton, Raymond Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
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US-10-193-002-350
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120

180 113 240 173

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Page 9

Best Local Similarity 95.2%; Pred. No. 6.6e-107; Matches 355; Conservative 3; Mismatches 9; Indels 6; Gaps 1;	59 RIKLEVSFKMRPAQPRCGSKPPSGSPETGAGAGTVATTPASSPVILAETGSTLL	DD 2 KIRLHTLLAVLTAAPLLLAAAGCGSKPPSGSPETGAGAGTVATTPASSPVTLAEFTGSTLL 61	OY 113 YELFNLMGPAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLM 172	Qy 173 NIALAISAQQVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVV 232	QY 233 PLHRSDGSGDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGGMVTGCAET 292	QY 293 PGCVAYIGISFLDQASQRGLGBAQLGNSSGNFLLPDAQSIQAAAGFASKTPANQAISMI 352	Oy 353 DGPAPDGYPIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASPLDQVHFQPLPPAV 412	Oy 413 VKLSDALIATISS 425 	RESULT 12 US-09-287-849-40 Sequence 40, Application US/09287849 Fatent No. US202020009459A1 FARENT NO. US202020009459A1 FARENT NO. US20202009459A1 APPLICANT: Reed, Steven G. APPLICANT: Steiky, Yasir A.W. APPLICANT: Campos Neto, Antonio APPLICANT: Campos Neto, Antonio APPLICANT: Campos Neto, Antonio APPLICANT: Alderson, Mark APPLICANT: Alderson, Mark APPLICANT: Alderson, Mark APPLICANT: Alderson, Mark APPLICANT: Alderson, Mark APPLICANT: Alderson, Mark APPLICANT: Alderson, Mark APPLICANT: Alderson, Mark APPLICANT: Alderson, Mark APPLICANT: Alderson, Mark APPLICANT: Alderson, Mark APPLICANT: Alderson, Mark FILE OF INVENTION NUMBER: US 09/287,849 CURRENT FILING DATE: 1997-03-13 PRIOR FILING DATE: 1997-03-18 PRIOR FILING DATE: 1997-03-18 PRIOR PILING DATE: 1997-03-18 PRIOR PILING DATE: 1998-04-07 PRIOR APPLICATION NUMBER: US 09/25,197 PRIOR APPLICATION NUMBER: US 09/25,197 PRIOR APPLICATION NUMBER: US 09/25,56 PRIOR APPLICATION NUMBER: US 09/25,56 FRIOR PILING DATE: 1998-04-07 PRIOR APPLICATION NUMBER: US 09/223,040 PRIOR APPLICATION NUMBER: US 09/223,040 PRIOR PILING DATE: 1998-04-07 PRIOR PILING DATE: 1998-04-07 PRIOR PILING DATE: 1998-04-07 PRIOR PILING DATE: 1998-04-07 PRIOR APPLICATION NUMBER: US 09/223,040 PRIOR PILING DATE: 1998-04-07 PRIOR DATE DATE DATE DATE DATE DATE DATE DATE	Query Match 36.1%; Score 1831; DB 9; Length 374; Best Local Similarity 95.2%; Pred. No. 6.6e-107; Matches 355; Conservative 3; Mismatches 9; Indels 6; Gaps 1;
Db 354 ATISSGGGSGGGSGGSVPTTAASPPSTAAAPPAATPVA 396	481 RFQEAANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGFTQSQTVTVDQQEILNR	7 60	QY 541 ANEVEAPMADPPTDVPITPCELTAAKNAAQQLVLSADNMREYLAAGAKERQ 591	QY 592	QY 619GBGTVQAESAGAVGGDSSAELTDTPRVATAGEPNFMDLKEAARKLETGD 667 	QY 668 QGASLAHFADGWNTFNLTLQGDVRRFRGFDNWEGDAATACEASLDQQRQWILHMAKLSAA 727	QY         728         MAKQAQYVAQLHVWARREHPTYEDIVGLERLYAENPSARDQILPVYAEYQQRSEKVLTEY         787           Db         601	OY 788 NNKAALEPVNPPKPPPAIKIDPPPPQEGGLIPGFLMPPSDGSGVTPGTGMPAAPWVPPT 847	Oy 648 GSPGGGLPA 856	; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-09-287-849-6

59 RIKLEVSFKMRPAQP-----RCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLL 112

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36.1%; Score 1831; DB 9; Length 374;

Query Match

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113 YPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLM 172
                                                                                                                                                                                                                                                                                                                                                                                                  13 NIALAISAQQVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVV 232
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                                                                                                                                                                                          Gaps
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Skeiky, Yasir A.W.
Skeiky, Yasir A.W.
Shavin C.
Campos Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                        . 9
                                                                                                                                                Length 374;
                                                                                                                                                                                        Indels
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COMPUTER READABLE FORKH:
BUILW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION UMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: vUnknown.
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                                                                                                                                           Score 1831; DB 12;
Pred. No. 6.6e-107;
3; Mismatches 9;
                   TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 153:
US-10-084-843-153
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-084-843-155; Sequence 155, Application US/10084843; Publication No. US20030143243A1; GENERAL INPORMATION:
    LENGTH: 374 amino acids
                                                                                                                                              36.1%;
larity 95.2%;
Conservative
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                                                                                                                                                                    Similarity
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                                                                YPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLM 172
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                                                                                                                                                NIALAISAQQVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVV 232
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                        61
YPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLM
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Twardzik, Daniel K.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

ZIF: 98104-708

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 210121.411C9 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 153, Application US/10084843; Publication No. US20030143243A1
GENERAL INFORMATION:
Seed, Steven G.
Skerky, Yasir A.W.
Dillon, Davin C.
Campos Neto, Antonio Houghton, Raymond Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 682-6031
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SEQUENCE CHARACTERISTICS
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STATE: Washington
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US-10-084-843-153
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62 YPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAGTVNIGASDAYLSEGDMAAHKGLM 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 374;
         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
FILING DATE: 10-011-2002
FILING DATE: 10-011-2002
FILING PAPE: 10-011-2002
FILING DATE: CALCATION DATA:
FRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Pred. No. 6.6e-107;
3; Mismatches 9;
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATORNEY/AGENT INCEMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHAX: (206) 622-4900
TELEPHAX: (206) 682-6031
FORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 148:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: November 21, 2003, 16:38:18 Job time : 42.3392 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 95.2%;
Matches 355; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLHRSDGSGDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAET 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLHRSDGSGDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAET 241
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KIRLHTILLAVLTAAPLLLAAAGGGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLL 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 600 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                              NAME: MAKI, DAVIG J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
REPEROMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAN: (206) 622-4900
TELEPAN: (206) 682-6031
INFORMATION FOR SEQ ID NO: 155:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
STRANDEDNESS: <Unknown>
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
US-10-084-843-155
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 36.1%; Score 1831, DB 12; Best Local Similarity 95.2%; Pred. No. 6.6e-107; Matches 355; Conservative 3; Mismatches 9;
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Dillon, Davin C.
Cangos-Neco, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
INVENTION: COMPOUNDS AND METHODS FO
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 148, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKLSDALIATISS 425
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US-10-193-002-148
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November 21, 2003, 15:57:31; Search time 20.507 Seconds (without alignments) 4609.825 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                    Title:
Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	phosphate specific	hypothetical prote	phosphate-binding	ABC transporter ph	able phospha	ABC phosphate tran	O)	phosphate-binding		phosphate-binding	O)		mic p		e-bin	phosphate-binding	hypothetical prote	l-i	PstS component of		Д	'n	phosphate-binding	phosphate-binding	phosphate-binding	periplasmic phosph	hypothetical prote	hypothetical prote
SUMMARIES	ΩI	G70803	F70584	H70802	AG2377	G82595	H72756	AD1920	H75611	S74423	AI0499	H91211	H86057	BYECPR	AB0956	D75081	F64426	C70473	C90194	C87183	B87171	D70584	F70833	S74876	H70583	I64120	S39852	D97110	H96597	A86840
	DB	. 21	Н	N	7	7	(7)	7	7	<del>, -1</del>	2	N	7	Н	N	7	٦	H	~	N	7	~	N	н	N	н	Н	~	N	N
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φo	Query Match	46.8	è.	9.6			•		•	•	•	8.3		•			٠		7.5	•	•		٠		•	٠	•	4.3	4.0	4.0
	Score	37	m	485	482.5	9	460.5	456	445	4	440	419	419	413	411	406	404	400	380.5	378	335.5	3	325	316.5	314	0	226.5	$^{\circ}$	0	202.5
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hypothetical prote	probable serine-th	phosphate ABC tran	phosphate ABC tran	probable large gly	hypothetical prote	conserved hypothet	hypothetical prote	3C3.18c protein -	hypothetical prote	phosphate ABC tran	tail length tape m	female sterile hom	CDA peptide synthe	hypothetical prote	
A83412	T35389	AC1387	AE1762	T36105	H86839	A75564	F75518	T10927	T10032	A69956	C90834	A43742	T36248	F75393	B75625
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4.0	4.0	9. 6.	9.6	э. В	3.7	3.7	3.7	3.7	3.6	3.6	3.6	3.6	3.6	3.6	3.5
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202.5	202	197.5	196.5	194	187.5	187.5	186.5	185.	18	184	183.5	18	182.	181	179.5

## ALIGNMENTS

Db 362 GGGGGGVPSAPLGSAIGGAESVRPAGAGDIAGLGQGRAGGGAALGGGGGMGMPWGAAHQGQ 421	OY 59 RIKLEVSFKMRPAQPRCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLL 112
945	Db 2 KIRLHTLLAVLTAAPLILLAAAGCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLL 61
	QY         113 YPLFNLWGPAFHERYPNYJITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLM 172
RESULT 2 F70584 phosphate specific transporter S precursor - Mycobacterium tuberculosis (strain H37RV) N;Alternate names: antigen b	Qy 173 NIALAISAQQVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVV 232
C.)Species: Mycobacterium tuberculosis C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000 C.Accession: F70584; JC5103; A42930; A49721; A45820	Qy 233 PLHRSDGSGDTFLFTQYLSKQDPGGWGKSPGFGTTVDFPAVPGALGENGWGGWVTGCAET 292
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.	182 PLHRSDGSGDTFLFTQYLSKQDPBGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAET
	OY 293 PGCVATIGISFILODASQRGLGEAQLGANSSGNFLEDDAGSIQAAAAGFASKTRANQAISMI 352  Db 242 PGCVAYIGISFLDQASQRGLGEAQLGNSSGNFLLPDAGSIQAAAAGFASKTPANQAISMI 301
A)TLILE: Decignaring the Diology of Mycobacterium tuberculosis from the complete genome A,Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: F70584	353 DGPAPDGYPIINYEYAIVNRRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQDLPPAV
A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1.374 <col/>	Db 302 DGPAFDGYPIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAV 361
A/Cross-references: GB 295209; GB:AL123456; NID:g3261750; PIDN:CAB08484.1; PID:g2078049 A;Experimental source: strain H37Rv R;Braibant, M.; Lefevre, P.; de Wit, L.; Peirs, P.; Ooms, J.; Huygen, K.; Andersen, A.B.	362 VKLSDALIATISS 37
tran	RESULT 3
	n.7000 hypothetical protein Rv3874 - Mycobacterium tuberculosis (strain H37RV) C.Species: Mycobacterium tuberculosis
	C;Date: 17-17-17-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 . C:Accession: H70802
show	R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
	Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
molec	A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;File: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & A;Reference number: A70500: WIID:98295987; PMID:9634230
	A;Accession: H70802 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
	A; Molecule type: DNA A; Residues: 1-100 cCOL> A: Cross-reference: GR-1/02/120: GR-1/122454. NID-03261558. DIDN. CAN17966 1. DID. G266022
 8	A.Experimental source: strain H37Rv
	A;Gene: Rv3874
A;Wolecule type: protein A;Residues: 25-34 <cha>. R.Indersen B R : Linnamist T : Olean M</cha>	ength 100;
7. The control of the	MACCHES 79; COURTY ALIVE U; MISMACCHES U; MIGGIS U; Gabs U; OX 426 APMKTDABATTADRAGANERATCHONISTONISTAGATOGOMAGAAGTBADAAATTADRAGAAGTAAAAAAAAAAAAAAAAAAAAAAAA
:	2 AEMKTDAATIAQEAGNFERISGDIKTQIDQVESTAGSLQQQWRGAAGTAAQAAVVRFQEA 61
A.Nolecule type: protein A.Residues: 'X', 27-28, 'X', 30-34,'XX', 37 <and2>. A.Note: confirmed presence of normal signal and absence of linoprotein attachment</and2>	486 ANKOKOELDEISTNIRQAGVOSKADEEQOQALISSOMGF 524
C,Genetics: A,Genetics: A.Gene	Db 62 ANKQKQELDEISTNIRQAGVQXSRADEEQQQALSSQMGF 100
Ancar Cocon. Step phosphate-repressible phosphate-binding protein C.Keyworfas: surface antiden	RESULT 4
F;1-25/Domain: signal sequence #status predicted <sig> F;26-374/Product: phosphate specific transporter S #status experimental <mat></mat></sig>	phosphate ABC transporter all4575 [im
Query Match 36.1%; Score 1831; DB 1; Length 374; Best Local Similarity 95.2%; Pred. No. 1.9e-80; Matches 355; Conservative 3; Mismatches 9; Indels 6; Gaps 1;	A,NOCE: NOSCOC Sp. Surrain F.C. /120 15 a Synonym Of Anabadna Sp. Strain F.C. /120 C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C,Accession: AG2377 Wolk, C.P., Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, R,Kanako, T.; Nakamura, Y., Wolk, C.P., Rutzi, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sucimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

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C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Accession: G82595
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A22515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: G82595
A;Status: preliminary
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: G82595
A;Status: preliminary
A;Mocoule type: DNA
A;Reserences: GB:AE004028; GB:AE003849; NID:g9107266; PIDN:AAF84940.1; GSPDB:GNO1
A;Experimental source: strain 9a5c
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A;Experimental source: strain 9a5c
A;Experimental source: strain 9a5c
A;Authors: Marchins, Marchins, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Miyaki, C.;
A;Authors: Marchins, E.M.; Madeira, A.; Menci, M.C.; Pernimental A;Authors: Marthins, E.M.; Madeira, M.C.; Marchins, E.C.; Miyaki, D.;
A;Authors: Marchins, E.M.; Madeira, M.C.; Genora, C.; C.; Miyaki, D.;
A;Authors: Marchins, E.M.; Madeira, M.; Mencie, M.C.; Franco, C.; E.C.; Miyaki, D.;
A;Authors: Ma
                                     Ana
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference umber: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2377
A;Status: preliminary
A;Residues: preliminary
A;Residues: 1-392 «VUR»
A;Cross-references: GB:BA000019; PIDN:BAB76274.1; PID:g17133711; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics: A;Gene: al14575
C;Superfamily: phosphate-repressible phosphate-binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGSKPPSGSPETGAG-AGTVATTPASSP-----VTLAETGSTLLYPLFNLWGPAFHE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDM-AAHKGLMNIALAISAQQVN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIGISFL 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDG---YP 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALIA 421
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                                                                                                                                                                                                                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 392;
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                                                                                                                                                                                                                                                                                                                                                            9.5%; Score 482.5; DB 2;
33.7%; Pred. No. 4.1e-16;
live 64; Mismatches 151;
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A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2141
C;Superfamily: phosphate-repressible phosphate-binding protein
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R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaha

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ki

BDA, Res. G, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyri

A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable phosphate-binding periplasmic protein APE0045 - Aeropyrum pernix (strain K1)
                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 B-HLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYL 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204
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C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                       21 GCKPSNDNQSTGVSQDGNSTTPPSAEQTKSVKISGAGASFIYPLISQWSADYNAATGN-K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKODPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIGISFLDQASQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKVSAE-WKQKVGEGTSVQW---PGGVGGKGNEGVASYVQQIKGSIGYVELAY---ALQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISAQQVNXNLPGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLGEAQLGNSSGNFLLPDAQSIQAAA--AGFASKTPANQAISMIDGPAPDGYPIINYEYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 KWSYTALQNAAGQWVQPSAESFAAAASNADBWSNAKDFNLVITNATGEA--AWPITATNFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 GSKPPSGSPETGAGAGTVATTPASS----PVTLAETGSTLLYPLFNLWGPAFHERYPNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALIAT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 373;
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C;Superfamily: phosphate-repressible phosphate-binding protein
                                                                                                                                                                                                                          9.1%; Score 463; DB 2; Length 36 llarity 32.8%; Pred. No. 3.2e-15; Conservative 67; Mismatches 151; Indels
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32.0%; Pred. No. 4.3e-15;
tive 65; Mismatches 150;
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les 112, Conserv
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A,Molecule type: DNA
A,Residues: 1-373 <KAW>
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S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
Arithle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A; Fitle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A; Reference number: A75250; MUID:20036896; PMID:10567266
A; Accession: H75611
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-403 < WHID
A; Coss-references: GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AAF12207.1; PID:g6460501
A; Experimental source: strain R1
C; Genetics:
A; Genetics:
A; A; Apposition: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 IALAISAQQVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVP 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SANAGAYPIASFIYLIFYKDQKYGNRTEAQAKALKNLLIYVVTSGQQ--YNEGLDYAKLP 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 LFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKG-LMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 GAIGYVELVY---AKONKLSFGAVKORRGKFILADNGPASNAALGVV--IPADTRVSLTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 PLCGTSPVFGSLDAPLTKPRHTRRRMKKTLLGLSALVMISTAAAQGAITGA--GASFPYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 VPTAIGAVVPAYNLPGVTKPLNFDGPTLANIYLGKIKTWGDPAIAKLNPGVTIPPLPITV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 LHRSDGSGDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCVAYIGISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.8%; Score 445; DB 2; Length 403;
31.5%; Pred. No. 2.6e-14;
ive 60; Mismatches 157; Indels
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Conservative 6
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Les 118; Conserv
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Best Local S:
Matches 118
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#17611
phosphate ABC transporter, periplasmic phosphate-binding protein - Deinococcus radiodura
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1399 #sequence_revision 03-Dec-1399 #text_change 31-Mar-2000
C;Accession: #175611
R;White, 0.; Eisen, 0.A.; Heidelberg, 0.F.; Hickey, E.K.; Peterson, 0.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
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                                               FGTTVDFF--AVPGALGENGNGGMVTGCAETPGCVAYIGISFLDQASQRGLGEAQLGNSS 321
                                                                                       GNFLLPDAQSIQAAAAGFASKTP-----ANQAISMIDGPAPDGYPIINYEYAIVNNRQ 374
                                                                                                                                                                                                                                                264 DVFLKPSPEGAQAAASGAVQNLPDSPDDDWSTGYDAIIYAPGKDSYPITSWSFLLFYKQY 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:BA000019; PIDN:BAB72868.1; PID:g17130257; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73
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                                                                                                                                                                                                                                                                                                                                                                 324 NDRDKAEAIKKFIEWINTEGOTKIIEGYI---PIPDEIROINMKAVEMIS 370
                                                                                                                                                                                                                                                                                                                         KDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALIATIS 424
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C;Superfamily: phosphate-repressible phosphate-binding protein
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114

---PETGAGAGT---VATTPASSPVTLAETGSTLLYP

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S. A.Reference number: S74322, MUID:97061201; PMID:8905231
A.Accession. S74423
A.Accession. S74423
A.Actaus: Nucleic acid sequence not shown; translation not shown
A.Status: nucleic acid sequence not shown; translation not shown
A.Actaus: 1-383 < KAN>
A.Molecule type: DNA
A.Actaus: 1-383 < KAN>
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A.A
phosphate-binding periplasmic protein pstS-1 - Synechocystis sp. (strain PCC 6803)

N.Alernate names: protein sl10680

C,Alernate names: protein sl10680

A,Variety: PCC 6803

A,Variety: PCC 6803

A,Variety: PCC 6803

C,Accession: Synechocystis sp.

C,Accession: S14423

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

K,Xokumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA, Res. J, 109-136, 1996

A,Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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Best Local Similarity
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phosphate-binding periplasmic protein PstS [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli (cjate: 18-Uul-2001 #text_change 03-Aug-2001 C;Accession: H91211 C;Accession: H91211 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genor A;Reference number: A99629; MUID:21156211; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphate-binding periplasmic protein PstS [imported] - Escherichia coli (strain O157:H7 C;Species: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Esc
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A)Cross-references: GB:AE005174; NID:g12518575; PIDN:AAG58924.1; GSPDB:GN00145;
A)Experimental source: strain O157:H7; substrain EDL933
C)Genetics:
A)Gene: pstS
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A,Experimental source: strain O157:H7, substrain RIMD 0509952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGKPVLPTEENFANAAKGADWSKTFAQ---DLTNQKGEDAWPITSTTFILIHKDQKKPEQ 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 GIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISAQQVNYNLPGV-SEHLKLNGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYLSKQDPEGWGK
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C;Superfamily: phosphate-repressible phosphate-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
8.3%; Score 419; DB 2; Length 34
Best Local Similarity 32.5%; Pred. No. 3.7e-13;
Matches 109; Conservative 56; Mismatches 144; Indels
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| | | | | :::: | | | | EFDWGYTHGAKQA--NELDYATLPAEVVE 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-346 <HAY>
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A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AI0499
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-346 <KUR>A;Residues: 1-346 <KUR>A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura A;Chura 
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                                                                   CGSKPPSG-SPETGAGAGTVATT--PASSPVTLAETGSTLLYPLFNLWGPAFHERYPNVT 131
                                                                                                                                                                                                             190
                                                                                                                                                                                                                                                          150 -EGLKLSQEALAGIMLGNITKWNDPKLVADNPDLTLPDRPITVVHRSDGSGTTAVFTWNL 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKODPEGWGKSPGFGTTVDFPAVPGA-LGENGNGGMVTGCAETPGCVAYIGISFLDQASQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNLTMASLQNKDGQFVVPTDENASATLA--AVELPENLREFITNPAGADSYPIVTYTWML 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYL 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71
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                                                                                                                                      CGGGGGGGDTAQTGGGDATTTTAADAFASKVSLTGAGASFPAPLYQGWFVALNQAVPNLE
                                                                                                                                                                                                             ITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKG-LMNIALAISAQQVNYNLPGV
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8.7%; Score 440; DB 2; Length 34:
Best Local Similarity 33.4%; Pred. No. 3.7e-14;
Matches 110; Conservative 60; Mismatches 141; Indels
69; Mismatches 152; Indels
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Conservative
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UWGP: Z52

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periplasmic phosphate-binding protein [imported] - Salmonella enterica subsp. enterica scroar Typhi (Species: Salmonella enterica subsp. enterica seroar Typhi (Species: Salmonella enterica subsp. enterica seroar Typhi (Species: Salmonella typhi (Species: Salmonella typhi (Species: Salmonella typhi (Species: Ob-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 (Species: Ob-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 (Species: Daylor) (Species: Ob-Nov-2001 #text_change 18-Nov-2002 (Species: Ob-Nov-2001 #text_change 18-Nov-2002 (Species: Ob-Nov-2001 #text_change 18-Nov-2002 (Species: Ob-Nov-2001 #text_change 18-Nov-2002 (Species: Ob-Nov-2001 #text_change 18-Nov-2002 (Species: Ob-Nov-2001 #text_change 18-Nov-2002 (Species: Ob-Nov-2001 #text_change 18-Nov-2002 (Species: Ob-Nov-2001 #text_change 18-Nov-2002 (Species: Ob-Nov-2002 A) (Species: Ob-Nov-2002 A) (Species: Ob-Nov-2002 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 A) (Species: Ob-Nov-2003 
                                                                                                                                                                                                                                                                         protein #status experimental <N
Asp, Arg, Ser, Thr) #status exi
    C;Comment: This protein is a component of the inducible, high-affinity, phosphate-specifi
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 SPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIGISFLDQASQRGLGBAQLGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGNFLLPDAQSIQAAAAGFA-SKTPANQAISMIDGPAPDGYPIINYEYAIVNNRQKDAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 TVATVVAATLSMSAFSVFAEASLTGAGATFPAPVYAKWADTYQKETGN-KVNYQGIGSSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 NVGTGSTVKWPI----GLGGKGNDGIAAFVQRLPGAIGYVEYAY----AKQNNLAYTKLISA
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                                                                    A/Gene: pstS; phoS
A/Map position: 84 min
C; Superfamily: phosphate-repressible phosphate-binding protein
C; Keywords: phosphate transport
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-346/Product: phosphate-repressible phosphate-binding protein #status
F;35,63,81,160,164,166/Binding site: phosphate (Thr, Ser, Asp, Arg, Ser, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                              8.1%; Score 413; DB 1; Length 346
32.2%; Pred. No. 7.2e-13;
ive 56; Mismatches 145; Indels
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C,Superfamily: phosphate-repressible phosphate-binding protein
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32.6%; Pred. No. 9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 32.2
Matches 108; Conservative
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A;Title: Structural gene for the phosphate-repressible phosphate-binding protein of Escherichia coli calcule type: DNA

A;Residues: 1-346 cSUR>
A;Residues: 1-346 cSUR>
A;Residues: 1-346 cSUR>
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Nature 347, 402-406, 1990
A; Title: High specificity of a phosphate transport protein determined by hydrogen bonds. A; Reference number: A30645; MUID:91015319; PMID:2215649
A; Contents: annotation; X-ray crystallography, 1.7 angstroms
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                                                                                                                                                         Gaps
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C; Superfamily: phosphate-repressible phosphate-binding protein
                                                                        ; Score 419; DB 2; Length 34; Pred. No. 3.7e-13; 56; Mismatches 144; Indels
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phosphate abc transporter, periplasmic phosphate-binding protein (phox) PAB2365 - Pyrocd C;Species: Pyrococcus abyssi.
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: D75081
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: D75081
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-383 < KAW>
A;Residues: 1-383 < KAW>
A;Cross-references: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB49953.1; PID:g545846
A;Cross-reference: strain Oreay
C;Genetics:
A;Gene: phox; PAB2365
C;Superfamily: phosphate-repressible phosphate-binding protein
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                           261 SPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIGISFLDQASQRGLGEAQLGNS 320
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LAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYLSKQDPEGWGK 260
                                                                                                                                         184 KVGAGSTVNWPT---GLGGKGNDGIAAFVQRLPGAIGYVEYAY---AKQNNLAYTKLVSA 237
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8.0%; Score 406; DB 2; Length 383;
Best Local Similarity 29.0%; Pred. No. 1.8e-12;
Matches 113; Conservative 64; Mismatches 149; Indels
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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 21, 2003, 15:51:11; Search time 11.5909 Seconds (without alignments) 3988.226 Million cell updates/sec Run on:

US-09-688-672A-54 5072 1 MGHHHHHHVIDIIGTSPTSW......RAWTEAVIGNRRRQDSKESK 983 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

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MIRDLINES-89307568, PubMed=2545626;
Andersen A. B., Hansen B.B.;
"Structure and mapping of antigenic domains of protein antigen b,
"Structure and mapping of Antigenic Mycobacterium tuberculosis.";
Infect. Immun. 57:2481-2488 (1989).
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PROSPACE-DINGING PROCES AND PROCESSOR (PBP-1) (PstS-1) (Protein antigen B) (PAB) (Antigen AG78).
PSTI_OR PHOSI OR RV0334 OR MT036I OR MTCY08D9.05C.
                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                         Length 460;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                7528743226AD7A71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAKSKGSQQEDEALYTEDRAWTEAVIGNRRRQDSKESK 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAKSKGSQQEDEALYTEDRAWTEAVIGNRRRQDSKESK 983
                                                                                                                                                                                                                                                                                     Score 2375; DB 1;
Pred. No. 1.1e-98;
    removed.
                                                                                                                                                                                                                                                                                                    100.0%; Pred. nc.
                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                             GLY-RICH
    not
                                                                              EMBL, AY029285; AAK31576.1, -.
EMBL, AL022120; CAA17973.1; -.
EMBL, AC007191; AAK48364.1; -.
PIR; G70800; G70803.
TIGR, MT3996; -.
Tuberculist; RV3881c; -.
  and this statement is
                                                                                                                                                                                                                                                SEQUENCE 460 AA; 47593 MW;
                                                                                                                                                                                                         Antigen; Complete proteome.
DOMAIN 306 428
                                                                                                                                                                                                                                                                                       46.8%;
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                                                                                                                                                                                                                                                                                                                              Matches 459;
                                                                                                                                                                                                                                                                                                                                                                       525
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ID PSTI_MY

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DT 01-APR

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Pleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Peterson J. DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 NIALAISAQQVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 PLHRSDGSGDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAET
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2 KIRLHT1LAVLTAAPL1LLAAGCGSKPPSGSPBTGAGAGTVATTPASSPVTLAETGSTLL
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-!- SIMILARITY: BELONGS TO THE PSTS FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Whole genome comparison of Mycobacterium tuberculosis clinical and
MEDLINE=9829597; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Gas S., Bary C.E. III. Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Compor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd E Hornsby T., Jagels K., Krogh A., Mclean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skalton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Encomplete genome sequence: ", Mycobacterium tuberculosis from the Complete genome sequence: ", Mycobacterium tuberculosis from the Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 9
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Tuberculist; Rv0934, -.
InterPro; IPR006059; SBP_bac_1.
Pfam, PF01547, SBP_bac_1, 1.
PR03ITE; PS00013; PS0XXR. LiPOPROTEIN, 1.
Phosphate transport; Transport; Membrane; Lipoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: Required for binding-protein-mediated phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 374;
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PHOSPHATE-BINDING PROTEIN 1.
N-ACYL DIGITCERIDE (POTENTIAL)
6334968191F738AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Indels
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95.2%; Pred. No. 1.1e-74;
tive 3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 295209; CAB08484.1; -...
EMBL; AB006981; AAK45208.1; -...
PIR; F70584; F70584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 24 N
374 AA; 38243 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M30046; AAA25374.1; -.
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TIGR; MT0961; -.
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                                                                                                                 DGPAPDGYPIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAV 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Bardock K., Basham D., Brown D., Chillingworth T., Comor R., Davies R., Devlin K., Feltwell T., Geneles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Rutter S., Geoger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CDC 1551 / Oshkosh,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fletschmann R.D., Hickey E.,
Feterson J., DeBoy R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nalson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
PGCVAYIGISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMI
                                                                   242 PGCVAYIGISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMI
                                                                                                DGPAPDGYPIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
10 kDa culture filtrate antigen cfpl0 (Secreted antigenic protein
MTSA-10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gioquel B.;
"A Mycobacterium tuberculosis operon encoding ESAT-6 and a novel low-molecular-mass culture filtrate protein (CFP-10).";
Microbiology 144:3195-3203(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Singh B., Siddiqui Z., Singh S., Sharma P.;
"Rv3874 (mtsa-10) gene of a clinical isolate of Mycobacterium
tuberculosis from India.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE ESAT6 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99061212; PubMed=9846755;
Berthet F.-X., Rasmussen P.B., Rosenkrands I., Andersen P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                             CFP10 OR LHP OR MISA10 OR RV3874 OR MI3988 OR MIV027.09.
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
                                                                                                                                                   413 VKLSDALIATISS 425
                                                                                                                                                                        362 VKLSDALIATISS 374
                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVFFQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             426 AEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEA
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100.0%; Pred. No. 9.7e-16;
live 0; Mismatches 0; Indels
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28-FEB-2003 (Rel. 41, Last annotation update)
Phosphate-binding periplasmic protein precursor (PBP).
PSTS OR XF2141.
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                                                                                                                                                                                                                                                                                                               EMBL, AF004671; AAC83445.1; -.
EMBL, AL022120; CAAL7966.1; -.
EMBL, AE007190; AAX48356.1; -.
EMBL, AF419854; AAL14999.1; -.
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INIT MET 0 0
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TIGR, MT3988; -.
Tuberculist; Rv3874; -.
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364 PHOSPHATE-BINDING PERIPLASMIC PROTEIN.
38736 MW; 8609CFAA1S9D4277 CRC64;
de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meidanis J., Setubal J.C., "The genome sequence of the plant pathogen Xylella fastidiosa."; Nature 406:151-159(2000).
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                                                                                                                                                                                                                                                       -!- FUNCTION: REQUIRED FOR BINDING-PROTEIN-MEDIATED PHOSPHATE TRANSPORT (BY SIMILARITY).
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4.1e-14;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphate-binding periplasmic protein precursor (PBP).
Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Phyllobacteriaceae; Mesorhizobium.
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32.8%; Pred. No. 4.1e-14;
Live 67; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPRO06059; SBP_bac_1.
PERM; PF01547; SBP_bac_1, PRO51FP; PRO51FP; PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Phosphate transport; Transport; Periplasmic; Signal;
                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Periplasmic (Potential).
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Best Local Similarity 32.89
Matches 116, Conservative
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364
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Kanako T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Watanabe A., Idesawa R., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Marsumoto M., Mateuno A.;
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Takeuoli C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
DNA Res. 7:331-338 (2000).
-!- FUNCTION: REQUIRED FOR BINDING-PROTEIN-MEDIATED PHOSPHATE
TRANSPORT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 TTPASSPVTLAETGSTLLYPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIG
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PHOSPHATE-BINDING PERIPLASMIC PROTEIN.
2710D1BC0417574D CRC64;
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PSTS ECOLI
STANDARD; PRT; 346 AA.

RC POSIZE: PT6744;

DT 01-2AN-1988 (Rel. 06, Created)
DT 01-3AN-1988 (Rel. 06, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT Prosphate-binding periplasmic protein precursor (PBP).
GN PSTS OR PHOS OR B3728 OR SF3727.

Scherichia coli, and
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HSSP: P06128; 1IXH.
InterPro; IPR06059; SBP_bac_1.
Pfan; PP01547; SBP_bac_1; 1.
Phosphate transport; Transport; Periplasmic; Signal;
                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Periplasmic (Potential).
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Matches 112; Conservative
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351 AA;
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EMBL;
    SPECIES=E.coli;
MEDLINE=84135579; PubMed=6321434;
Surin B.P., Jans D.A., Fimmel A.L., Shaw D.C., Cox G.B., Rosenberg H.;
Structural gene for the phosphate-repressible phosphate-binding
protein of Escherichia coli has its own promoter: complete nucleotide
sequence of the phoS gene.";
J. Bacteriol. 157:772-778(1984).
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MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Jin Q., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Xan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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MEDLINE=97443975; PubMed=9298646;
Link A.J., Robison K., Church G.M.,
Comparing the predicted and observed properties of proteins encoded
in the genome of Eschericia coli K.12.";
Electrophoresis 18:1259-1313(1997).
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MEDLINE=97372887; PubMed=9228942;
Wang Z., Luecke H., Yao N., Quiocho F.A.;
"A low energy short hydrogen bond in very high resolution structures of protein receptor-phosphate complexes.";
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SPECIES=E.coli; STRAIN=K12 / MG1655;
MEDLIKE=93315143; PubMed=7686882;
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Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
"DNA sequence and analysis of 136 kilobases of the Escherichia coligenome: organizational symmetry around the origin of replication.";
Genomics 16:551-561(1993).
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MEDLINE=8413559; PubMed=6365894;
MEDLINE=8413559; PubMed=6365894;
MAGOTA K., Otsuil N., Miki T., Houchi T., Tsunasawa S., Kondo J.,
Sakiyama F., Amemura M., Morita T., Shinagawa H., Nakata A.;
"Nucleotide sequence of the phoS gene, the structural gene for the phosphate-binding protein of Escherichia coli.";
J. Bacteriol. 157:909-917(1984).
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Luecke H., Quiocho F.A., "High specificity of a phosphate transport protein determined by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=E.coli;
MEDLINE=9833779; PubNed=9671506;
Hishberg M., Henrick K., Haire L.L., Vasisht N., Brune M.,
Corrie J.E., Webb M.R.;
"Crystal structure of phosphate binding protein labeled with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.89 ANGSTROMS) OF MUTANT ASN-81
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                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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MEDLINE=91015319; PubMed=2215649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hydrogen bonds.";
Nature 347:402-406(1990).
                                    NCBI TaxID=562, 623;
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SEQUENCE FROM N.A.
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 Shigella flexneri
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coumarin fluorophore, a probe for inorganic phosphate.";
Biochemistry 37:10381-1038(1998).
-!- FUNCTION: THIS IS ONE OF THE PROTEINS REQUIRED FOR BINDING-PROTEIN
-MEDIATED PHOSPHATE TRANSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EcoGene; EG10714; psts.
InterPro; IPR005673; Peri-phosph.
InterPro; IPR006059; SBP_bac_1.
Pfam; PF01547; SBP_bac_1.
IGRPAMS; TIGR00975; 3ā0107803; 1.
Phosphate transport; Transport; Periplasmic; Signal; 3D-structure;
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                                                   -!- SUBCELLULAR LOCATION: Periplasmic.
-!- INDUCTION: BY PHOSPHATE DEPRIVATION AND SUBJECT TO POSITIVE CONTROL BY THE PHOB GENE PRODUCT AND TO NEGATIVE CONTROL BY PHOR GENE PRODUCT AND TO NEGATIVE CONTROL BY PHOR GENE PRODUCT
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L10328; AAA62079.1; -.
AE000449; AAC76751.1; -.
AE015380; AAN45173.1; -.
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PDB, 1DBP, 15-OCT-94.
PDB, 1DQUT, 11-JUL-96.
PDB, 1QUT, 11-JUL-96.
PDB, 1QUT, 11-JUL-96.
PDB, 1QUT, 11-JUL-96.
PDB, 1QUT, 11-JUL-96.
PDB, 1XK9, 04-FEB-98.
PDB, 1XX1, 22-OCT-97.
PDB, 1AX1, 22-OCT-97.
PDB, 1AX6, 23-WAR-99.
PDB, 1AX6, 14-OCT-98.
PDB, 1AX5, 14-OCT-98.
PDB, 1AX5, 14-OCT-98.
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STRAIN=Rd / KW20 / ATCC 51907;
STRAIN=Rd / KW20 / DEDMED47542800;
FIGHSCHMANN R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlaschean R.D., Adams M.D., Tomb J.F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fithugh W., Fields C.A., Gocayne J.D., McKenney K., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                         POTENTIAL.
PHOSPHATE-BINDING PERIPLASMIC PROTEIN
6378650112CF9161 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                        344;
FUNCTION: REQUIRED FOR BINDING-PROTEIN-MEDIATED PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                       59; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NUV-1995 (Rel. 32, Last section update)
28-FBB-2003 (Rel. 41, Last annotation update)
Phosphate-binding periplasmic protein precursor (PBP)
PSTS OR HI1383.
                                                                                                                                                                                                                          HSSP; P06128; 11XH.
Pfam; PF01547; SBP bac_1; 1.
Phosphate transport; Transport; Periplasmic; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 FKQGKVAA--TELDYVPLPEEVIQKIQAQWKTEVKSSDGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 391 ITDGNKASFLDQVHFQPLPPAVVKLSDALIAT-ISSAEMKT
               TRANSPORT (BY SIMILARITY).
SUBCELLULAR LOCATION: Periplasmic (Potential).
SIMILARITY: BELONGS TO THE PSTS FAMILY.
                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                          Score 411.5; DB 1
Pred. No. 7.4e-12;
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                                                                                                                                                                                                            EMBL; AE006079; AAK02520.1; ALT_INIT.
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01-NOV-1995 (Rel. 32, Last seq
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                         37362 MW;
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                                                                                                                                                                                                                                                                                                                           344 AA;
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Matches 108; Conserv
                                                                                                                                                                                                                                                                             Complete proteome.
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P45192;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVKQIIANTVDFGASDAPLSD-EKLAQEGLFQFPTVIGGVVLAVNIPGLKSGELVLDGKT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYLSKQDPEGWGK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGDIYLGKIKKWDDEAIAKLNPGLKLPSQNIAVVRRADGSGTSFVFTSYLAKVNEE-WKN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPGFGTTVDFFAVPGALGENGNGGMVTGCAETPGCVAYIGISFLDQASQRGLGEAQLGNS 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGNFLLPDAQSIQAAAAGFA-SKTPANQAISMIDGPAPDGYPIINYEYAIVNNRQKDAAT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVATVVAATLSMSAFSVFAEASLTGAGATFPAPVYAKWADTYQKETGN-KVNYQGIGSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NVGTGSTVKWPI - - - GLGGKGNDGIAAFVQRLPGAIGYVEYAY - - - AKONNLAYTKLISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISAQOVNYNLPGV-SEHLKLNGKV
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MEDGLINE=21145866; PubMed=11248100;
MEDGLINE=21145866; PubMed=11248100;
MEDGLINE=21145866; PubMed=11248100;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc., Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                           26;
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                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
PSTS OR PM0436.
                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 6.4e-12;
56; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVK 414
                                                                                                                                                                                                                                                                                                                                                            867DA7199C2C87ED
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                                                                                                                                                                                                                                                                                                                                                                                          Score 413;
                                                                                                                                                                                                                                                                                                                                                             37024 MW;
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Pasteurellaceae, Pasteurella
NCBL_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 32.2
nes 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
     Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                                            346 AA;
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                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                         Whole-genome random sequencing and assembly of Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 DFGASDDPMKSBLLQQHQ-LVQFPAVIGGIVPVVNLPEIKPGKLKLSGKLLAEIFLGKIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 TVATTPASSPVTLAETGSTLLYPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 PAVPGALGENGNGGMYTGCAETPGCVAYIGISFLDQASQRGLGEAQLGNSSGNFLLPDAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 LTGQGGKGNEGVASYVRQMKYSIGYVEYA-----YAKQNQLAWISLQNQAGQFVQPSNE
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Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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                                                                                                                                                                                                                                                PHOSPHATE
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                                                                                                                                                                                                            1 19 POTENTIAL.
20 334 PHOSPHATE-BINDING PERIPLA.
334 AA; 36665 MW; FFC44EEB53FEGB62 CRC64;
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InterPro; IPR06659; SBP bac_1.
Pfam, PF01547; SBP bac_17; ITGRPMs; TIGRPMs; AG0107803; I.
Phosphate transport; Transport; Periplasmic; Signal;
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HSSP; P06128; 1IXH.
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                                                                                                                                 Science 269:496-512(1995).
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                                                                                                                                                                         CONCEPTUAL TRANSLATION.
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                                                                    Jenter J.C.;
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28-FEB-2003
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PST3_MYCAV
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Identification of Mycobacterium avium DNA sequences that encode
"Identification of Mycobacterium avium DNA sequences that encode
exported proteins by using phoa gene fusions.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBU databases.
-!- PUNCTION: Required for binding-protein-mediated phosphate
transport (By similarity).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
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Pfam; PF01547; SBP bac 1; 1.
PROSITE; PS001013; PROKĀR_LIPOPROTEIN; 1.
Phosphate transport; Transport; Membrane; Lipoprotein; Signal. SIGNAL 1 22 POTENTIAL.
CHAIN 23 369 PHOSPHATE-EINDING PROTEIN 3.
TIPID 23 NACYL DIGLYCERIDE (POTENTIAL).
TIPID 23 23 NACYL DIGLYCERIDE (POTENTIAL).
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphate-binding protein 3 precursor (PBP-3) (PstS-3)
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31.0%; Pred. No. 1.2e-08;
iive 46; Mismatches 161;
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HSSP; P06128; 1A54.
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Best Local Similarity 31.0%;
Matches 114; Conservative
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                                                                                                                                                                                                                                                                    Mycobacterium avium
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Content J., Three different putative phosphate transport receptors are encoded by "Three different putative phosphate transport receptors are encoded by the Mycobacterium tuberculosis genome and are present at the surface of Mycobacterium bovis BCG.";
J. Bacteriol. 179:2900-2906(1996).
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                   247 SF---ASARKLINTAKIATSAD----PEPIAISVDSVG---KTISGATIIGEGNDLVLDTV
                                                                        302 SFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPAN------QAI
                                                                                                                                                                     SMIDGPAPDGYPIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLP
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MEDLINE-89255987, PubMed=9634230,
MEDLINE-98255987, PubMed=9634230,
MEDLINE-98255987, PubMed=9634230,
MEDLINE-98255987, PubMed=9634230,
Gordon S.T., Brosch R., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborns J., Quartes M., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Complete genome sequence ",
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Brdmann;
MBDINE=97284492; PubMed=9139906;
Lefevre P., Braibant M., de Wit L., Kalai M., Roeper D.,
Groetzinger J., Delville J.-P., Peirs P., Ooms J., Huygen K.,
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphate-binding protein 2 precursor (PBP-2)
PSTS2 OR WY0932C OR WT0959 OR WTCY08D9.07.
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Submitted (JAN-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 NYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDT 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
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                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21128732; PubMed=11234002;

Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,

Cole S.T., Eiglmeier K., Parkhill J., Churcher C., Harris D.,

Mungall K., Bacham D., Brown D., Chillingworth T., Connor R.,

Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,

Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,

Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,

Barrell B.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:1007-1011(2001).
-!- FUNCTION: Required for binding-protein-mediated phosphate transport (By similarity)
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006059; SBP_bac_1.
Pfam; PF01547; SBP_bac_1; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Phosphate transport; Transport; Membrane; Lipoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.6%; Score 335.5; DB 1; Length 369; 28.9%; Pred. No. 1.9e-08; ive 50; Mismatches 159; Indels 59
                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corymebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
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22 369 PHOSPHATE-BINDING PROTEIN 3.
22 22 N-ACYL DIGYCERIDE (POTENTIAL).
369 AA; 37733 MW; 697DECBGGAB4B9AC CRC64;
                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphate-binding protein 3 precursor (PBP-3) (PstS-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Massive gene decay in the leprosy bacillus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE PSTS FAMILY.
                                                    369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL583924; CAC31050.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                       STANDARD;
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HSSP; P06128; 11XH.
Leproma; ML2095; -.
                                                                                                                                                                                                                       Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (By similarity)
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109; Conserv
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                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                    MYCLE
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Matches
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bishai W.;
    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 KGVST-LNLDGPTTAKIFNGTITVWNDPQ1QALNSGTDLPPTPISVIFRSDKSGTSDNFQ 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLWGPAFHERYPNVTITA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 NANGSGAGVTQFLNNETDFAGSDVPLNPSTGQPDRSAERCGSPAWDLPTVFGPIAITYNI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIGISFLDQA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 KYLDGASNGAWGK--GASETFNGGVGVGASGNNGTSALL---QTTDGSITYNEWSF---A 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SORGIGEAQLGNSSGNFILPDAQSIQAAAAGFASKTPANQAI-----SMIDGP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 QGTGSGAGIAQAAAGTVNIGASDAYLS----EGDMAAHK---GLMNIALAISAQQVNYNL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 VGKQLNMAQIITSAG----PDPVAİTTESVG---KTİAGAKİMGQGNDLVLDTSSFYRPT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APDGYPIINYBYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAV-VK 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 QPGSYPIVLATYEIVCSKXYPDATIGTAVRAFMQAAIGPGQEG--LDQYGSIFLFKSFQAK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 CGGGTNSSS - - SGAG-GTSGSVHCGGKKELHSSGSTAQENAMEQFVYAYVRSCPGYTLDY 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                        INDUCTION: ACCUMULATION OF PROTEIN IS ENHANCED UNDER PHOSPHATE STARVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
                                                                                                                                                                                                                                                                                                                                                                                                                           Tuberculist; Rv0932c; -.
InterPro; IPR006059; SBP bac_1.
Ffam, PF01547; SBP_bac_1; 1.
PRO$TIE; PS00013; PROXAR, LIPOPROTEIN; 1.
Phosphate transport; Transport; Membrane; Lipoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
PHOSPHATE-BINDING PROTEIN 2.
N-ACYL DIGHYCERIDE (POTENTIAL).
97F5116CEE9B3B5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.5%; Score 330.5; DB 1; Length 31.1%; Pred. No. 3.1e-08; Live 44; Mismatches 168; Indels
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086343; 0260794;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphate-binding protein 3 precursor (PBP-3)
PSTS3 OR PMOS2 OR RV0928 OR MT0955 OR MTCY21C12.22.
Mycobacterium tuberculosis.
                                                  STARVATION. SIMILARITY: BELONGS TO THE PSTS FAMILY.
                                                                                                                                                                                                                                                                                         EMBL; Z48056; CAA88137.1; -.
EMBL; Z95209; CAB08486.1; -.
EMBL; AB006581; AAK45206.1; -.
PIR; D70584; D70584.
'HSSP; P06128; 1IXH.
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23 370 PH
23 23 N-,
370 AA, 37864 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 31.1<sup>3</sup>
Matches 114; Conservative
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PST3 MYCTU
1D PST3 M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Pleischmann R.D., Alband D., Eisen J.A., England D., Hickey E.,
Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=H37RV;

MEDLINE=9829587; PubMed=9634230;

A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

B Badcock K., Basham D., Chillingworth T., Connor R.,

A Badcock K., Davin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Cliver S., Seeger K., Skalton S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

T Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Content J.;
"Three different putative phosphate transport receptors are encoded the Mycobacterium tuberculosis genome and are present at the surface of Mycobacterium bovis BCG.",
J. Bacteriol. 179:2900-2906(1997).
-!- FUNCTION: Required for binding-protein-mediated phosphate
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                                                                                                                                                MEDIINE=97000022; PubMed=8843165;
Braibant M., Lefevre P., de Wit L., Ooms J., Peirs P., Huygen K., Wattiez R., Content J.;
"Identification of a second Mycobacterium tuberculosis gene cluster encoding proteins of an ABC phosphate transporter.";
FEBS Lett. 394:206-212(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE=97284492, PubMed=9139906,
Lefevre P., Braibant M., de Wit L., Kalai M., Roeper D.,
Groetzinger J., Delville J.-P., Peirs P., Ooms J., Huygen K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FICORDIE).
-!- INDUCTION: By phosphate starvation.
-!- SIMILARITY: BELONGS TO THE PSTS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, Z95209, CAB08488.1; -.
EMBL, Z48057; CAA81138.1; -.
EMBL, AE006981; AAK45202.1; ALT_INIT.
PIR; H70583; H70583.
HSSP, P06128; 1IXH.
                                                                            SEQUENCE FROM N.A., AND INDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tuberculist, Rv0928; -.
InterPro, IPR006059; SBP bac_1.
Pfam; PF01547; SBP_bac_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Erdmann;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Probable)
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SNAKKISDAAVSLPV-----GQQPAAEQPHVPIAPGGPSQTG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAAPQIGATKPAATAKTTPQRPRGSDADAGSRAQSQYGFGDPPGGGALKGAVDAASDAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----QASQRGLGEAQ----LGNSSGNFL-LPDAQSIQAAAAGFASKTPANQAISMIDGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----QGPVQSQPGRRQEPAASATK---LHVADGLPARPVQPAVSATDLQTDTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 GTVATTPASSPVTLAETGSTLLYPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 QDVGGGSGACAPAPDESHWGL------THRDQGHDERIS------QTAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RD-----TPSLSAVAGPVTLSGSSSSSGRNSSSNSNTSTSSTSNGVTITSNVGVNGASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----DLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIRQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAGKITYRIKLEVSFKMRPAQPR----CGSK-----PPSGSPETG-----AGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVAAASPA--PAGISDQLSTPACP-----PEREPQ---AGKPRASGRAPAPGVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 VNIGASDAYLSEGDMAAHKGLMNIALAISAQQVNYNLPGVSEHLKLNGKVLAAMYQGTIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 KSPGFGTTVDFPAVPGAL-----GENGNGGMVTGCAETPGCV---AYIGISFLD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLGRTIQGRIARLQAAREALRAARHARVGAAMQPPPV------QARPVQGQSGQVPQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TWDDPQIAA -- LNPGVNLPGTAVVP -----LHRSDGSGDTFLFTQYLSKQDPEGWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 OERLMAARRAVVTMOWNTHLGRRGRSFAPLPTGGMSIATSAASSSTSSASSSSSMDG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478 ASAVAAQAPSSAMPTAAMAATMGSATIGSAATLPTAAVVSSAAAEGTQPSGLLLAGGRPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1783;
                                                                                                                                                                                                      mRNA processing; mRNA splicing.
CHLOROPLAST (POTENTIAL).
TRANS-SPLICING FACTOR RAA3.
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SER-RICH.
ALA-RICH.
ALA-RICH.
GLN-RICH.
ARG-RICH.
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POLY-ALA.
POLY-PRO.
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POLY-GLY.
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                                                                                                                                                           EMBL; AF310675; AAG40000.1; -.
EMBL; AF310674; AAG39999.1; -.
Chloroplast; Transit peptide; MENA
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343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 NIDGPTLAKIFNGSITQWNNPALQALNRDFTLPGERIHVVFRSDESGTTDNFQRYLQAAS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 GEAQLGNSSGNFLLPDAQSIQAAAAGFASKT---PANQAISMIDG----PAPDGYPIINY 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TMANIVISAGGD--PVAITIDSVGQTIAGATISGVGNDLVLDTDSFYRPKRPGSYPIVLA 313
                                                                                                                                                                                                                                                                                                                                                                                                              98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGISEFNGNOTDFGGSDVPLSKDEAAAAORRCGSPAWNLPVVFGPIAVTYNLNSVSS-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGIAQAAAGTVNIGASDAYLSEGDMAAHK-----GLMNIALAISAQQVNYNLPGVSEHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLNGKVILAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYLSKQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 NGAWGKGAG-----KSFQGGVGEGARGNDGTSAAAKNTPGSITYNEWSF---AQAQHL
                                                                                                                                                                                                                                                                                                                                                                 TGAGAGTVATTPASSPV-----TLAETGSTLLYPLFNLWGPAFHERYPNVTITAQGTGS
                                                                                                                                                                                                                                                                                                                                                                                                              TGGGA---TTGQASAKVDCGGKKTLKASGSTAQANAMTRFVNVFEQACFGQTLNYTANGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEGWGKSPGFGTTVDFPAVPGALGE--NGNGGMVTGCAETPGCVAYIGISFLDQASQRGL
                                                                                                                                                                                                                                                                                                                        Gaps
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SUBCELLULAR LOCATION: Chloroplast stroma.
DOMAIN: The N-terminal 453 amino acids are dispensable, while
C-terminal 630 amino acids are required for function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Required for trans-splicing of exons 1 and 2 of the chloroplast encoded psaA mRNA (a group II intron). May be requirer stability of the chloroplast RNA-protein complex in which is found.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydomonas reinhardtii.
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in chloroplast
                                                                                                                                                                                                                                                                                                                        38;
                          Phosphate transport; Transport; Membrane; Lipoprotein; Signal
                                                                                        PHOSPHATE-BINDING PROTEIN 3.
N-ACYL DIGLYCENIDE (POTENTIAL).
AAA - PSG (IN STRAIN ERDWAN).
Q -> A (IN STRAIN ERDMAN).
MISSING (IN STRAIN ERDMAN).
OH -> HD (IN STRAIN ERDMAN).
W; 7D557829A9118E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND CHARACTERIZATION.
STRAIN=137C / CC-125,
MEDIAIN=13C / CC-125,
PubMed=11285239;
Rivier C., Goldschmidt-Clermont M., Rochaix J.-D.;
Rivier C., Goldschmidt-Clermont M., Rochaix J.-D.;
"Identification of an RNA-protein complex involved in chlorogy group II intron trans splicing in Chlamydomonas reinhardtii."
EMBO J. 20:1765-1773 (2001)
                                                                                                                                                                                                                                                                           Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLP 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYEİVCSKYPDSQVGTAVKAFLQSTİGAĞQ--SGLGDNGYIPIP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Part of a 1700 kDa complex that includes the
                                                                                                                                                                                                                                                                                              ; Pred. No. 1.7e-07;
39; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Last annotation update)
Trans-splicing factor Raa3, chloroplast precursor
                                                                                                                                                                                                                                                                           DB 1;
1.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1783 AA
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Last annotation update
                                                                                                                                                                                                                                                                           Score 314;
    PROKAR LIPOPROTEIN; 1
                                                                       POTENTIAL.
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SIGNAL 1 22
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Best Local Similarity 30.8°
Matches 106, Conservative
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    PS00013;
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                                                                                                                                                                                                                                                                       POLAAVVAGYAAAGH----RHEPLLEALAGVALAKAGGAGGIGGGAAGAVPRGQAASELK 845
                                                                                                                                                                                                                                                                                                              RDQI-----BVYAEYQQRSEKV-----BTEYNNKAALEPVNPPKPP----- 802
GTVQAESAGAVGGDSSA----ELTDTPRVATAGEPNFMDLKBAARKLETGDQGASLAHFA 676
                                                                                                                                                                                      -----LLGRLSRYQPAGRDDGPAVLAPHARYSPAAYQAAAAAAQPQLLLAPLSL 789
                                                                                                                                                                                                                                                                                                                                                                                                                                      906 LWAYATLEQLPAAAPTPPPPPASAAAASTAPRAAESRPAAAPAPAFAEATATR--TPLLTAP 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MVPP---TGSP----GGGLPADTAAQLTSA------GREAAALSGDVAVKAASLG 884
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RSRLTFRAACVFLTALARLGYRGGAVTRLAAALAVWLARQLNTGAVTPRAKWKGTWLAAA
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Harris S.D., Hamer L., Sharpless K.E., Hamer J.E.;
"The Aspergillus nidulans sepA gene encodes an FH1/2 protein involved
in cytokinesis and the maintenance of cellular polarity.";
EMBO J. 16:3474-3483(1997).
                                                                                                                                                                                                                                -----LERLYAENPSA
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                                                                                                                                                 DGWNTFNLTLQGDVKRFRGFDNWEGDAA------TACEASLDQQRQWILHMAKL
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DISRUPTING THE GBD-DAD INTERACT
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STRAIN=FGSC 26;
MRDLIN=9522965; PubMed=7713416;
Marhoul J.F., Adams T.H.;
"identification of developmental regulatory genes in Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nidulans by overexpression.";
Genetics 139:537-547(1995).
-!- FUNCTION: INVOLVED IN CYTOKINESIS. OVEREXPRESSION RESULTS IN
                                                                                                      GTVRAPTOTAAPAASPAATAPALASTPFATPAAAP----LPEPPEVVAARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
SIMILARITY: Contains 1 GTPase-binding (GBD) domain.
SIMILARITY: Contains 1 Formin homology 1 (FH1) domain.
SIMILARITY: Contains 1 Formin homology 2 (FH2) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
REVISIONS TO 143-153; 207; 1071-1109 AND 1644.
Hamer L., Harris S.D., Sharpless K.E., Hamer J.E.;
submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                SAAMAKQAQYVAQLHVWARREHPTYEDIVG------
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DOMAIN: DRFS ARE REGULATED
RHO-GTP ACTIVATES THE DFRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1658 FH2. (FOCULED COIL (POTENTIAL).
1566 COILED COIL (POTENTIAL).
1610 DAD. ARG/LYS-RICH (BASIC).
1109 PAPPEPPERGREPPPPPRGGGFG
1109 -> LESPSGTGAFWHYPRASSPSTWWFNRSTSAAASYWWCI
C (IN REF. 3).
1476 D -> V (IN REF. 3).
1504 V -> L (IN REF. 3).
1504 V -> L (IN REF. 3).
1504 V -> L (IN REF. 3).
4, 197355 MW; 192136DEZEF2A75B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 NAGLSHHSSSTVDSSTNSRMSIDQASIHSSLSSNTRGSSYISTDGSSRTTLPSHSNDRSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --LHRSDGSGDTFLFTQYLSKQDPEGWGKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 GPA---PDGYPIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWESLAPPSSAAGSRSSRYSKRSSIQSVDFGADIDPSLLSTSAGPITSIPFESLSTDTQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.7%; Score 189; DB 1; Length 1790;
larity 19.4%; Pred. No. 0.36;
Conservative 145; Mismatches 430; Indels 38
-:- SIMILARITY: Contains 1 Formin homology 3 (FH3) domain.
-:- SIMILARITY: Contains 1 DRF autoregulatory (DAD) domain.
-:- SIMILARITY: BELONGS TO THE FORMIN HOMOLOGY FAMILY. BNI1
SUBFAMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWEQAA---AEAVQRA----RDSVDDIRVARVIEQDMAVDSAGKIT-
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EMBL, L36341; AAA33306.1; ALT_SEQ.
InterPro; IPR003104; FH2.
Ffam, PF02181; FH2; 1.
SMART; SM00498; FH2; 1.
Cell division; Coiled coil.
EMAIN
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DLKTQID---QVESTAGSLQGQWRGAAGTA----AQAAVVRFQEAANKQKQELDEIST
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Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
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Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Barrell B.G.;
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Nature 409:1007-1011(2001).
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16: Sp.Dacterlap:*	) 	Corynebacterinea	terinea
	N CX	NCBI_TAXID=1767; [1]	D=1767;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Q49590 mycobacteri	Q49589 mycobacteri	Q8paf7 xanthomonas	Q8ynj0 anabaena sp	Q8pm56 xanthomonas	O9yg56 aeropyrum p	Q8yyd9 anabaena sp	Q8u247 pyrococcus	Q49675 mycobacteri	Q9ryz6 deinococcus	Q55199 synechocyst	Q8z9s9 yersinia pe	Q8pm55 xanthomonas	Q56833 xanthomonas	Q8ky90 edwardsiell	Q9am16 edwardsiell
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		Match Length DB	374	374	363	392	363	373	347	375	336	403	383	346	339	339	346	314
	*	Match	30.6	27.8	9.5	9.5	9.3	9,1	0.6	9.0	8.9	8.8	8.8	8.7	9.8	9.8	8.5	8.4
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Q8PAF6 Q32484 Q8XXD3 Q8XXZ73 Q8ZKX5 Q8ZKX5 Q8ZKX5 Q9ZKX8 Q9ZKX8 Q9ZKX8 Q97ZX8 Q50043 Q50043 Q50043 Q50099 P73785 Q5771 Q50099 P73785 Q8ZKN6 Q8	PRT; reated) ast sequent; ast sequent; inobact inobact inocae; sequent; A7F2D A7F2D Score 1	Pred, No. 5.6 5; Mismatches
	X;  01, Cre 123, Las 123, Las 13, Las 14, Actin 0bacteria ed=890006 0.1, De Si encoding 11, 14, 235-2, 14, 235-2, 14, 235-2, 16, 268 MW; 0.6%; Sc	o 40
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SEQUENCE 363 AA
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  SEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYL 250
                        SKODPEGWGKSPGFFTVDFPAVPGALGENGNGGWVTGCAETPGCVAYIGISFLDQASQR 310
                                                                                                                          SKODPDGWGKSPGFGTTVAFPTVPGALGENGNGGWVTGCADTPGCVAYIGISFLDQAQGK 258
                                                                                                                                                                GLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGYPIINYEYAIV 370
                                                                                                                                                                                           GLGEAQLANASDKYLLPDAKSIQAAAAGFASKTPANQAISLINGPAPDGYPIVNYEYAIV 318
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                                                                                                                                                                                                                                                       NNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALIATIS 424
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"Duplication of gnenes encoding the immunodominant 38 kDa antigen improbacterium intracellulare.";

FEMS Microbiol. Lett. 144:235-240(1996).

EMBL; X95538; CAA64783.1; --.

EMSL; R96128; LAS4.

InterPro; IPR060659; SBP_bac_1.

Pfam; PF01547; SBP_bac_1; 1.

SEQUENCE 374 AA; 37998 MW; 45796D4E9F6F513D CRC64;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Last annotation update)
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; Pred. No. 7.2e-64;
33; Mismatches 49;
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STRAIN=ATCC 35761;
MEDLINE=97055782; PubMed=8900068;
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76.5%;
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Best Local Similarity 76.5%
Matches 267; Conservative
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 33333 / NCPPB 528;

MEDLINE-2202145; PurbMcd=12024217;

A Guaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Alves L.M.C., do Amaral A.M., Bertolini, M.C., Camargo L.B.A.,

Alves L.M.C., do Amaral A.M., Derreiro A.M.C., Ferro M. I.E.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciqpina L.P.,

Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Ratia J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Ratia J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

Antina E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Spinola L.A.F., Takita M.A., Sana J.A.D., Silva C., de Souza R.F.,

A Trindade dos Santos M., Tudfin D., Tsai S.M., White P.F.,

Trindade dos Santos M., Tuffil D., Tsai S.M., White P.F.,

Mormanian M.C., Kitalina J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Setubal J.C., Kitajima J.P.,
"Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.";
Nature 417:459-463(2002).
EMBL, AE012554, AAM40822.1; -.
InterPro, IPR006059; SBP_bac_1.
Pfam; PF01547; SBP_bac_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPD
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                                                                                                                                                                                                                                                                                 Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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                                                                              Created)
Last sequence update)
Last annotation update)
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                                                                                                                     01-OCT-2002 (TrEMBLrel. 22, Last sequence l-VAR-2003 (TrEMBLrel. 23, Last annotation ABC transporter phosphate binding protein. PSTS OR XCC1527.
    363
    PRT;
                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gamm
Xanthomonadaceae; Xanthomonas.
PRELIMINARY;
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Xanthomonadaceae; Xanthomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                               LFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIGISFL 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 IINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALIA 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                   RYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDM-AAHKGLMNIALAISAQQVN 184
                                                                                                                                                                                                                                                                                                                                                                                                    CGGOOGSDNTATODGSSGTAKDATASSPAKLDLGGNVSLTGAGASFPAPLYASWFTDLNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 VFTKHLAAVSPE-WKSKVGEGKSVSWPV---GVGGKGNEGVTAQIKQTQGAIGYIEYGY-
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                            MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria; Gammaproteobacteria, Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                               29;
                                                                                                                                                                                                                                                                                                                                         DB 16; Length 392;
                                                                                                                                                                                                                               "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."; DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                       Match 9.5%; Score 482.5; DB 16; Length Local Similarity 33.7%; Pred. No. 8.5e-17; nes 124; Conservative 64; Mismatches 151; Indels
                                                                                                       Anabaena sp. (strain PCC 7120).
Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc
                                  01-MAR-2002 (TrEMBirel. 20, Created)
01-MAR-2002 (TrEMBirel. 20, Last sequence update)
01-MAR-2003 (TrEMBirel. 23, Last sannotation update)
Phosphate-binding periplasmic protein of phosphate ABC
                                                                                                                                                                                                                                                                                                                  392 AA; 41343 MW; FF28D266FB59C950 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
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             392 AA
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01-0CT-2002 (TrEMBLrel. 22, Last sequence
01-MAR-2003 (TrEMBLrel. 23, Last annotatio
ABC transporter phosphate binding protein.
PSTS OR XAC1577.
Xanthomonas axonopodis (pv. citri).
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              PRT;
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InterPro, IPR06059; SBP bac_1.
Pfam, PF01547, SBP bac_1; 1.
Complete proteome.
SEQUENCE 392 AA, 41343 MW, I
                                                                                                                                                                                                                                                                                                                                                               Matches 124; Conservative
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             PRELIMINARY;
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                                                                                                                            NCBI_TaxID=103690;
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            Q8YNJO,
Q8YNJO,
01-MAR-2002 (
                                                                                 transporter
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                                                                                                                                                   SEQUENCE
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MEDINE=2202145; PubMed=1202417;

MEDLINE=22022145; PubMed=1202417;

A da Silva A.C.R., Ferro J.A., Reinach C.S., Furlan L.R.,

A duaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

RA alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

RA cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Formighleri B.F., Franco M.C., Grappio C.C., Gruber A.,

RA Faria J.B., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

RA Stuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos D.H.,

Martins E.C., Machadus J.M., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machadus J.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Drindade Gos Santos M., Tamura R.B., Teixeira B.C., Tezza R.I.D.,

RA Trindade Gos Santos M., Tuuffi D., Tsai S.M., White F.F.,

RA Trindade Gos Santos M. Julfi D., Tsai S.M., White F.F.,

RA Troncities M. C., Kitajima J.P.;

R. "Comparison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16; Length 363;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
373AA long hypothetical phosphate-binding periplasmic protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.3%; Score 469.5; DB 16; Best Local Similarity 32.2%; Pred. No. 3.5e-16; Matches 119; Conservative 69; Mismatches 157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 417:459-463 (2002).
EMBL; AB011790; AAM36445.1; -.
InterPro; IPR006059; SBP_bac_1.
Pfam; PF01547; SBP_bac_1.
Complete proteome.
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                                                                SEQUENCE FROM N.A.
STRAIN=306 / ATCC 13902
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NCBI_TaxID=92829
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Q8U247
              RAT RAT RAY OR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR RAY DR R
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                                                                                                                                                                                                                                            Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jun-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi Bosoyama A., Fukui S., Nagai Y., Nishijiama K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Kl.";
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MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
ABC phosphate transport system phosphate-binding periplasmic ALL0911.
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
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HSSP; P06128; 1IXG.
Interbro; IPR006059; BB-bac_1.
Interbro; IPR006051; SBP-dom1.
Pfam; PP01547; SBP-bac_1; 1.
PROSITE; PS01037; SBP_BACTERIAL_1; 1.
                                                                                                                                                                                                          MEDLINE=99310339; PubMed=10382966;
                                            Desulfurococcaceae; Aeropyrum
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Matches 112; Conservative
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                                                                                                                                            SEQUENCE FROM N.A.
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                                                                  NCBI_TaxID=56636;
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RA Yasuda M., Tabata S.;

RY Yasuda M., Tabata S.;

RT 'Complete genomic sequence of the filamentous nitrogen-fixing RT 'Complete genomic sequence of the filamentous nitrogen-fixing RL DNA Res. 8:205-213 (2001).

RE EMBL: AP003584; BAB72868.1; -.

RICHARD PROGROSS9; SEP_bac_1.

RE EMBL: PF01547; SEP_bac_1: 1.

RE EMBL: PF01547; SEP_bac_1: 1.

RE EMBL: AP00589; SEP_bac_1: 2.

RE Complete proteome.
                                                                                                                                                            nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                         Length 347;
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Weiss R.B., Dunn D.M., Robb P.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ABCI0212; AAAB1127.1, -..
InterPro; IPR06659; SBP_bac_1.
Pfam; PF01547; SBP_bac_1; 1.
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13.0%; Pred. No. 1.6e-15;
ve 69; Mismatches 142; Indels
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Last sequence update)
Last annotation update)
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32.1%; Pred. No. 1.7e-15;
tive 58; Mismatches 149;
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Matches 114; Conservative 6
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2003 (TrEMBLrel. 23,
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hes 115; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pyrococcus furiosus
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GCVAYIGISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMID 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPAPDGYPIINYEYAIVNNRQK----DAATAQTLQAFLHWAITDGNKASFLDQVHFQPLP 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SANAGAYPIASFTYLIFYKDQKYGNRTEAQAKALKNLLTYVVTSGQQ--YNEGLDYAKLP 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLCGTSPVFGSLDAPLTKPRHTRRRMKKTLLGLSALVMISTAAAQGAITGA--GASFPYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDWAAHKG-LMN
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                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN=R1;

MEDLINE=20036896; PubMed=10567266;

Minte O., Eisen J.A., Heidelberg J.F., Hickey B.K., Peterson J.D.,

Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,

Moffat K.S., Qin H., Jiang L., Pamphille W., Crosby M., Shen M.,

Wamathevan J.J., Lam P., McDonald L., Iterback T., Zalewski C.,

Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,

Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                        01-MAY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Phospipate ABC transporter, periplasmic phosphate-binding protein.
DRA0157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
8.8%; Score 445; DB 16; Length 403;
Best Local Similarity 31.5%; Pred. No. 6.9e-15;
Matches 118; Conservative 60; Mismatches 157; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                              Deinococcus radiodurans.
Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcus.
NCBI_TaxID=1299;
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                                                                                                                 403 AA
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R HSSP; P06128; AAF12207.1; -. R HSSP; P06128; 11XG.

TITRR, DRAD157; -. InterPro; IPR006059; SBP_bac_1. Pfan; PF01547; SBP_bac_1. Complete proteome.
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                                                                                                                   PRELIMINARY;
294 IDGP 297
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                                                                                            249
                                                                                                                                                                                                                          248 IEENLKIVALKONAKAGNFVKPTEETIKAAVAAFIPDPAEGYKEDIRQLLNAPGENSYP 307
                                 LSKQDPEGWGKSPGFGTTVDFPA--VPGALGENGNGGMVTGCAETPGCVAYIGISFLDQA 307
SGAGIAQAAAGTVNIGASD------AYLSEGDMAAHKGLMNIALAISAQQVNYNLPG 189
                                                                                                                                                                                                                                                                                           SORGLGEAQLGNSSGNFLLPDAQSIQAAAGFASKTP----ANQAISMIDGPAPDGYP 361
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                                                                                                                                                                                                                                                                                                                                                                                        IINYEYAIV----NNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKL 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 VATTPASSPVTLAETGSTLLYPLFNLWGP-AFHERYPNVTITAQGTGSGAGIAQAAAGTV
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                                                                                            VSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQY
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                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=96084954; PubMed=7489918;
Doukhan L., Predich M., Nair G., Dussurget O., Mandic-Mulec I.,
Cole S.T., Smith D.R., Smith I.;
"Genomic organization of the mycobacterial sigma gene cluster.";
Gene 165:67-70(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          049675 PRELIMINARY; PRT; 336 AA.
049675;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
PabB.
Mycobacterium leprae.
Mycobacterium leprae.
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TAXID=1769;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
8.9%; Score 452; DB 2; Length 33
Best Local Similarity 40.1%; Pred. No. 2.4e-15;
Matches 122; Conservative 22; Mismatches 74; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGYPIINYEYAI 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyalima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 CGSKPPSG-SPETGAGAGTVATT--PASSPVTLAETGSTLLYPLFNLWGPAFHERYPNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 CGGGGGGDTAQTGGGDATTTTAADAFASKVSLTGAGASFPAPLYQGWFVALNQAVPNLE
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                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence analysis of the genome of the unicellular cyanobacterium Synchopoytis sp. strain PCC6603. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136
                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=96127529; PubMed=8590279;
MEDLINE=96127529; PubMed=8590279;
Kaneko T., Tanaka A.,
Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium Sequence analysis of the genome of the unicellular cyanobacterium Sequence positions positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 383;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 AA; 40023 MW; 1A1E2CE2EDCFBFFC CRC64;
                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Phosphate-binding periplasmic protein precursor (PBP)-
PSTS OR SLL0680.
                                                                                                  Bacteria; Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 8.8%; Score 444; DB 16; Similarity 31.5%; Pred. No. 7.3e-15; DB; Conservative 69; Mismatches 152;
                                                                                    Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro, IPR006059; SBP_bac_1.
Pfam; PF01547; SBP_bac_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D64001; BAA10341.1; -. HSSP; P06128; 2ABH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 383 AA;
                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                  STRAIN=PCC 6803;
Tabata S.;
                                                                                                            NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                    Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108;
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MEDLIKE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21470413; PubMed=11586360; ParkINI=20.92 / Biovar Orientalis; MEDLINE=21470413; PubMed=11586360; ParkInil J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., ParkInil J., Wene B.W., Thomson N.E., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Feltwell T., Mamlin N., Holroyd S.D., Jagels K., Karlyshev A.V., Feltwell T., Wallin N., Holroyd S., Jagels K., Karlyshev A.V., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTVATTPAS -- SPVTLAETGSTLLYPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAA
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                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
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                                 U1-MAR-2003 (TrEMBLrel. 20, Last sequence update)
Putestive phosphate-binding periplasmic protein (Periplasmic PSTS OR YPO4117 OR Y4131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 346;
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Hypothetical protein; Complete proteome.
SEQUENCE 346 AA; 36710 MW; 0C9B4FCF55D3C181 CRC64;
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8.7%; Score 440; DB 16;

Best Local Similarity 33.4%; Pred. No. 1e-14;

Matches 110; Conservative 60; Mismatches 141;
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J. Bacteriol. 18:4601-4611(2002).
EMBL; AJ414160; CAC93566.1;
EMBL; ABC14014; AAM87673.1;
EMBL; AF01575; IPR006659; SBP_bac_1.
Pfam; PF01547; SBP_bac_1; 1.
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346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 413:523-527(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=632;
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RESULT 15
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REQUENCE FROM N.A.

REQUESTRAIN=306 / ATCC 13902 / XV 101;

REDINE=20202145; PubMed=20204217;

REDINE=20202145; PubMed=20204217;

RA Gasilora A.C.R., Ferro J.A., Refrach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Gamarotte G., Cannavan F., Candaro J., Chambergo F., Clapina L.P.,

RA Camarotte G., Cannavan F., Ferrollini M.C., Camargo L.B.A.,

RA Camarotte G., Cannavan F., Ferrollini M.C., Camargo L.P.,

RA Camarotte G., Ferrella A.U.S., Ferrellini R.C., Caparago L.P.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Ferrol M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Formighieri E.F., Franco M.C., Madeira A.M.B.N., Mayaki C.Y., Moon D.H.,

RA Martins E.C., Machado M.J., Madeira A.M.B.N., Mayaki C.Y., Moon D.H.,

RA Martins E.C., Machado M.J., Madeira A.M.B.N., Mayaki C.Y., Moon D.H.,

RA Sphnola L.A.F., Takita M.A., Tamura R.B., Teixaira B.C., Tezza R.I.D.,

RY Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RY Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RY Comparison of the genomes of two Xanthomonas pathogens with differing RT host specificities ".

RMES, AB01730; AAN36466.1; -.

RMES, AB01730; AAN36466.1; -.

RIMERPRO, IPRO0659; SPP bac.];

RY TIGRAPAM; TIGRROBES J. 1.

RY TIGRAPAM; TIGRROBES J. 1.

RY TIGRAPAM; TIGRROBES J. 1.

RY TIGRAPAM; TIGRROBES J. 1.

RY TIGRAPAM; TIGRROBES J. 1.

RY TIGRAPAM; TIGRROBES J. 1.

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RY TIGRAPAM; TIGRROBES J. 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YNLPGVSE-HLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 PLFTOYLSKODPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIGISF 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 IDQASQRGLGEAQLGNSSGNFILPDAQSIQAAAAGFASKTPANQAISMIDGFAPDGYPII 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFKWRPAQPRCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLWGPAFH 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 ERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISAQQVN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FNFTNYLSKVNPD-WKGKVGEGTAVQWPT---GIGGKGNEGVAAYVKQIKGGIGYVELSY 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 SFKTRLA-------VGVLAASLALCAQAADVTGA--GASFIYPVMSKWS-ADY 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                  Gammaproteobacteria; Xanthomonadales;
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                                                                                (TremBLrel. 22, Created)
(TremBLrel. 22, Last sequence update)
(TremBLrel. 23, Last annotation update)
                                             339 AA.
                                           PRT;
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                                                                                                                                                                                                  Bacteria; Proteobacteria; Gamm
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                               Xanthomonas axonopodis (pv.
                                                                                                                                        Phosphate binding protein. PHOX OR XAC1578.
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                                           PRELIMINARY;
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SEQUENCE 339 AA:
                                                                                                                                                                                                                                         NCBI_TaxID=92829;
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01-OCT-2002 (
01-MAR-2003 (
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                                         Q8PM55
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RESULT 13
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65 SFWARPAQPRCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLWGPAFH 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---ALONKMAYTAMKNAAGKFVQPSDETFAAANSADWGSSKDFYLVMTNAAGDNAWPIT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 ERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISAQQVN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLFTQYLSKQDPBGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIGISF 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 ENFTNYLSKVNPD-WKSKVGEGTAVQWPT---GIGGKGNEGVAAYVKQIKGGIGYVELSY 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AINFILVQKKRRAPTGLKATLDFFRWVYSKGDAQA--KQLDYVPLPDALVTQIBAYMAT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 YNLPGVSE-HLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDT
                                                                                                                                                                                                                                            4 SFKTRLA--------VGVLAASLALCAQAADVTGA--GRSFIYPVMSKWS-ADY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gammaproteobacteria; Enterobacteriales;
                                                                                                                                Xanthomonas oryzae.
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.6%; Score 435; DB 2; Length 33 ilarity 32.0%; Pred. No. 1.7e-14; Conservative 60; Mismatches 156; Indels
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SEQUENCE FROM N.A.
Tan Y.P., Leung K.Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR005673; Peri-phosph.
InterPro; IPR006059; SBP bac_1.
Pfam; PF01547; SBP bac_1; 1.
TIGREAM; TIGR00975; 3a0107303; 1.
SEQUENCE 339 AA; 35632 MW; B15241EF192ED72E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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339
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PRT;
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Enterobacteriaceae, Edwardsiella.
NCBI_TaxID=636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23, Phosphate-binding protein.
                                  01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2003 (TrEMBLrel. 23,
Phosphate binding protein.
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PRELIMINARY;
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                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                             NCBI_TaxID=347;
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Best Local Simil
Matches 115; (
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32; Gaps 14;
                                                                                                                    87 GAGAGTV--ATTPASSPVTLAETGSTLLYPLFNLWGPAFHERYPNVTITAQGTGSGAGIA 144
                                                                                                                                                                                          145 QAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISAQQVNYNLPGV-SEHLKLNGKVLAA 203
                                                                                                                                                                                                              69 QIIANIVDFGASDAPLSDEKLAA-DGLFQFPTVIGGVVMAVNLPGVKSGELTLDGFTLGD 127
                                                                                                                                                                                                                                                           204 MYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYLSKQDPEGWGKSPG 263
                                                                                                                                                                                                                                                                                264 FGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIGISFLDQASQRGLGEAQLGNSSGN 323
                                                                                                                                                                                                                                                                                                                                                       324 FLLPDAQSIQAAAAG-----PASKTPANQAISMIDGPAPDGYPIINYEYAIVNNRQ-KD 376
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
8.5%; Score 431; DB 2; Length 346;
Best Local Similarity 35.7%; Pred. No. 2.9e-14;
Matches 121; Conservative 50; Mismatches 136; Indels
EMBL; AF248495; AAM45393.1; -.
SEQUENCE 346 AA; 36264 MW; 9DA3670A6684B821 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  377 AATAQTLQAFLHWAITDGNK-ASFLDQVHFQPLPPAVVK 414
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Search completed: November 21, 2003, 16:08:17 Job time : 50.3698 secs

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10-OCT-2000; 2000WO-US28095
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                                                                                                                                                                                                                                                              Mycobacterium tuberculosis
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                   07-OCT-1999;
                                                                                                                                                                                                                                                                             Key
Binding-site
                                                                                                                                                                                                                                                                                                                                 12-APR-2001
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        11268
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7086.58
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M. tuberculosis an M. tuberculosis an M. tuberculosis an Polypeptide encode M. tuberculosis an M. tuberculosis an Mycobacterium spc. Mycobacterium spc. M. tuberculosis an M. tuberculosis an
                                November 21, 2003, 15:50:31 ; Search time 32.6333 Seconds (without alignments) 2621.664 Million cell updates/sec
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                                                        2737
1 MHHHHHTAASDNFQLSQGG.....RAPVEADAGGGQKVLVRNVV
                                                                                              1107863
    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                             Total number of hits satisfying chosen parameters:
                                                                                    1107863 segs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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AAW73765
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/label= Histidine_tag
/note= "Nickel chelating region used to aid
purification of the protein"
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AAG83275
ABB94246
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AAU74588
AAO22142
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/note= "In frame
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(first entry)

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Antigen; M.tuberculosis protein; immunotherapy; tuberculosis; diagnosis;
                        M. tuberculosis antigen clone hTcc#1 protein sequence
                                                                                Mycobacterium tuberculosis
                                                                                                                                                                                                         (CORI-) CORIXA CORP.
 24-MAR-1999
                                                                                                                                                                                                                                  Alderson MR,
                                                                                                                                                   20-MAY-1998;
                                                                                                      WO9853075-A2
                                                                                                                                                                         05-MAY-1998;
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                                                                                                                            26-NOV-1998
                                                           nfection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKTLINATQLLKLLAKLAELVAAAIADIISDVADIIKGILGEVWEFITNALNGLKELWDK 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGMGGPVGMGGMHPSSGASKGTTTKKYSEGAAAGTEDAERAPVEADAGGGQKVLVRNVV 539
                                                                                                                                                The sequence represents Mycobacterium tuberculosis fusion protein, TDRAL2-HTCC#1 and includes a His tag at the N-terminus to aid purification. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSLEYFEKALEELAAAFPGDGWLGSAADKYAGKNRNHVNFFQELADLDRQLISLIHDQAN
                                                                                                                                                                                                                                                                                                                                                                MHHHHHHTAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSLEYFEKALEELAAAFPGDGWLGSAADKYAGKNRNHVNFFQELADLDRQLISLIHDQAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHHHHHTAASDNRQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD
                                                                                                                                                                                                                                                                                                                                                                                              NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASLPALAGIGGGSGFGGLPSLAQVHAASTRQALRPRADGPVGAAAEQVGGQSQLVSAQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASLPALAGIGGGSGFGGLPSLAQVHAASTRQALRPRADGPVGAAAEQVGGQSQLVSAQGS
                                             Σ.
                                                                                         infections in mammals using fusion of heterologous antigens -
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0
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                                             Dillon DC,
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                                                                                                                                                                                                                                                                                                   100.0%; Score 2737; DB 22;
100.0%; Pred. No. 1.2e-219;
iive 0; Mismatches 0;
                                             PD,
                                             McNeil1
                                             RL,
                                                                                         Vaccinating against Mycobacteria proteins comprising combinations
                                                                                                                         Claim 17; Fig 8; 168pp; English
                                            Houghton
 99US-0158425
                                                                                                                                                                                                                                                                                                                           Conservative
                    (CORI-) CORIXA CORP.
                                                                  WPI; 2001-290576/30
                                            Reed S,
                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                            543 AA;
 07-OCT-1999;
                                                                                        Vaccinating
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                                            Skeiky Y,
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Skeiky YAW;

Dillon DC,

Campos-Neto A,

98US-0073010. 98WO-US10407

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This sequence represents an immunogenic portion of a Mycobacterium tuberculosis antigen of the invention. The polypeptides are useful for immunotherapy to treat or prevent tuberculosis (especially in humans), e.g. they can be included with an acceptable carrier in pharmaceutical compositions or included in vaccines, and administered to induce protective immunity in a patient against M. tuberculosis. Tuberculosis a chronic, infectious disease generally caused by M. tuberculosis is a chronic, infectious disease generally results in serious complications and death. Pasion proteins containing the artigen, or DNA molecules can similarly be included with an acceptable carrier in pharmaceutical compositions or in vaccines and administered as above. The polypeptides are also useful for diagnosis of tuberculosis, by contacting dermal cells with at least one polypeptide and detecting an immune response (especially induration) on the patient's skin. Inhibiting the spread of tuberculosis requires vaccination and accurate diagnosis, since antibiotic therapy may not be effective due to the existence of an asymptomatic but contagious stage and to patient non-compliance. The polypeptides overcome concerns of safety and efficacy of current vaccination with live bacteria (usually Bacillus Calmette-Guerin) and care of ensitivity and specificity of existing diagnostic techniques.
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                                                                                                      Polypeptide comprising immunogenic Mycobacterium tuberculosis antigen - useful for immunisation against M. tuberculosis infection to treat or prevent tuberculosis, and in diagnosis of tuberculosis
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                                                                                                                                                                                                                                                       Claim 2; Page 87-88; 100pp; English.
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99.78;
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WPI; 1999-045314/04.
N-PSDB; AAX01177.
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Matches 39
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AAW73765 standard; Protein; 392

AAW73765;

AAW73765 ID AAW7 XX AC AAW7 XX RESULT 2

Length 392;

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Query Match
Best Local Similarity
Matches 391; Conserv
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                            241 GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA 300
                                                           507
                                                                                 STRQALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKY 360
                                                                                                                                                                                                                                                                                                                          Antigen; M.tuberculosis protein; immunotherapy; tuberculosis; diagnosis;
     GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA
                                                         STRQALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated Mycobacterium tuberculosis antigens - used to develop products for the prevention, treatment and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                M. tuberculosis antigen clone hTcc#1 protein sequence
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                                                                                                                SEGAAAGTEDAERAPVEADAGGGQKVLVRNVV 539
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                                                                                                                                                                                                               AAW73655 standard; Protein; 392 AA
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                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA
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                                                                                                                   148 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA
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                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tuberculosis, Mycobacterium infection, gene therapy, anti bacterial, immunostimulant, clone hTcc.
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                                                           Indels
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Score 1963; DB 20;
Pred. No. 3e-155;
0; Mismatches 1;
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     71.78;
99.78;
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                                                              Conservative
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N-PSDB; AAS12487.
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4059 /label= Peptide_4 /note= "Used for T-cell epitope mapping"	5372 /Jabel= Peptide_5 /note= "Used for T-cell epitope mapping"	6685 /label= Peptide 6 /note= "Used for T-cell epitope mapping"	7998  /label= Peptide_7  /nabel= "Used for T-cell epitope mapping"   9211	/label= Peptide_8 /note="Used for T-cell epitope mapping" 105, 124	/label= Peptide_9 /note= "Used for T-cell epitope mapping"	11813/ /note= "Used for T-cell epitope mapping" 131150	/label= Peptide_11 /note= "Used for T-cell epitope mapping" 144163	<pre>/label= Peptide_12 /note= "Used for T-cell epitope mapping" 157176</pre>	/label= Peptide_13 /note= "Used for T-cell epitope mapping"	//sy /locte= Peptide_14 /note= "Used for T-cell epitope mapping" 183202	<pre>/label= Peptide 15 /note= "Used for T-cell epitope mapping" 156215</pre>	/label= Peptide_16 /note=_"Used for T-cell epitope mapping"	/Jabel= Peptide_17 /Jabel= Peptide_17 /note="Used for T-cell epitope mapping"	/label= Peptide 18 /label= Peptide 18 /note= "Used for T-cell epitope mapping"	735-1294  /Jacels   Peptide 19  /note= "Used for T-cell epitope mapping"	248267 /Jacel= Peptide_20 /note= "Used for T-cell epitope mapping"	261280 /label= Peptide_21 /note= "Head for T-cell enitone manning"	) ) ) 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	<pre>/note= "Used for T-cell epitope mapping" 287.306</pre>	/label= Peptide_23 /note= "Used for T-cell epitope mapping"	300319 /label= Peptide_24 /note= "Used for T-cell epitope mapping"	25 Treall enitone	) 1 1 1	/race= "Used for T-cell epitope mapping" 339358	/label= Peptide 27 /note= "Used for T-cell epitope mapping" 352371
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cc encoding them. The invention describes compounds and methods for the diagnosis of tuberculosis. The compounds callest one immunogenic portion of the compounds comprise at least one immunogenic portion.	encoding such polypepti	or mytobacterium intection in parients and biologic compounds of the invention and antibodies directed Mycobacterium proteins may be used in vaccines for Mycobacterium infontion The middle of all a fortion of the middle of all a fortions and the middle of all a fortions and the middle of all a fortions are all and the middle of all a fortions and a fortions are all a fortions and a fortions are all a fortions and a fortion and a for		Sequence 392 AA; Query Match 71	Similarity 99.7%; Pred. No. 38-15; 1; Conservative 0; Mismatches 1; Indels	OY 148 MSRAFIIDPTISAIDGIYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA 207 	Qy 208 DKXAGKNRHVNPFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT 267	268	Db 121 YIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIAD 180	OY 328 IISDVADIIKGILGEVWEFITNALNGLKELWDKLTGWYTGLFSRGWSNLESFFAGVPGLT 387		Db 24.1 GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA 300	301 STRQALRPRADGPVGAAAAEQVGGSQCLVSAQGSQGWGGPVGMGGNHPSSGASKGTTTKKY	OY 508 SEGAAAGTEDAERAPVEADAGGGOKVLVRNVV 539  OH	00 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	RESULTS AAUO1882 ID AAUO1882 standard; Protein; 392 AA.	XX AC AAU01882; XX	-AUG-2001 (fi	tuberculosis antigen HTCC#1/Mtb40.	KW HTCC#1; Mtb40; antigen; vaccine; tuberculosis; AIDS; KW acquired immunodeficiency disease.	AAA DS Mycobacterium tuberculosis. XX	y Locatio ptide 1.20 /label=	ptide		ין Peptide 2746 יין /label= Peptide 3 יין /note= "Used for T-cell epitope mapping"

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The sequence represents Mycobacterium tuberculosis HTCC#1 (also known as Mtb40), an M. tuberculosis antigen. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease, AIDS.
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              /note= "Used_for_T-cell epitope mapping" | 25..38 | /label= Peptide_29 | /note= "Used for T-cell epitope mapping" | 33..39 | /label= Peptide_30 | /label= Peptide_30 | /label= Peptide_30 | /note= "Used for T-cell epitope mapping" |
 /label= Peptide_28
/note= "Used for T-cell epitope mapping"
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N-PSDB; AAS03773.
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This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and selecting a polymucleotide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. Species. The method of the invention is useful for detecting M. Toperae infection. The method reduces the number of potential new targets and protective antigens for new drugs and vaccine compositions to treat and prevent mycobacterial diseases, particularly protein from Mycobacterium tuberculosis, and Mycobacterium leprae requence represents a marker protein from Mycobacterium tuberculosis, and Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLBFVRPVAVDLT 120
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                                                                                                                                                                                                                                                                                                                                  Mycobacterioses; survival; virulence; protective antigen; vaccine; mycobacterial disease; tuberculosis; leprosy.
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Mycobacterium leprae.
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                                                                                                                 300
                                                                                                                                                                             507
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                                                        447
181 IISDVADIIKGTLGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and
                                                                                                              241 GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA
                                                                                                                                                                                                                                   301 STROALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKY
                                                        GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA
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                                                                                                                                                                                                                                                                                                  539
                                                                                                                                                                                                                                                                                                                                     361 SEGAAAGTEDAERAPVEADAGGGQKVLVRNVV 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTCC#1 antigenic protein.
                                                                                                                                                                                                                                                                                                     SEGAAAGTEDAERAPVEADAGGGQKVLVRNVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE29714 standard; Protein; 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-MAR-2001; 2001US-275837P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to fusion proteins containing at least two Mycobacterium species antigons, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigons which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and
                                                                                                                                                                                                                                                                                   241 GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA
                    1 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGLLYSSLEYFEKALEELAAAFFGDGWLGSAA
                                                                                  YIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIAD
                                                                                                                                                      121 YIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIAD
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                                                               DKYAGKARNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT
                                                                                                                                                                                            IISDVADIIKGILGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLT
                                                                                                                                                                                                                          IISDVADIIKGTLGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusion protein, antigen; serological sensitivity, immune response; tuberculosis; infection; vaccine; MTB40; HTCC #1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTB39 antigen and MTB32A antigen from useful for eliciting immune response in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium species MTB40 (HTCC #1) protein
                                                                                                                                                                                                                                                                                                                                                                                        SEGAAAGTEDAERAPVEADAGGGQKVLVRNVV 539
                                                                                                                                                                                                                                                                                                                                                                                                                     SEGADAGTEDAERAPVEADAGGGGKVLVRNVV 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE17578 standard; Protein; 392 AA.
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2001US-265737P.
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01-FEB-2001;
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Gaps

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Score 1963; DB 23; Length 392; Pred. No. 3e-155; 0; Mismatches 1; Indels 0

Query Match Best Local Similarity 99.7%; Matches 391; Conservative

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         useful for eliciting an immune response in a mammal, e.g., human, mamusided with BGC. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polymucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a non-human animal. Sequences of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for interadermal skin test. The present sequence is Mycobacterium species MTB40 (HTCC #1) protein.
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tuberculosis infection. Sequences of the invention are
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HTCC#1(TM-1) protein sequence"
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Pred. No. 3e-155;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tuberculosis antigen HTCC#1(TM-1)
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                                                                                                                                                                                                                                                           71.7%;
99.7%;
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                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                               392 AA;
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Best Local Simil
Matches 391; C
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Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is Mycobacterium tuberculosis HTCC#1(TM-1)
representing HTCC#1 (an M. tuberculosis antigen) lacking the first
transmembrane domain and includes a His tag at the N-terminus to aid
purification. Compositions comprising at least 2 heterologous antigens,
as a fusion protein, and vectors expressing the fusion proteins are used
as a fusion protein, and vectors expressing the fusion proteins are used
as a fusion protein by Mycobacteria. The compositions contain at least 2
against infection by Mycobacteria. The compositions contain at least 2
individuals infected with tuberculosis, a disease frequently affecting
patients with acquired immunodeficiency disease, AIDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384 PGLTGATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   444 VHAASTRQALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGCMHPSSGASKGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 VHAASTRQALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                      MĽ;
                                                                                                                                                                                                                                                                                                                                                               fusion
                                                                                                                                                                                                                                                                    Lodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 408;
                                                                                                                                                                                                                                                                                                                                                         Vaccinating against Mycobacteria infections in mammals using proteins comprising combinations of heterologous antigens
                                                                                                                                                                                                                                                                      DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                  Dillon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1941; DB 22;
Pred. No. 2.1e-153;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       504 TKKYSEGAAAGTEDAERAPVEADAGGGOKVLVRNVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 TKKYSEGAAGTEDAERAPVEADAGGGOKVLVRNVV
                                                                                                                                                                                                                                                                  McNeill PD,
                                   /note= "In frame STOP codon"
                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Fig 9a; 168pp; English.
                                                                                                                                                                                                                                                                    Houghton RL,
                    /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.7%;
Matches 391; Conservative
                                                                                                                                           10-OCT-2000; 2000WO-US28095
                                                                                                                                                                             99US-0158338
                                                                                                                                                                                                                                                                                                    2001-290576/30.
                                                                                                                                                                                                                                  (CORI-) CORIXA CORP
Misc-difference 405
                                                                                                                                                                                                                                                                  Skeiky Y, Reed S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  408 AA;
                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS03777
                                                                       WO200124820-A1
                                                                                                                                                                             07-OCT-1999;
                                                                                                                                                                                              07-OCT-1999;
                                                                                                       12-APR-2001
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RESULT 10 AAU01887

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The sequence represents Mycobacterium tuberculosis fusion protein, HTCC#1(1-149) TDH9-HTCC#1(161-392) and includes a His tag at the HTCC#1(1-149). TDH9-HTCC#1(161-392) and includes a His tag at least 2 N-terminus to aid purification. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease,
                                                                                                                          443
                                                                                                                                                                                                        503
                                                                                                                                                                                                                                             368
LTYIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAI
                                                                                                                                                         249 PGLTGATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQ
                                           3 6 ADIISDVADIIKGILGEVWEFITNA--LNGLKELWDKLTGWVTGLFSRGWSNLESFFAGV
                                                                             189 ADIISDVADIIKGTLGEVWEFITNAKLLNGLKELWDKLTGWVTGLFSRGWSNLESFFAGV
                                                                                                                        PGLTGATSCLSQVTGLFCAAGLSASSCLAHADSLASSASLPALAGIGGGSGFGGLPSLAQ
                                                                                                                                                                                                        444 VHAASTRQALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTT
                                                                                                                                                                                                                                          309 VHAASTRQALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lodes ML;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccinating against Mycobacteria infections in mammals using proteins comprising combinations of heterologous antigens
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C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTCC#1(1-149)-TbH9-HTCC#1(161-392); antigen; vaccine;
AIDS; acquired immunodeficiency disease; His Tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region used
                                                                                                                                                                                                                                                                                          539
                                                                                                                                                                                                                                                                                                                      369 TKKYSEGAAAGTEDAERAPVEADAGGGGKVLVRNVV 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M. tuberculosis antigen HTCC#1 fusion protein #2.
                                                                                                                                                                                                                                                                                        504 TKKYSEGAAAGTEDAERAPVEADAGGGOKVLVRNVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3..8
/label= Histidine_tag
/note= "Nickel_chelating
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU01903 standard; Protein; 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= OTHER
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99US-0158425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-290576/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reed S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200124820-A1
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07-0CT-1999;
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Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                          384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDKLILEGAKKGLEFVRPVAVD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is Mycobacterium tuberculosis HTCC#1(TM-1) representing HTCC#1 (an M. tuberculosis antigen) lacking all the transmembrane domains and includes a His tag at the N-terminus to aid purification. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease, AIDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKYAGKNRNHVNFFQELADLDROLISLIHDQANAVQTTRD--ILEGAKKGLEFVRPVAVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccinating against Mycobacteria infections in mammals using fusion proteins comprising combinations of heterologous antigens
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                                                                                                                                                                                                                                                                                                                                                                                         /note= "These residues are deleted to form the HTCC#1(TM-2) protein sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.9%; Score 1941; DB 22; Length 408; 98.7%; Pred. No. 2.1e-153; ive 0; Mismatches 1; Indels 4;
                                                                                                                                                                                                                                                                                          1..8
/label= Histidine tag
/note= "Nickel chelating region used to aid
purification of the protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dillon DC,
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                                                                                                                                                                   HTCC#1(TM-2); antigen; vaccine; tuberculosis; AIDS;
acquired immunodeficiency disease; His Tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= OTHER
/note= "In frame STOP codon"
                                                                                                                          M. tuberculosis antigen HTCC#1(TM-2)
                                                                                                                                                                                                                                                                    Location/Qualifiers
      standard; Protein; 408 AA
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                                                                                                                                                                                                                              Mycobacterium tuberculosis.
                                                                                    (first entry)
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Best Local Similarity 98.7
Matches 391; Conservative
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N-PSDB; AAS03778.
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Binding-site
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    AAU01887
                                             AAU01887;
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148 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328 IISDVADIIKGILGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVFGLT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSGAFIIDPTLKAIEAWHALLGIGVPNDGGVLYSSLSFFEKALEHLAAAFPGDGWLGSAA
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es 248; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                      369 QLAQPIQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGF 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PALAGIGGGSGFGGLPSLAQVHAASTRQALRPRADGPVGAAAEQVGGQSQLVSAQGSQGM 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PALAGIGGGSGFGGLPSLAQVHAASTRQALRPRADGPVGAAAAEQVGGQSQLVSAQGSQGM 728
                                                                                                                  89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --NATOLLKLLAKLAELVAAAIADIISDVADIIKGILGEVWEFITNALNGLKELWDKLTG
                                                                                                                                        DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WVTGLFSRGWSNLESFFRAGVPGLTGATSGLSQVTGLFGAAGLSASSGLAHADSLASSASL
                                                                                           148 MSRAFIIDPTISAIDGLYDLLGIGIPNOGGILYSSLEYFEKALEELAAAFPGDGWLGSAA
                                                                                                                 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGPVGMGGMHPSSGASKGTTTKKYSEGAAAGTEDAERAPVEADAGGGOKVLVRNVV 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGPVGMGGMHPSSGASKGTTTKKYSEGAAAGTEDAERAPVEADAGGGQKVLVRNVV
                                                                   384;
                                              Length 788;
                                                                     Indels
                                                                                                                                                                                      YIPVVGHALSAAFQAPFCAGAMAVVGGALAYLV-----
                                             Score 1718; DB 22;
Pred. No. 2.2e-134;
2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M. tuberculosis and M. leprae marker protein #53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU05402 standard; Protein; 394
                                                                                                                                                                                                                                                                                                                                  --ITLITII---
                                             62.8%;
49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                     Conservative
                                                        Similarity
                     788 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-APR-2003
                                                                     384;
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                                                                                                                                        802
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                                                                                                                                                                                       268
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                      Sequence
                                                                                                                                                               69
                                                                                                                                                                                                                                                                                                                                  301
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                                             Query Match
                                                                   Matches
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ABU05402
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AC ABU0
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DE M. t
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360

KYSEGAAAGTEDAERAPVEADAGGGQKVLVRNVV

Mycobacterioses; survival; virulence; protective antigen; vaccine; mycobacterial disease; tuberculosis; leprosy.

505

240

DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT 267

9

.; 3

Indels

46.1%; Score 1263; DB 23; 62.9%; Pred. No. 7.8e-97; iive 55; Mismatches 89;

Conservative

Length 394;

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This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and selecting a polymucleotide sequence that is highly conserved in both genomes with no conterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. Tuberculosis or M. leprae infection. The method reduces the number of potential new targets and protective antigens for new drugs and vaccine compositions to treat and prevent mycobacterial diseases, particularly tuberculosis and Mycobacterium tuberculosis and Mycobacterium ieprae infention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mycobacteria by a comparative genomic analysis of the sequences Mycobacterium tuberculosis and M. leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genes for survival
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; Page 224-225; 874pp; English
                                                                                                                                                                                                                                                                                                                                            22-FEB-2001; 2001US-270123P.
Mycobacterium tuberculosis.
Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying and selecting
                                                                                                                                                                                                                                                                                                                                                                                                                      (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-759885/82.
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                                                                                                              WO200274903-A2
                                                                                                                                                                                                                                                                  32-FEB-2002;
                                                                                                                                                                                        26-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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The sequence represents Mycobacterium tuberculosis fusion protein, HTCC#1(184-392)-TDH9-HTCC#1(1-129) and includes a His tag at the N-terminus to aid purfication. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease,
128′YIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIAD 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 DVADIIKGILGEVWEPITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 DVADIIKGILGEVWEFITUNALNGLKELWDKLTGWYTGLFSRGWSNLESFFAGVPGLTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lodes ML;
                                                                                                                                                                                                                                                                     tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fusion
                                                   328 IISDVADIIKGILGEVWEFIINALNGLKELWDKLTGWVTGLFSRGWSNLESF 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccinating against Mycobacteria infections in mammals using proteins comprising combinations of heterologous antigens -
                                                                                                                                                                                                                                                                                                                                                                                3..8
/label= Histidine tag
/note= "Nickel chelating region used to aid
purification of the protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                   HTCC#1(184-392)-TbH9-HTCC#1(1-129); antigen; vaccine;
AIDS; acquired immunodeficiency disease; His Tag.
                                                                                                                                                                                                                                   M. tuberculosis antigen HTCC#1 fusion protein #1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 38.7%; Score 1060; DB 22; Best Local Similarity 100.0%; Pred. No. 1.7e-79; Matches 209; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= OTHER
/note= "In frame STOP codon"
                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                         AAU01902 standard; Protein; 744 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Skeiky Y, Reed S, Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; Fig 10; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .0-OCT-2000; 2000WO-US28095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0158338
                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-290576/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAS03790.
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                                                                                                                                                                                                                                                                                                                                                                 Key
Binding-site
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07-OCT-1999;
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                                                                                                                                                                                                       29-AUG-2001
                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                       AAU01902;
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                                                                                                                          AAU01902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIAD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALBELAAAFPGDGWLGSAA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             representing the first transmembrane domain of HTCC#1 (an M. tuberculosis antigen) and includes a His tag at the N-terminus to aid purification: Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodefliciency disease, AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFERALEELAAAFPGDGWLGSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lodes ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccinating against Mycobacteria infections in mammals using fusion proteins comprising combinations of heterologous antigens
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.7%; Score 1168; DB 22; Length 242; 99.6%; Pred. No. 3.3e-89; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                   region used to aid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is Mycobacterium tuberculosis HTCC#1(1-223),
                                                                                                                                                                       HTCC#1(1-223); antigen; vaccine; tuberculosis; AIDS;
acquired immunodeficiency disease; His Tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McNeill PD,
                                                                                                                                                                                                                                                                                                                                                /label= OTHER
/note= "In frame STOP codon"
                                                                                                                                                                                                                                                                                /label= Histidine tag
/note= "Nickel chelating reg
purification of the protein"
                                                                                                                                         M. tuberculosis antigen HTCC#1(1-223).
                                                                                                                                                                                                                                                    Location/Qualifiers
                                             AAU01883 standard; Protein; 242 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 7a; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reed S, Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0158338
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000WO-US28095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0158425
                                                                                                                                                                                                                      Mycobacterium tuberculosis.
                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 99.6
es 231; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-290576/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAS03774.
                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                               WO200124820-A1
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Binding-site
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                                                                                                           29-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 897
                                                                            AAU01883;
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Best Local S
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               RESULT 13
                               AAU01883
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390

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The sequence represents Mycobacterium tuberculosis fusion protein, HTCC#1(184-392) TDH9-HTCC#1(1-200) and includes a His tag at the N-terminus to aid purification. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease,
                                                        510
                                                                         129 QALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKYSEG 188
450
                     SGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAASTR
SGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAASTR
                                                        QALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKYSEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lodes ML
                                                                                                                                                                                                                                                                                                                                       HTCC#1(184-392)-TbH9-HTCC#1(1-200); antigen; vaccine; tuberculosis; AIDS; acquired immunodeficiency disease; His Tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccinating against Mycobacteria infections in mammals using fusion proteins comprising combinations of heterologous antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                3..8
/label= Histidine_tag
/note= "Nickel chelating region used to aid
purification of the protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dillon DC,
                                                                                                                                                                                                                                                                                                         M. tuberculosis antigen HTCC#1 fusion protein #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= OTHER
/note= "In frame STOP codon"
                                                                                                                  539
                                                                                                                                             189 AAAGTEDAERAPVEADAGGGOKVLVRNVV 217
                                                                                                                511 AAAGTEDAERAPVEADAGGGOKVLVRNVV
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 12; 168pp; English.
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                                                                                                                                                                                                                     AAU01904 standard, Protein; 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-2000; 2000WO-US28095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0158338.
99US-0158425.
                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-290576/30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 815 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200124820-A1
                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-OCT-1999;
07-OCT-1999;
                                                                                                                                                                                                                                                                               29-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                  AAU01904;
391
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Length 815;

38.7%; Score 1060; DB 22;

Query Match

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                                                                                                                                                      128
                                                                                         68
                                                                                                                                                                                                        331 DVADIIKGILGEVWEFITNALNGLKELMDKLTGWVTGLFSRGWSNLESFFAGVPGLTGAT
                                                                                 9 DVADIIKGILGEVWEFIINALNGLKELMDKLIGWVIGLFSRGWSNLESFFAGVPGLTGAT
                                                                                                                                            69 SGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAASTR
                                                                                                                                                                                        451 QALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKYSEG
                                                                                                                         391 SGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLFSLAQVHAASTR
                               Gaps
                               ô
                               Indels
              1.9e-79;
hes 0;
              Pred. No. 1.9 ; Mismatches
                                                                                                                                                                                                                                                   511 AAAGTEDAERAPVEADAGGGQKVLVRNVV 539
                                                                                                                                                                                                                                                                               189 AAAGTEDAERAPVEADAGGGGKVLVRNVV 217
                                                                                                                                                                                                                                                                                                                            Search completed: November 21, 2003, 16:03:21 Job time : 33.6333 secs
100.0%; Pre-
                               Conservative
             Best Local Similarity
Matches 209; Conser
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ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EMB PC Compatible
COMPUTER: EMB PC Compatible
COMPUTER: EMB PC Compatible
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,009
FILING DATE: 05-MAY-1998
CLEASOFFICATION NUMBER: 31.392
REGISTRATION NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 210121.441C1
TELEFAM: 206-622-4900
TELEFAM: 206-622-4900
TELEFAM: 206-622-4900
TELEFAM: 392 amino acids
FENGTH: 392 amino acids
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Fatent No. 6555653
GENERAL INFORMATION:
APPLICANT: Alderson, Mark
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
CORRESPONDENCES: 144
CORRESSEE: SEED and BERRY
STREET: 6300 Coumbia Center, 701 Fifth Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.7%; Score 1963; DB 4; ilarity 99.7%; Pred. No. 4.5e-166; Conservative 0; Mismatches 1;
US-09-620 412C-325
US-09-528 419-325
US-09-508 419-325
US-09-606-421B-354
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Best Local Similarity
Matches 391; Conserv
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CITY: Seattle
STATE: Washingt
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TOPOLOGY: lin
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                    GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Minimum DB Maximum DB

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348 ALQQLAQPTQGTTPSSKLGGLWXTVSPHRSP-----ISNWVSMANNHMSMTNSG 396
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                                       288 ODAAAMFGYAAATATATLIPPEEAPEMTSAGGILEQAAAVEEASDTAAANQLMNNVPQ
                                                                             -LGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS F
TITLE OP INVENTION: DIAGNOSIS OF CHLAMYDIAL I
FILE REPERBNCE: 210121.46907
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING BATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FASTSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 337, Application US/09620412C Patent No. 6448234 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 585
7 TYPE: PRT
ORGANISM: Chlamydia trachomatis
US-09-620-412C-337
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Best Local Similarity
Matches 231; Conserv
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US-09-620-412C-337
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Patent No. 6544522

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Alderson, Mark

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

TITLE OF INVENTION: Pusion Proteins of Mycobacterium tuberculosis Antigens

TITLE OF INVENTION: and Their Uses

TITLE OF INVENTION: WIGHER: US/09/223,040

CURRENT APPLICATION NUMBER: US/09/223,040

CURRENT FILING DATE: 1998-12-30

NUMBER OF SEQ. ID NOS: 10

SOFTWARE: Patentin Ver. 2.1

SEQ. ID NO 2

LENGTH: 729
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                                                                                                    XIPVVGHALSAAFQAPFCAGAMAVVGGALAXLVVKTLINATQLIKLLAKLAELVAAAIAD
                                                                                                                                                                                    181 IISDVADIIKGTLGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLT
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                                                                                                                                                                                                                                       GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA
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DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT
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ORGANISM: Artificial Sequence
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Best Local Similarity 40.0
Matches 221; Conservative
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364 LINNTSEKHGGGAFVTKEISQTYTSDVETIPGIT-PVHGETVITGNKSTGGNGGGVCTKR 422
                                                          LAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAASTRQALRPRADGPVGAAAEQVGG 470
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                                                                                                                                             464 ASAATSTPKS----APVSTALSTPSSSTVSSLTLLAASSQASPATSNKETQDPNAD 515
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                                                                                                                                                                                                               Sequence 337, Application US/09598419
Patent No. 6565856
GENERAL INFORMATION:
TELE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DAGGES OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: UNMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARES FASES OF Windows Version 3.0/4.0
SEQ ID NO 337
LENGTH: 585
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26.9%; Score 737.5; DB 4;
Best Local Similarity 38.8%; Pred. No. 5.5e-57;
Matches 231; Conservative 40; Mismatches 174;
                                                                                    423 LALSNLQSISISGNSAAENGGG-----
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TYPE: PRT
ORGANISM: Chlamydia trachomatis
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OSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKYSEGAAAGTEDAERAPVEAD
                                           464 ASAATSTPKS ----APVSTALSTPSSSTVSSLTLLAASSOASPATSNKETODPNAD
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                                                                                                                                                                                                                                                                   FOR TREATMENT AND INFECTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 26.6%; Score 728; DB 4; Best Local Similarity 37.8%; Pred. No. 3.8e-56; Matches 228; Conservative 49; Mismatches 186
                                                                                                                                          Sequence 353, Application US/09620412C
Sequence 353, Application US/09620412C
Patent No. 6446234
GENERAL INFORMATION:
FAPPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFP;
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT APPLICATION NUMBER: US/09/620,412C
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
IENGTH: 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Chlamydia trachomatis
US-09-620-412C-353
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US-09-620-412C-353
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Matches
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                                                                                                                                                                                                                                                                                                                         26.6%; Score 728; DB 4; Length 583; 37.8%; Pred. No. 3.8e-56; ive 49; Mismatches 186; Indels 140;
            Sequence 313, Application US/09598419
Fatent No. 656556
GENERAL INFORMATION:
APPLICANT: Scholler, John
TITLE OF INVENTION:
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: 10121.46906
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT APPLICATION NUMBER: US/09/598,419
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, ORGANISM: Chlamydia trachomatis
US-09-598-419-353
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Matches 228; Conservative
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; Sequence 333, Application US/09620412C; Patent No. 6448234

RESULT 7 US-09-620-412C-333

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                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 175;
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.46907
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILIG DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: PastSEQ for Windows Version 3.0/4.0
SEQ ID NO 333
                                                                                                                                                                                                                                                                                                                                                                               Length 518;
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APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C6
CURRENT APPLICATION NUMBER: US/09/598,419
NUMBER OF SEQ IN NOS: 357
                                                                                                                                                                                                                                                                                                                                                                         ; Score 722.5; DB 4;
; Pred. No. 9.9e-56;
44; Mismatches 132;
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Local Similarity 37.3%;
hes 209; Conservative 4
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                                                                                                                                                                                                                                                                                                                            US-09-620-412C-333
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US-09-598-419-333
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Query Match
Best Local Similarity
Matches 149; Conserv
                                                          Local Similarity
les 149; Conserv
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       US-09-556-877-196
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                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                 171 GIPNQGGILYSSLE----YFEKALBELAAAFPGDGWLG-----SAADKYAGKURNHV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 NFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLTYIPVVGHALSA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 AFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIADIISDVADIIKG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 ILGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLTGATSGLSQVTG 398
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                                                                                                                                                                                                                                                                                                                                                        TKSGGTRTGNVTLAEGPPAEF-----LVPRGSMSRAF-IIDPTISAIDGLYDLLGI 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 CPPEPKELNFSRVETSSSTTFTETIGEAGAEXIVSCNASFTKFTNIPTTDTTTPTNSNSS 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 VLSFMTRSGTEGSLTLSEI--KMTGEGGAIFSQG----ELLFTDLTSLT-IQNNLSQLSG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --LFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAASTRQALRPR 456
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                                                                                                                                                                                                       1 MHHHHHHAASDNFQLSQGGQFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD
                                                                                                                                                                      Indels 175;
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APPLICANT: Bhatia, Ajay
APPLICANT: Bhatia, Ajay
APPLICANT: Bhatia, Ajay
APPLICANT: Fling, Steve
APPLICANT: Fling, Steve
APPLICANT: Maisonneuve, Jeff
APPLICANT: Maisonneuve, Jeff
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: COMPOSITIONS OF CHLAMYDIAL INFECTION FILE REFERENCE: 210121.469C5
CURRENT APPLICATION NUMBER: US/09/556,877
CURRENT APPLICATION NUMBER: US/00-04-19
NUMBER OF SEQ ID NGS: 305
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                 Length 518;
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                                                                                                                                 26.4%; Score 722.5; DB 4; 37.3%; Pred. No. 9.9e-56; ive 44; Mismatches 132;
SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ ID NO 333 LENGTH: 518
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Patent No. 6432916
GENERAL INFORMATION:
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                                                          TYPE: PRT
ORGANISM: Chlymadia trachomatis
                                                                                                                                                  Similarity 37.3
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ORGANISM: Chlamydia
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US-09-556-877-196
                                                                                  ; UKGANISM: C11.1
US-09-598-419-333
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LENGTH: 525
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Best Local S
Matches 209
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Length 525;
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; Sequence 196, Application US/09620412C
; Sequence 196, Application US/09620412C
; GENERAL INPORMATION:
    APPLICANT: Steven P. Fling
    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
    FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: PRESEDE for Windows Version 3.0/4.0
; SEQ ID NO 196
; LENGTH: 525
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Sequence 196, Application US/09598419

Patent No. 665886

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C6
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     DB 4;
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Score 717.5; DB 4;
Pred. No. 2.8e-55;
6; Mismatches 13;
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Pred. No. 2.8e-55;
6; Mismatches 13
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  26.2%;
llarity 71.3%;
Conservative
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ilarity 71.3%;
Conservative
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286 AGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIADIISDVADIIKGILGEVWE
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Parent No. 6565856

GENERAL INFORMATION

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Scholler, John

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND

TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

FILE REFERENCE: 210121.469C6

CURRENT APPLICATION NUMBER: US/09/598,419

CURRENT FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 357

SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.9%; Score 709.5; DB 4; Best Local Similarity 37.5%; Pred. No. 2.3e-54; Matches 214; Conservative 53; Mismatches 187;
                                                                                                                                                                                                                                                                                                                                      3460 KRLSYHGYSSASKGYTVSSQASGAHGHKFLL 490
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LENGTH: 715
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ORGANISM:
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                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 321, Application US/09620412C
Patent No. 6448234
GENERAL INPORMATION:
ASPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.464926
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                     Length 525;
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                                                                                                                                                                                   Score 717.5; DB 4;
Pred. No. 2.8e-55;
6; Mismatches 13;
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FactSEQ for Windows Version 3.0/4.0
SEQ ID NO 196
LENGTH: 525
TYPE: PRT
ORCANISM: Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                    TKSGGTRTGNVTLAEGPPAEFPLVPRGSP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-321
                                                                                                                                                                                   26.2%;
71.3%;
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Best Local Similarity 71.3
Matches 149; Conservative
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260 ---MIFNGRLS-IVDENYESVYDSMDLSRGKAE-----QLILSIETTNDGQLDSNWQ 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56
                                                                                         346 FITNALN-----GLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLTGATSGLSQV
                                                                                                                                                         ---SSLNTSLLSPPHYGYOGLW--TPNWITTTYTITLNNNSS----APTSATSIAEO-
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                                                                            454 RPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSS-----GASKGTTTKKY 507
                                                                                                            61 NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ 120
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397 TGLFGAAGLSASSGLAHADSLASSASLP---ALAGIGGGSGFGGLPSLAQVHAASTRQAL
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Patent No. 6565856
GENERAL INPORMATION:
APPLICANT: SCHOLLEY, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: LAGGOGE
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 329
                                                                                                                                                                                                                                                                                                                                           GENERAL INCORNATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: 0209/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
ENGTH: 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 25.9%; Score 708; DB 4; Length 715; Best Local Similarity 70.7%; Pred. No. 3.1e-54; Matches 152; Conservative 13; Mismatches 26; Indels
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                                                                                                                                                            508 SEGAAAGTEDAERA-PVEADAGG--GOKVLV 535
                                                                                                                                                                                                    460 KRLSYHGYSSASKGYTVSSQASGAHGHKFLL 490
                                                                                                                                                                                                                                                                                                      Sequence 329, Application US/09620412C
Patent No. 6448234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Chlamydia trachomatis
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; ORGANISM: Chlamydia trachomatis
US-09-598-419-329
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US-09-620-412C-329
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61 NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ 120
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                                                                                                                                                            1 MHHHHHHTAASDNFQLSQGGQGFAIPIGQAMAIAGQIK----LPTVHIGPTAFLGLGVVD 56
                                                                                                          1 MHHHHHHAASDNFQLSQGGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD
                                                        24;
     Length 715;
                                                        Indels
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Score 708; DB 4;
Pred. No. 3.1e-54;
13; Mismatches 26
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ne : 12.3667 secs
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25.9%;
ilarity 70.7%;
Conservative 13
Query Match
Best Local Similarity
Matches 152; Conserv
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Sequence 324, App. Sequence 324, App. Sequence 136, App. Sequence 132, App. Sequence 129, App. Sequence 1876, Ap. Sequence 1876, Ap. Sequence 1884, Ap. Sequence 1864, Ap. Sequence 1864, Ap. Sequence 1864, Ap. Sequence 1864, Ap. Sequence 1864, Ap. Sequence 1864, Ap. Sequence 1864, Ap. Sequence 1864, Ap. Sequence 1863, Ap. Sequence 1863, Ap. Sequence 1863, Ap. Sequence 1863, Ap. Sequence 1863, Ap. Sequence 1863, Ap. Sequence 1863, Ap. Sequence 1863, Ap. Sequence 1863, Ap. Sequence 1863, Ap. Sequence 1863, Ap. Sequence 1863, Ap. Sequence 1863, Ap. Sequence 1852, App. Sequence 1852, App. Sequence 1853, Ap. Sequence 1853, Ap. Sequence 1853, Ap. Sequence 1853, Ap. Sequence 1853, App.

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November 21, 2003, 16:08:22 ; Search time 21.0222 Seconds (without alignments) 4680.740 Million cell updates/sec
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2737
1 MHHHHHHTAASDNFQLSQGG......RAPVEADAGGGQKVLVRNVV 539
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               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                666188 seqs, 182559486 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match
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Perfect score:
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ALIGNMENTS

US-09-073-009-138

Sequence 118, Application US/09073009
Patent No. US2001001288A1
GRERAL INPORMATION:
APPLICANT: Alderson, Mark
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
ITILE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
ADDRESSES: SEED and BERRY
STREET: 6300 Coumbia Center, 701 Fifth Ave.
CITY: Seattle
STATE: Washington
COUNTY: Washington
COUNTY: Washington
COUNTY: Bathole
STAME: Pabable FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pc-Dos/Ms-Dos
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,009
FILING DATE: 06-MAY-1998
CLASSIFICATION NUMBER: 31,392
REFERENCE/DOCKET VUMBER: 210121.441C1
TELECOWNUNICATION INFORMATION:
NAME: MARK, David J.
REGISTRATION NUMBER: 210121.441C1
TELECOWNUNICATION INFORMATION:
TELECOMPUTS FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LINFORMATION FOR SEQ ID NO: 138:
TYPE: amino acids
TYPE: amino acids

Sequence 29, Appl Sequence 51, Appl Sequence 53, Appl Sequence 2, Appl Sequence 16, Appl Sequence 18, Appl Sequence 65, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 337, Appl Sequence 337, Appl Sequence 337, Appl Sequence 337, Appl Sequence 337, Appl Sequence 337, Appl Sequence 333, Appl

US-09-073-009-138 US-09-793-366-138 US-10-080-170-610 US-10-080-170-610 US-10-080-170-610 US-10-080-170-63 US-10-080-170-63 US-10-098-732A-18 US-09-841-28 US-09-841-132-333 US-09-841-132-353 US-09-841-132-353 US-09-841-132-333

1963 1963 1963 1963 1263 1263 809 809 809 809 739 739 737.8

Sequence 138, App

Sequence 138,

9

387

447

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61 DKYAGKARNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT 120
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APPLICANT: Skeiky, Yasir

APPLICANT: Guderian, Jeffrey

APPLICANT: Guderian, Jeffrey

APPLICANT: Guderian, Jeffrey

APPLICANT: Griss Corporation

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

CURRENT APPLICATION NUMBER: US,10/098,732A

CURRENT PILING DATE: 2003-04-29

PRICR FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 80

SCOTTANE: PALCHIN Ver. 2.1
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ORGANISM: Mycobacterium tuberculosis
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US-10-098-732A-29
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Best Local Similarity 99.73
Matches 391; Conservative
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APPLICANT: John, Shyian
APPLICANT: Lodes, Michael
APPLICANT: Lodes, Michael
APPLICANT: Lodes, Michael
APPLICANT: Corrixa Corporation
ITILE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
ITILE OF INVENTION: Of Tuberculosis
ITILE OF INVENTION: Of Tuberculosis
ITILE OF INVENTION WINBER: US, 69/793, 306
CURRENT APPLICATION NUMBER: US, 60/185, 037
PRIOR APPLICATION NUMBER: US, 60/185, 037
PRIOR APPLICATION NUMBER: US, 60/223, 828
PRIOR APPLICATION NUMBER: US, 60/225
PRIOR APPLICATION NUMBER: US, 60/223, 828
NUMBER OF SEQ ID NOS: 164
SEQ ID NOS: 164
SEQ ID NO 038
LENGTH: 392
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
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99.7%; Pred. No. 4.9e-145;
iive 0; Mismatches 1;
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Similarity 99.7%; Pred. No. 4.9e-145;
91; Conservative 0; Mismatches 1;
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; Patent No. US20020098200A1
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Ovendale, Pamela
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Best Local Similarity 99.7
Matches 391; Conservative
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                       TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-073-009-138
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GENERAL INFORMATION:
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US-09-793-306-138
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Best Local Simil
Matches 391;
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TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYDAXIS OR TITLE OF INVENTION: TEATHENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495.0218
CURRENT PERIOR TON NUMBER: US/10/080,170
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
SOFTWARE: PALENTIN VEY: 2.1
SEQ ID NOS: 652
SOFTWARE: PALENTIN VEY: 2.1
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GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA 447
                                  241 GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA 300
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71.7%; Score 1963; DB 16;
Best Local Similarity 99.7%; Pred. No. 4.9e-145;
Matches 391; Conservative 0; Mismatches 1;
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; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-610
                                                                                                                                                                                                                                                                                                   Sequence 610, Application US/10080170 Publication No. US20030129601A1 GENERAL INFORMATION:
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US-10-080-170-610
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US-10-080-170-53
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Sequence 53, Application US/10080170 Publication No. US20030129601A1

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APPLICANT: Reed, Steven G.
APPLICANT: Seed, Steven G.
APPLICANT: Seed, Y. Masir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neco, Antonio
APPLICANT: Campos-Neco, Antonio
APPLICANT: Campos-Neco, Antonio
APPLICANT: Campos-Neco, Antonio
APPLICANT: Campos-Neco, Antonio
APPLICANT: Campos-Neco, Antonio
APPLICANT: Campos-Neco, Antonio
APPLICANTON: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: 1999-04-07
FILE OF INVENTION NUMBER: US 08/918,112
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1998-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 IISDVADIIKGILGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLT 387
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APPLICANT: COLE, S.T.

TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR

TITLE OF INVENTION: COMPARATIVE MYCOBACTERIOSES.

TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR

TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES.

FILE REFERENCE: 03495,0218

CURRENT APPLICATION NUMBER: US/10/080,170

PRIOR APPLICATION NUMBER: 60/270,123

PRIOR APPLICATION NUMBER: 60/270,123

PRIOR FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 652

SOFTWARE: PATENTIN VET. 2.1
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46.1%; Score 1263; DB 16;
Best Local Similarity 62.9%; Pred. No. 2.1e-90;
Matches 248; Conservative 55; Mismatches 89;
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Patent No. US20020009459A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Mycobacterium leprae
US-10-080-170-53
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LENGTH: 394
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
FILE REPERENCE: 014058-009020US
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                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
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                                                                                                                                                                                                                 29.6%; Score 809; DB 9; Length 729;
40.0%; Pred. No. 1.4e-54;
Live 69; Mismatches 170; Indels
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION UNMBER: US 09/223,040
PRIOR FLING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SSEQ ID NO 2
LENGTH: 729
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; Publication No. US20030147911A1
; GENERAL INFORMATION:
                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 221; Conserv
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US-10-359-460-2
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276 LSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIAD-IISDVAD 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TKSGGTRTGNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSASLVAAAQMWD----- 174
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; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
US-10-359-460-2
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Best Local Similarity 40.0%; Pred. No. 1.4e-54;
Matches 221; Conservative 69; Mismatches 170;
CURRENT APPLICATION NUMBER: US/10/359,460
CURRENT FILING DATE: 2003-02-05
PRIOR PELLING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FLING DATE: 1997-03-13
PRIOR PLING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR PILING DATE: 1997-10-01
PRIOR PILING DATE: 1997-03-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/056,56
PRIOR PILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.1
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US-10-058-732A-16

Gequence 16, Application US/10098732A

; Publication No. US20030175294A1
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ORGANISM: Artificial Sequence
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APPLICANT: Skeiky, Yaair
APPLICANT: Skeiky, Yaair
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Leishhania Antigen
FILE REFERENCE: 014058-012010/098,732A
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2001-04-29
FRIOR APPLICATION NUMBER: US 60/275,837
FRIOR PELING DATE: 2001-03-13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MHHHHHHTAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD
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US-10-098-732A-16
                                                                                                                                                                                                                                                                                                                                                                                                        92;
                                                                                                                                                                                                                                                                                                                                                                     29.6%; Score 809; DB 12; Length 729; llarity 40.0%; Pred. No. 1.4e-54; Conservative 69; Mismatches 170; Indels 9
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US-10-098-732A-18
Sequence 18, Application US/10098732A
; Publication No. US20030175294A1
                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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LENGTH: 729
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Best Local S:
Matches 221
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APPLICANT: Skelky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Brannon, Mark
APPLICANT: Goderian, Jeffrey
APPLICANT: Gorixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Heterologous Fusion Protein Constructs
TITLE OF INVENTION: Heterologous Fusion Protein Constructs
FILE REFERENCE: 01408-01201008;
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2001-04-29
PRIOR PILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence:MTB72FMutSA; OTHER INFORMATION: (Ra12-TbH9-Ra35MutSA)
US-10-098-732A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.6%; Score 809; DB 12; 39.5%; Pred. No. 1.4e-54; iive 66; Mismatches 169;
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, Sequence 65, Application US/10098732A
; Publication No. US20030175294A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 39.5'
Matches 220; Conservative
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TYPE: PRT
ORGANISM: Artificial Sequence
                              Skeiky, Yasir A.W.
Dillon, Davin C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :: ; | | : | | : | 348 ALQQLAQGTTPSSKLGGLWKTVSPHRSPI------SNMVSMANN 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  383 VPGLTGATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIG---GGSGFGG-- 437
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                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Description of Artificial Sequence:WTB72F-WAPS
CTHER INFORMATION: (r95f) fusion construct, TB MTB72F (Ra12-TbH9-Ra35)
OTHER INFORMATION: linked to Leishmania thiol-specific antioxidant
CTHER INFORMATION: (TSA or MAPS)
US-10-098-7328-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
              APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising
TITLE OF INVENTION: Leishmania Antigen
FILE REPERENCE: 014058-012010US
CURRENT PELLING DATE: 2003-04-29
PRIOR PELLING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 19.6%; Score 809; DB 12; Length 930; Local Similarity 39.5%; Pred. No. 1.9e-54; ness 220; Conservative 66; Mismatches 169; Indels 102;
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                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
Skeiky, Yasir
                                                                                                                                                                                                                                                                               SEQ ID NO 65
LENGTH: 930
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Matches
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US-09-287-849-28 ; Sequence 28, Application US/09287849 ; Patent No. US20020009459A1

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APPLICANT: Alderen, Mark
APPLICANT: Alderen, Mark
APPLICANT: Alderen, Mark
APPLICANT: Alderen, Mark
APPLICANT: Alderen, Mark
APPLICANT: Corists or Corporation of Mycobacterium tuberculosis Antigens
FILES DESTRUCTION WINDER: US 08/181.112
PRING PILLNO DATE: 1999-04-07
CTREENT FILLYOLGATION WINDER: US 08/181.12
PRING PILLNO DATE: 1999-04-07
CTREENT PILLYOLGATION WINDER: US 08/181.12
PRING PILLNO DATE: 1999-04-07
CTREENT PILLYOLGATION WINDER: US 08/181.12
PRING PILLNO DATE: 1999-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 ----GGI-----YTEKSLTITGITGTIDFVSNIATDSGAGVFTKENLSCTNTNSLQFLK 218
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                                                                               269 IPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIADI
                                                                                                                                                                                                                                                                                                                                                                                  -----AHTCPDSFPTAD----TABOPAA
                                                                                                              THITG-IELANNKATDVGGGAYVKGTL-----TCENSHR-LQFLKNSSDKQGG----
                                                                                                                                                                329 ISDVADIIKGILGEVWEFITNALNGLKELWDKLTGWVT--GLFSRG-----WSNLESF-
                                                                                                                                                                                                                                                                                          364 LINNTSEKHGGGAFVTKEISOTYTSDVETIPGIT-PVHGETVITGNKSTGGNGGGVCTKR
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37.8%; Pred. No. 2.1e-4%;
ive 49; Mismatches 186; Indels 140; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 353, Application US/09841132
Patent No. US20020061848A1
GENERAL INFORMATION:
APPLICANT: Breatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.465C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 37.8<sup>1</sup>
Matches 228; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TKSGGTRTGNVTLAEGPPAEFCRYPSHWRPLGDLS---IQSSKQSLFNSNYSKQGGGLY 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217
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                                                                                                                                                                                                                                                                                                                                                                                      1 MHHHHHHTAASDNFQLSQGGGGFAIPIGQAMAIAGQIRSGGGGSPTVHIGPTAFLGLGVVD 60
                                                                                                                                                                                                                                                                                                                                                                                                                               MHHHHHHHTAASDNFQLSQGGGGGGAIPIGQAMAIAGQIRSGGGSPTVHIGFTAFLGLGVVD 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 NQGGILYSSLE----YFEKA------LEELAAAFPGDGWLGSAADKYAGKNRNH
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                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion US-10-359-460-28
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                                                                                                                                                                                                                                                                                                          Length 231;
                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                   27.0%; Score 739; DB 12;
llarity 100.0%; Pred. No. 8.1e-50;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 26.9%; Score 737.5; DB 9; Similarity 38.8%; Pred. No. 3.8e-49; 17; Conservative 40; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Breatie, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Brobst, Beter
APPLICANT: Brobst, Beter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
ITILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFE
FILE REPRENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 337
LENGTH: 585
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-04-07
PRIOR PLILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFUMARE: Patentin Ver. 2.1
LENGTH: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKSGGTRTGNVTLAEGPPAEF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 337, Application US/09841132; Patent No. US20020061848A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Chlamydia trachomatis
                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 141; Conserva
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US-09-841-132-337
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Best Local S:
Matches 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 GIPNOGGILYSSLE-----YFEKALEELAAAFPGDGWLG-----SAADKYAGKNRNHV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 CFPEPKELNFSRVETSSSTTFTETIGEAGABYIVSGNASFTKFTNIPTTDTTFTNSNSS 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLTYIPVVGHALSA 278
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                  ------GAIYĞKXAKLSRINNLE-----LSĞNSŞQDVGGĞLCLTESVEPDALĞ- 427
                                                                                                                      SASSGLAHADSLASSASL----PALAGIGGGSGFGGLPSLAQVHAASTRQALRPRADGP 460
                                                                                                                                                                                     VGAAAE----QVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKYSEGAAAGTE 516
                                                                                                                                                      ---SLLSHYNSAAKEGGVIHSKTVTLSNLKSTFTFADNTVKAIVESTPEAPEEIPPVEGE 484
-IIKGILGEVWEFITNALNG 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ
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                                                             LKELWDKLTGWVTGLFSR--GWSNLESFFAGVPGLTGATS----GLSQVTGL-FGAAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                       Sequence 333, Application US/09841132
Fatent No. US2020061848A1
GENERAL INFORMATION:
APPLICANT: Bhatia, Ajay
APPLICANT: Breiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INPECTION
FILE REFERENCE: 210121.469C8
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: PastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 26.4%; Score 722.5; DB 9;
Best Local Similarity 37.3%; Pred. No. 4.8e-48;
Matches 209; Conservative 44; Mismatches 132;
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 ATOLLKLLAKLAELVAAAIADIISDVAD----
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US-09-841-132-333
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd Copyright

OM protein - protein search, using sw model

November 21, 2003, 15:57:31 ; Search time 11:2444 Seconds (without alignments) 4609.825 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-688-672A-64 2737 1 MHHHHHHTAASDNFQLSQGG......RAPVEADAGGGQKVLVRNVV 539

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5.4 783	49 5.4 2174	1510	5.4 1660	5.4 539	684	5.4 792	5.4 960	5.4 1381	5.4 515	5.3 805	46 5.3 957	5.3 667	.5 5.3 694	.5 5.3 882	•

## ALIGNMENTS

RESULT 1
A70957
hypothetical protein Rv3616c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence revision 17-Jul-1998 #hext change 22-Oct-1000
C, Accession: A70957
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris D. Gardon s
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin N. Holroyd e
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Seegers, C.; Relton, S.; Seegers, C.; Relton, S.; Seegers, C.; Seegers, S.; Seege
Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Tavlor, K.; Whitehead, S.; Rarrell B.C.
A) Title: Deciphering the biology of Mycobacterium furbarculosis from the complete genome of
A;Reference number: A70500; MUID:98295987; PMID:9634223
A; Accession: A70957
A)Status: preliminary, nucleic acid sequence not shown: translation not shown
A.Molecule tyme. DNA

A;Molecule type: DNA A;Rodecules: 1-392 <COL> A;Cross-references: GB:Z95557; GB:AL123456; NID:g3242276; PIDN:CAB08950.1; PID:e316833; i B;Experimental source: strain H37Rv C;Genetics: A;Genetics:

. 0 Gaps . 0 Query Match
71.7%; Score 1963; DB 2; Length 392;
Best Local Similarity 99.7%; Pred. No. 2.4e-108;
Matches 391; Conservative 0; Mismatches 1; Indels

207 267 120 327 180 328 IISDVADIIKGIIGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVFGLT 387 240 388 GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA 447 241 GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA 300 9 148 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA 61 DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT 268 YIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIAD 181 IISDVADIIKGTLGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLT 208 DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT 임 ò d  $\delta$ PP QQ  $\delta$ ò g  $\delta$ Dp

SEGAAAGTEDAERAPVEADAGGGQKVLVRNVV 539

508

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126 342

282 99

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Paritable secreted serine proteinase [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Dec-2002
C;Caccession: A87242
R;Cole. S.T.: Eiglimeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, Nature 409, 1007-1001, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: A87242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CiAccession: S47170
K.Cameron, R.M.; Stevenson, K.; Inglis, N.F.; Klausen, J.; Sharp, J.M.
Submitted to the EMBL Data Library, June 1993
A; Description: Isolation and characterisation of a 34KDa protein of Mycobacterium paratuk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-361 <CAM>
A;Cross-references: EMBL:223092; NID:g505550; PIDN:CAA80638.1; PID:g505551
C;Superfamily: Escherichia coli trypsin-like proteinase degs; GLGF domain homology; tryps
trypsin-like proteinase degS; GLGF domain homology; tryps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 VQRVVNTGPAAAGIAPGDVITGVDTVPINGATSMTEVLVPHHPGDTIAVHFRSVDGGER 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein 34K - Mycobacterium paratuberculosis
C;Species: Mycobacterium paratuberculosis
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 VORVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGAR
                                                                                                                                                                 7 HTAASDNFQLSQGGQGFALPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGA
                                                                                                                                                                                                               223 NTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGFTAFLGLGVVDNNGNGA
                                                                                                                                                                                                                                                                                   67 RVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGT
                                                                                                                                                                                                                                                                                                             283 RVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 361;
                                                          2; Length 355;
                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.3%; Score 474.5; DB 2;
69.7%; Pred. No. 7.6e-21;
tive 17; Mismatches 22;
                                                          Score 676; DB 2;
pred. No. 1e-32;
1; Mismatches
                                                       24.7%;
Local Similarity 99.2%;
les 132; Conservative
     C; Superfamily: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                     127 RTGNVTLAEGPPA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 KTGNVTLAEGPPA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 TGNVTLAEGPPA 139
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A:Residues: 1-361 <CAM>
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Gene: ML2659
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Best Local S:
Matches 92
                                                                         Query Match
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Dec-2002
C;Accession: F70983
R;Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.: Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atterence number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70983
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70983
A;Residues: 1-355 <COL>
A;Accession: GB:296071; GB:AL123456; NID:93242254; PIDN:CAB09453.1; PID:92181967
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: pepA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIAD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STROGTRSOAGVSABLSTBOFGGOOFPVSAOGSOGMGGSOGMGGMTPASTKSKKDERKKK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                            hypothetical protein B1620_C2_213 - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C;Accession: S72814
S;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Reference number: S72584
A;Reference number: S72584
A;Accession: S72814
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .Cross-references: EMBL:U00015; NID:9466931; PIDN:AAC43223.1; PID:9466935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

46.1%; Score 1263; DB 2; Length 394;
Best Local Similarity 62.9%; Pred. No. 3.6e-67;
Matches 248; Conservative 55; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KYSEGAAAGTEDAERAPVEADAGGGOKVLVRNVV 539
                    SEGAAAGTEDAERAPVEADAGGGQKVLVRNVV 392
                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: DNA
Residues: 1-394 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208
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289

Gaps

Indels

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probable serine proteinase Rv0983 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: C70821
R;Cole S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Cole S.T.; Brosch, R.; Davinh, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, Ma.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Mhitchead, S.; Barrell, B.G.
A;Aitle: Decliphering the biology of Mycobacterium tuberculosis from the complete genome & A;Reference number: A70500; MUID:9829597; PMID:9634230
A;Accession: C70821
A;Actus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DMA
A;Accessions: 1464 c/COL>
A;Accessions: 1464 c/COL>
A;Accessions: 1464 c/COL>
A;Accessions: 1464 c/COL>
A;Accessions: Rycose-references: GB:Alol1999; GB:All23456; NID:g3261538; PIDN:CAA17582.1; PID:e125391(
A;Gene: Rv0983
C;Genetics: A;Gene: Rv0983
C;Superfamily: Escherichia coli trypsin-like proteinase deg8; GLGF domain homology; tryps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C, Superfamily: Escherichia coli trypsin-like proteinase degs; GLGF domain homology; tryps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-382 <STO>
A;Cross-references: GB:AL450380; NID:g13092536; PIDN:CAC29684.1; GSPDB:GN00147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      337 TLGADSADAQSGSIGLGFAIPVDQAKRIADELISTGKA-----SHASLGVQVTNDKDTL 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 GARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AASDNFOLSOGGOGFALPIGOAMAIAGOIRSGGGSPTVHIGPTAFLGLGVVDNNGN-GAR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 TAASDNFQLSQG--GQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVV-DNNGN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match
Local Similarity 38.9%; Pred. No. 0.00015;
es 51; Conservative 21; Mismatches 50; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 GTRIGNVTLAE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451 GSRTVOVTLGK 461
   525 ADAGGGQK 532
                                                                   388 AGTAASOR 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C.Accession: B7066
R.Josephania, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Decipharing the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Residues: 1-402 col.
A; Residues: 1-402 col.
A; Residues: 1-402 col.
A; Cross-references: GB:Z83864; GB:ALI23456; NID:93261687; PIDN:CAB06237.1; PID:e301440; A; Experimental source: strain H37Rv
C; Generics:
A; Generics:
A; Generics:
C, Superfamily: Escherichia coli trypsin-like proteinase degs; GLGF domain homology: tryg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 TISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAADKYAGKNRN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 QQLRAQYMGDLDKLTGNMISNQAKYVSDTRDVLRAMKKMIDGVYKVCKGLEKIPLLGHLW 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 HVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLTYIPVVGHAL 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 RGILGRIIBMLTTLPKFPGLPGLPDIIDGLWPPKLPDIPIPGLPDIPGLPDFKWPPT 224
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                                                                                                                                                                                                                                        67 RVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGT 126
                                                                                                                                                                                                                                                                                                                                                                                              282 RVARVVATGPAAMAGISVGDIITSVDGVPISEATAMTNVLVPHHPGETVAVNYRSAGGGD 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
14.1%; Score 385.5; DB 2; Length 402;
Best Local Similarity 30.4%; Pred. No. 1.5e-15;
Matches 130; Conservative 47; Mismatches 156; Indels 95; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       406 -SASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAASTRQALRPRADGPVGAA
                                                                                                                                       1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein Rv3864 - Mycobacterium tuberculosis (strain H37RV)
                                                                DB 2; Length 354;
                                                            Query Match 16.8%; Score 460.5; DB 2; Length 3
Best Local Similarity 66.2%; Pred. No. 4.9e-20;
Matches 88; Conservative 18; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 RIGNVTLAEGPPA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 LTANVTLAEGPPA 354
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258 ADSGDAQSGSIGLGFAIPVDQAKRIADELISTGKATHASLGVQVATDKGTPGAK 311 68 VQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTR 127	Db 66 TEAARGVNIPVDVNVDKDTKGGFLSRLLGGKKGLSSLGDDAAKASSQVQHLGKSFLDLTR 125  Qy 51 TAFLGLGVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATA 101
VIDVVAGGAAAAAAAYFNGVVII.NVIDKII.SSABALVAAVKSKAFGGKVSEII.IQDQSGSSK TGNVILAE 135         : TVQVTLGK 379	128 IAMIGWGIVAIAAFDVGLVAGLLAGLESELSAFGAGGGVVALGMDGIAA-AAFI 17  102 MADALNGHHPCDVISVTWQTKSGGTRTCNVTLAEGPPAFFLV 14
THESULT 9  145448  probable serine proteinase (EC 3.4.21) MLCB373.28 [similarity] - Mycobacterium leprae (Species: Mycobac	09 144 PRGSMSRAFIIDPTISAIDGLYDLGIGIPNOGGILVSSLEYFEKALEEL 193 237 GPGLQQLQNILDRTGEFFTGLGPVISTGTQAFLTLSNAGANAFGHLAPLQFFANGFNDM 296 09 194 AAAFPGDGWLGSAADKYAGKNRUHVNFFQELAD
breinase degs, GLGF domain h s predicted DB 2; Length 452; 0066; 351, Indels 7; Gaps 35PTVHIGPTAFLGLGVVDNNGN-GAR                          KATHASLGVQVATDKGTPGAK MADALNGHHPGDVISVTWQTKSGGTR	296 LAYLVVKTLINA
441	Qy S01 GTTTKKYSEGAAAGTEDAERAPVEADA 527  Db 690 GISTKELKQYSAALEQERKRIQVEKNA 716
RESULT 10 H72802 minor tail subunit protein - Mycobacterium phage D29 C;Species: Mycobacterium phage D29 C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 20-Apr-2001 C;Accession: H72802 R;Ford, M.E.; Sarkis, G.J.; Belanger, A.E.; Hendrix, R.W.; Hatfull, G.F. J. Mol. Biol. 279, 143-164, 1998 R;Ford, M.E.; Sarkis, G.J.; Belanger, A.E.; Hendrix, R.W.; Hatfull, G.F. J. Mol. Biol. 279, 143-164, 1998 A;Accession: H72802 A;Accession: H72803 A;Accession:	RESULT 11 RESULT 11 RESULT 11 RESULT 11 RESULT 11 RIGH 239 Rivolae-rich protein Rv0109 - Mycobacterium tuberculosis (strain H37RV) C; Species: Mycobacterium tuberculosis C; Date: 17-101-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C; Accession: H70839 R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davines, R.; Devilni, K.; Feltwell, T.; Gencles, S.; Harris, D.; Gordon, S.; Sandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 A; Authors: Squares, R.; Sultston, J.E.; Taylor, K.; Mhitchead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome shallon H70839 A; Status: preliminary: nucleic acid sequence not shown; translation not shown A; Residues: 1-496 cools. A; Cross-references: GB:Alo21926; GB:All23456; NID:g3261520; PIDN:CAA17303.1; PID:g290957; A; Experimental source: strain H37Rv
Length 837; Indels 212; Gaps 25; IRSGGGSPTVHIGP 50	C;Genetics: Rv0109 A;Gene: Rv0109 C;Superfamlly: Phaseolus glycine-rich cell wall protein 1.8 Query Match Query Match Best Local Similarity 25.5%; Pred. No. 0.01; Matches 83; Conservative 26; Mismatches 107; Indels 110; Gaps 14;

Db 1037 ALGG	SULT 13 3323 3425 Species Lactococcus phage bIL170 Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 05-Nov-1999 Accession: T03323 Crutz-Cody, A.M., Desselin, B.; Commissaire, J.; Anba, J.; Kyriakidis, Description: Sequence and organization of the lactococcal isometric bIL17 Reference number: Z14903 Accession: T03323 Status: preliminary; translated from GB/EMBL/DDBJ Accession: T03323 Cross-references: EMBL:AF009630; NID:g3282260; PIDN:AAC27195.1; PID:g3282 Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Guary Match Best Local Similarity 21.8%; Pred. No. 0.029; Matches 119; Conservative 70; Mismatches 189; Indels 168; Gaps	Db 229 TTFIGLGESAKTAVSKTEALVKANQAFGGTGENLKGVVQAYGGMSAAGKV 278  Qy 92 DGAPINSATAMADALNGHHPGDVISVIWQTKSGGTRIGHIS 136  Qy 92 DGAPINSATAMADALNGHHPGDVISVIWQTKSGGTRIGHIS 136  Qy 137 PFAEFLVPRGSMSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEY 185  Db 339 SSSATKIRDTWSGFNEDLSQALIPTLEALTPVINALIDKMDDMGKGAGKAIENVVKY 396  QY 186 FEKALEERAAFPG-DGMLGSAADKYAGRNHV 218
Qy         262 VAVDLTYIPVVGHALSAAFQAPFCAGAMAVVG	RESULT 12 A83080 hypothetical protein PA4541 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: A83080 C;Accession: A83080 C;Accession: A83080 C;Accession: A83080 C;Accession: A83080 C;Accession: A82950; MUID:20437337; PMID:10984043 C;Accession: A83080 C;Accession	.⊒ ψ

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A; Accession: A30878
A; Status: preliminary
A; Modecule type: mRNA
A; Modecule type: mRNA
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A; Modecule type: mRNA
A; Cross-references: GB: J04035; MID: g207442; PIDN: AAA42268.1; PID: g207443
A; Cross-references: GB: J04035; MID: g207442; PIDN: AAA42268.1; PID: g207443
A; Franzblau, C.; Pratt, C.A.; Faris, B.; Colannino, N.M.; Offner, G.D.; Mogayzel Jr., P., Biol. Chem. 264, 15115-15119, 1989
A; Title: Role of tropoelastin fragmentation in elastogenesis in rat smooth muscle cells. A; Reference number: A36523; MUID: 89359327; PMID: 2768256
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A;Note: the list of introns may be incomplete
C;Superfamily: elastin
C;Superfamily: elastin
C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-664/Product: elastin #status predicted <MAT>
F;854-859/Disulfide bonds: #status predicted
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A;Resdidae: 1864 SEEMS0647; GB:U05292; NID:g207444; PIDN:AAA42269.1; PID:g207445
A;Cross-references GB:Mo647; GB:U05292; NID:g207444; PIDN:AAA42269.1; PID:g207445
R;Deak, S.B.; Pierce, R.A.; Belsky, S.A.; Riley, D.J.; Boyd, C.D.
J. Biol. Chem. 263, 13507, 1368
J. Biol. Chem. 263, 13507, 1368
A;Title: Rat tropolastin is synthesized from a 3.5-kilobase mRNA.
A;Reference number: A30878; MUID:88330868; PMID:2971041
                                                                                                 668 IENAHSNVHVAAQSTERNSLGGVGGLVGLNVGLNRAKGMIRASGSQGKVET--YRPGLNVGGLVG 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cispecies: Rattus norvegicus (Norway rat)
Cibate: 11-20a-1991 #sequence revision 16-Aug-1996 #text_change 22-Jun-1999
Cibates: 11-20a-1991 #sequence revision 16-Aug-1996 #text_change 22-Jun-1999
Cibates: As a sequence revision 16-Aug-1996 #text_change 22-Jun-1999
Ripterce, R.A.; Deak, S.B.; Stolle, C.A.; Boyd, C.D.
Biochemistry, 29, 9677-9683, 1990
A;Title: Heterogeneity of rat tropoclastin mRNA revealed by cDNA cloning.
A;Reference number: A36106; MUID:91104868; PMID:1702999
                            --VSAQGSQ-----GMGGPVGMG--GMHPSSGASKGTTTKKYSEGAAAG----
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Residues: 558-864 <RB2>
Cross-references: GB:M86376; NID:g207459; PIDN:AAA42272.1; PID:g207462
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A; Title: Elements of the rat tropoelastin gene associated A; Reference number: 154172; MUID:92241859; PMID:1572637
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A,Residues: 22-31 <FRA>
R,Rich, C.B.; Foster, J.A.
Arch. Biochem. Biophys. 268, 551-558, 1989
A,Title: Characterization of rat heart tropoelastin.
A,Reference number: 802173; MUID:89117149; PMID:2913947
A,Accession: S02173
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                                                                                                                                                                                                                                                      -----TEDAERAPVEADAGGGKVLV 535
                                                                                                                                                                                                                                                                                                                                                       726 YNMFGHVSDSSASGQVEAGGAGNTGGLV 753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                elastin precursor - rat
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H83135
Froble adhesin PA4082 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: H83136
C;Accession: H83136
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
R;Stover, C.K.; Pham, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
A.; Corry, S.; Olson, M.V.
Nature 406, 959-664, 2000
A.Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathon,
A;Recision: H83135
A;Accession: H83135
A;Accession: H83135
A;Accession: H83135
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                                                                    637 WITVIGGIQSVWGGVTGFFSGIFDAVSSVVSTVFSAIGGFASSAWNVLVSVWSAVAGFFG 696
-SRGWSNLESFFAGVPGLTG 388
                                                                                                                                                                                                                                                                                        697 GIFNAVSGV--VSSVFSAIGSFASSAMGVVQSIWSAVSGFFSGIFNSVSSVVSGVFSALG 754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HHHTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDN---
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     - TNALNGLKELWDKLTGWVTGLF
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                                                                                                                                  244 GGQOPGVPLGYPIK-APKLPGGYGLPYTN-GKLPYGVAGAGGKAGYPTGTGVGSQAAVAA 301
                                                                                                                                                                                     75 APAAS-LGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTL 133
                                                                                                                                                                                                                                                                                                                             351 AAAKAAKYGAAGGLVPGGPGVRVPGAGIPGVGIPGVGGIPGVGGIPGVGGIPGVGG---- 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------GARGGVG------IPTYG--VGAGGFPGYGVGAGAG 464
                                                                                        19 GGQGFAIPIGQAMAIAGQIRSGGGSPTVHIG--PTAFLGLGVVDN--NGNGARVQRVVGS 74
Query Match
6.0%; Score 165; DB 1; Length 864;
Best Local Similarity 23.2%; Pred. No. 0.035;
Matches 130; Conservative 48; Mismatches 210; Indels 172; Gaps
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(c) 1993 - 2003 Compugen Ltd
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                                                                                                                                                                                                                                                                    Genomics 12:651-658(1992).
-!- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY.
-!- SUBUNIT: THE POLYWERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER INTO AN EXTENSIBLE 3D NETWORK.
-!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
-!- ALTERNATIVE PRODUCTS:
-- ALTERNATIVE PRODUCTS:
-- Event-Alternative splicing; Named isoforms=8;
Comment=Experimental confirmation may be lacking for some
                                                                                ----TLGTALTTALQAIQPMLPTLVDSFKQLSETLVTSLGPYLPQIGEAFGQIVGAVIQ
                                                                                                                         531 SIASFLIGGISRLYGVLADCVGAVAE------W-GSWSSGVQQVSDFVGQLPGKIKSW
            ---ILEGAKKGLEFVRPVAVD
                                   356 MPALTSVSSLLGNVLGTLGTQLAPITTALTPAFTTLADTLGTMLTGALQALGPVLTVVAE
                                                          --PFCAGAMAVVGGA---
                                                                                                         -----TQLLKLLAKLAELV---AAAIADIIS
                                                                                                                                                         331 DVADIIKGILGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLTGA-
                                                                                                                                                                                                                            583 FDDAGSWLIEACKNVVQCLINGIGSMISSAVSKAKELASSVK-----NAVTGFLGIHS
                                                                                                                                                                                                                                                     441 LAQVHAASTRQALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASK
                                                                                                                                                                                                       -----TSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=91104868; PubMed=1702999;
MEDLINE=91104868; S.B., Stolle C.A., Boyd C.D.;
Blerce R.A., Deak S.B., Stolle C.A., Boyd C.D.;
"Heterogeneity of rat tropcalastin mRNA revealed by cDNA cloning.";
Blochemistry 29:9677-9683(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                558-864 FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 264-533 AND 558-864 FROM N.A., AND ALTERNATIVE SPLICING MEDLINE=92241859; PubMed=1572637; Plerce R.A., Alatawi A., Deak S.B., Boyd C.D.; Elements of the rat tropoelastin gene associated with alternative splicing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 781-864 FROM N.A.
MEDLINE=88330868; PubMed=2971041;
Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.,
"Rat tropoelastin is synthesized from a 3.5-kilobase mRNA.'
J. Biol. Chem. 263:13504-13507(1988).
              LDROLISLIHDOANAVOTTRD-
                                                                                                                                                                                                                                                                                                                                                                                                              01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
10-5SP-2003 (Rel. 42, Last annotation update)
Elastin precursor (Tropoelastin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                        864 AA.
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GISTKELKQYSAALEQERKRIQVEKNA 715
                                                                                                                                                                                                                                                                                                     GTTTKKYSEGAAAGTEDAERAPVEADA 527
                                                                                                            LAYLVVKTLINA-----
                                                             266 LTYIPVVGHALSAAFQA-
                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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IsoId=099372-1; Sequence=Displayed;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEGPPAEF----LVPRGSMSRA-----FIIDPTISAIDGLYDLLGI-GIPNOGGILYS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---SAADKYAGKNRNHVNFFOELADLDROL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isoform
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 AAAKAAKYGAAGGLVPGGPGVRVPGAGIPGVGIPGVGGIPGVGGIPGVGGIPGVGGIPGVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 APAAS-LGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTCNVTL
                                                                                                                                                                                                                                                     VSP_004245, VSP_004246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210; Indels 172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interPro, IPR003979, tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
Structural protein; Connective tissue; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
                                                                                                                                 IsoId=Q99372-5; Sequence=VSP_004244, VSP_004245;
                                                                                                                                                                      IsoId=099372-6; Sequence=VSP_004245, VSP_004246;
                                                                                                                                                                                                              IsoId=Q99372-7; Sequence=VSP_004244, VSP_004246;
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/FIG=VSP 004244.
Missing (in isoform 3, 6 and isoform 8).
/FIId=VSP 004245.
                                                                                                                                                                                                                                                     ISOId=099372-8; Sequence=VSP_004244, VSP_0042
PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Missing (in isoform 7 and isoform 8).
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ELASTIN.
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Name=2;
IsoId=Q99372-2; Sequence=VSP_004244;
                                                      IsoId=Q99372-3; Sequence=VSP_004245;
                                                                                           IsoId=Q99372-4; Sequence=VSP_004246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.0%; Score 165;
23.2%; Pred. No. 0.
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AAA42271.1; JOINED.
AAA42271.1; JOINED.
AAA42271.1; JOINED.
AAA42271.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M60647; AAA42269.1; -.
EMBL; J04035; AAA42268.1; -.
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AAA42271.1;
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les 130; Conservative
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Matches
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                                                                                                                                                                                  PMLPSIMQSFQQISDVLVTSLAPHIPALATALGQVAGAVLQLAPTIISTLVPA--FVQLV 488
                                                                                                                                                                                                                 -TGATSGLSQVT 397
                                                                                                                                                                                                                                                                                                                          SNVIK------KVSEWVSS-FSSGAQQIAAKAAELPGMIQSALANLMAIGLQAGKDLVQ 600
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                                       ----GPLSTFINGFGDLFVSLMPALTSVSGLIGNVLGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome 7.";

Genomics 23:125-131 (1994).

-!- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND

-!- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND

NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY.

-!- SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER

-!- SUBCELLULAR LOCATION: SYTRACELLULAR MATRIX OF ELASTIC FIBERS.

-!- PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
                                                                         LDRQLISLIHDQANAVQTTRDILEGAKKG-LEFVRPVAVDLTYI-PVVGHALSAAFQA--
                                                                                                                                                                                                                                                     489 PKVÄELVPIIVNLVQSFANLMPVVLPLAQALVSVÄGÄVIQVGVSIGGALIGALANLTEII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TATAIN-BABLE/C; TISSUB-Lung;
MEDLINE-95130069; PubMed-7829060;
Wydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
"Use of an intron polymorphism to localize the tropoelastin gene t mouse chromosome 5 in a region of linkage conservation with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                       TNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGL-----
       FEKALEELAAAFPGDGWLGSAADKYAGKNRNHVNFFQE--
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Last annotation update)
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(Rel. 34, Last sequ
(Rel. 42, Last anno
                                       FNRLMESGLOAM - - - GOLG -
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MGI:95317; Eln.
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01-OCT-1996 (
15-SEP-2003 (
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                                     291
                                                                                                                                            --SQAAAAAA---AKAAKYGAGGAGTLGGLVPGAV 499
                                                                                                                                                                          352 NGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPG-LTGATSGLSQVTGLFGAAGLSASSG 410
                                                                                                                                                                                                              PG-----ALPGAVPGALP-----GAVPGALPGAVPGVPGTGGVPGAGTPAAAA 543
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                                                                                                                                                                                                                                                                                       ---GDLG 600
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                                                                     ----GARGGVG------IPTYG--VGAGGFPGYGVGAGAG 464
                                                                                                       VGGALAYLVVKTLINATQLLKLLAKLAELVAAAIADIISDVADIIKGILGEVWEFITNAL 351
                                                                                                                                                                                                                                                                                                                                                       601 GAGTPAAAKSAAKAAKAQYRAAAGLGAGVPGLGVGAGVPGFGAGAGGFGAGAGVPGFGA 660
                                 232 ISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLTYIPVVGHALSAAFQAPFCAGAMAV
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Mycobacteriophage L5.
Mycobacteriophage L5.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
L5-like viruses.
NCBI_TaxID=31757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.0%; Score 164; DB 1; Length 836;
22.5%; Pred. No. 0.034;
:ive 75; Mismatches 203; Indels 146;
                                                                                                                                                                                                                                                                                 544 AAAAKAAAKAGQYGLGPGVGGVPGGVGVGLPGGVGPGGVTGIGTGPGTGLVP
PGIGGPGIVGGPGAVSPAAAAAAAAAKAAKY-
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(Rel. 28, Last sequence update)
(Rel. 28, Last annotation update)
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Hatfull G.F., Sarkis G.J.;
"DNA sequence, structure and gene expression a
phage system for mycobacterial genetics.";
Mol. Microbiol, 7:395-405(1993).
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Best Local Similarity 22.5
Matches 123; Conservative
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Minor tail protein GP26.
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                                                                                                                                                                                                     EGPPAEFLVPRGSMSR - - - AFILDPTISALDGLYDLLGIGIPNOGGILYSSLEYFEKALE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                   Indels 165;
                                                                               DB 1; Length 860;
                                                                                                                                                                                                                                                                                                                                                ---BGALGGL---
                                                 BY SIMILARITY.
0COBESAAEIEDD7F1 CRC64;
                    Connective tissue.
                                                                                                   186;
                                                                                        .063;
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                                                                                                                                                                                                                                                                ---PGIVGGPGAVSPAAAAAAAKAAKY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       730 AA
                                                                                                   38; Mismatches
                                                                              5.8%; Score 159.5;
23.3%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGGM-HPSSGASKGTTTKKYSEGAAAG 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGGAGSPAAKSAAKAAAKAQYRAAAG 611
InterPro; 1Pkoussys, property PRO1500; TROPOELASTIN.
Structural protein; Repeat; Signal; Constructural protein; Repeat; Signal, 27
                                       ELASTIN
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TISSUE=Skin fibroblast;
                                      860 EI
855 BY
71955 MW;
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Conservative 3
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                                      28 8
850 8
860 AA;
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Matches 118; Conserv
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND NUCHAL LIGAMENT, WHICH MUST EXPAND RAFIDLY AND RECOVER COMPLETELY.
-: SUBBUILT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER INTO AN EXTENSIBLE 3D NETWORK.
-: SUBGELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
-: ALTERNATIVE RODOUTS:

Event-Alternative splicing; Named isoforms=2;

Comment-Additional isoforms seem to exist;
Fazio M.J., Olsen D.R., Kauh E.A., Baldwin C.T., Indik Z., Ornstein-Goldstein N., Yauh H., Rosenbloom J., Uitto J., "Cloning of full-length elastin cDMAs from a human skin fibroblast recombinant cDNA library: further elucidation of alternative splicing utilizing exon-specific oligonucleotides.";

J. Invest. Dermatol. 91:458-464 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Hippocampus, and Placenta,
MEDLINE=66291399; PubMed=8689688;
Arangiskakis J.M., Bwart A.K., Morris C.A., Mervis C.B.,
Bertrand J., Robinson B.F., Klein B.P., Ensing G.J., Everett L.A.,
Green E.D., Proeschel C., Gutowski N.J., Noble M., Atkinson D.L.,
                                                                                                                                                                                                                                                                                                                   MEDIANE=88156138, PubMed=2831431;
Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M.,
Rosenbloom J., Uitto J.
"Isolation and characterization of human elastin cDNAs, and age-
associated variation in elastin gene expression in cultured skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Green E.D., Proeschel C., Gutowski N.J., Noble M., Atkinson D. Odelberg S.J., Kearing M.T.;
"LIM-kinasel hemizygosity implicated in impaired visuospatial constructive cognition.";
Cell 86:59-69(1996).
                                                                                                                                                                                                                                                       SEQUENCE OF 164-724 FROM N.A. (ISOFORM B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P15502-1; Sequence=Displayed;
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EMBL; M16983; AAC98394.1; JOINED.
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Lab. Invest. 58:270-277(1988).
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M17271;
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M17267;
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M36860;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --GPQPG------VPLGY-PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYP 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLINATQLLKLLAKLAELVAAALADIISDVADIIKGILGEVWEFITNALNGLKELWDKLT 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GWVTGLFSRGWSNLESFFAGVPGLTGATSGLSQVTGLFGAAGLSASSGLAHADSLASSAS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 -----AGVPGVPGA----IPGIGGIAGVGTPAAAAAAAAKAAK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423 LPALAG-IGGGSGFG-----GLPSL-----AQVHAASTRQALRPRADGP 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 YGAAAGLVPGGPGFGPGVVGVPGAGVPGAGIPVVPGAGIPGAAVPGVVSPEAAK 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GOSQLVSAQGSQGMGGPVGM 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 SAP-AASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 GVPGVGGLGVSAGAVVPO-PGAGVKPGKVPGVGLPGVYPGGVLP-----GARFPGVG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 LEGAKKGLEFVRPVAVDLTYIPVVGHALSAAFQAPFCAGAMAV-----VGGALAYLVVK 302
                                                                                                                                                                     DR GO; GO:0005578; C:extracellular matrix; TAS.

DR GO; GO:0005519; C:extracellular space; TAS.

GO; GO:0005519; F:extracellular space; TAS.

DR GO; GO:0005203; P:extracellular matrix structural constituent; TAS.

DR GO; GO:0008203; P:exl proliferation; TAS.

CO; GO:0007203; P:circulation; TAS.

CO; GO:0007304; P:histogenesis and organogenesis; TAS.

R GO; GO:0007585; P:respiratory gaseous exchange; TAS.

R Interpro; IPR003979; tropoglassin.

N Structural protein; Connective tissue; Repeat; Signal;

M Williams-Beuren syndrome; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNG--NGARVQRVVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5:6%; Score 152.5; DB 1; Length 730; Best Local Similarity 20.4%; Pred. No. 0.13; Matches 117; Conservative 46; Mismatches 182; Indels 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 730 ELASTIN.
720 725 BY SIMILARITY.
472 477 Missing (in isoform 2).
FITIGE-USP 004243.
730 AA; 63260 MW, AB06DISBAS67AE46 CRC64;
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EMBL; M24782; AAA53190.1; --
EMBL; U62292; AAB17544.1; --
EMBL; X15603; CAA33627.1; --
PIR; A32707; EAHU.
HSSP; P50099; 1ZFU.
Genew; HGNC:3327; ELN.
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WA22 MYCTU RESULT 6

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMIL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bishal W.;
"Whole genome comparison of Mycobacterium tuberculosis clinical and
"Whole genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINES 2025997; PubMed=9634230;

MEDLINES 2025997; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglameier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Bacham D., Chillingworth T., Connor R.,

Hornsby T., Jagels R., Feltwell T., Gentles S., Hamiin N., Holroyd Hornsby T., John K., Kroph A., McLean J., Moule S., Murphy L.,

Oliver S., Osborne J., Quali M.A., Rajandream M.A., Rogers J.,

Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157;
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                                                                                                                                                                   Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                          Corynebacterineae; Mycobacteriaceae; Mycobacterium
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larity 24.5%; Pred. No. 0.17;
Conservative 40; Mismatches 213;
   (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
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SIGNAL 30 POTENTIAL.
CHAIN 31 914 WAG22 ANTIGEN.
                                                                                                       WAG22 antigen precursor.
WAG22 OR RV1759C OR MT1807 OR MTCY28.25C.
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InterPro, IPR000084; PE_region.
Pfam; PF00934; PE; 1.
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30-MAY-2000 (
16-OCT-2001 (
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Best Local Simil
Matches 133; (
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           AEGPPAEFLVPRGSMSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEEL 193
                                                                                                                                                             300 VVKTLINATQLLKLLAKLABLVAAAIADIISDVADIIKGILGEVWEFITNALNGLKELWD 359
                                                                                                                                                                                                                                       623 TTTGGVGG--AGGNAGLLIGAAGLGGCGGGAFTAGVTTGGAGGTG--GAAGLFANGGAGG 678
                                                                                                                                                                                                                                                                                                                                      GAGGPGGLYGAGGSGCAGGHGGMAGGGGGVGGNAGSLTLNASGG--AGGSGGSSLSGKAG 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann G.D., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.E., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                             360 KLTGWVTGLFSRGWSNLESFFAGVPG-----LTGATSGLSQVTGLFGAAGLSASSGLAH
                                                                                                                                                                                                                                                                                                                -VGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKYSEGAAAGTEDAERAPVEAD
                                                                                AGKSGFGGFGGLLLGADGY-----NAPESTSPWHNLQQDILSFINEPTEAL-TGRPLIGN
                                                                                                            ------BGAKKGLEFVRPVAVDLTYIPVVGHALSAAFQAPFCAGAMAVVGGALAYL
                                                                                                                                    GDSGTPGTGDDGGAGGWLF------GNGGNGGAGAAGTNGSAGGAGGALL
                                                                                                                                                                                    ADSLASSASLPALAGIGGGSGFGGLPSLAQVHAASTRQALRPRADGPVGAAAEQ-----
                                     -----GAL
                                                             A--AAFPGDGWLGSAADKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDIL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=9829587; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Gas S., Bary C.E. III. Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Comnor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd E. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                   --NAV----LIGNG--GEGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2011 (Rel. 40, Last annotation update)
Hypotherical PB-PGRS family protein Rv0747 precursor.
RV0747 OR MI0772.5 OR MIV041.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                    801 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
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                                   AGG-
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ID Y747_MYC
AC 053810;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENEL GUESTATION. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GAGGLFGSGG-----AGGASTDVAGGAGGAGGAGG--NAGMLFGAAGVGGV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 DIIKGILGEVWEFITNALNGLKELWDKLIGWVTGLFSRGWSNLESFFAGVPGLTGATSGL 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 SQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAASTRQAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 ALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKL-AELVAAAIADIISDVA
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POTENTIAL.
HYPOTHETICAL PE-PGRS FAMILY PROTEIN
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01-JUL-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Discs large-1 tumor suppressor protein.
Discs large-1 tumor suppressor protein.
Discsophila melanogaster (Fruit fly).
Discophila melanogaster (Fruit fly).
Neoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
[1]
PGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Pred. No. 0.2;
23; Mismatches 111; Indels
SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EA54C9BF45A00F41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G -> S (IN REF. 2)
R -> G (IN REF. 2)
K -> G (IN REF. 2)
K -> G (IN REF. 2)
S -> G (IN REF. 2)
T -> I (IN REF. 2)
T -> A (IN REF. 2)
T -> A (IN REF. 2)
MISSING (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 150; DB Pred. No. 0.2;
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Tuberculist; Rv0747; -..
InterPro; IPR000084; PE_region.
Pfan; PF00934; PE; 1.
Hypothetical protein; Repeat; Sig SIGNAL
                                                                                                                                                                                                                                                      EMBL; AL021958; CAA17514.1; -. EMBL; AE006968; AAK45011.1; -.
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601 AA;
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P31007;
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                                                                        Query Match
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Q50594;
                        DOMAIN
                                     DOMAIN
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YI40_MYCTU
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                            Isold=P31007-1; Sequence=Displayed;
TISSUE SPECTFICITY: In embryos, expression is seen in epithelial
Cells and some nervous tissue. In larvae, expression is seen as a
belt around salivary glands and imaginal disks, also in
proventriculus and parts of the brain. Expressed in adult
reproductive tissues.

DEVELOPMENTAL STAGE: Expressed both maternally and zygotically
throughout development.
SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
SIMILARITY: Contains 3 PDZ-DHR domains.
SIMILARITY: Contains 1 SH3 domain.
SIMILARITY: Contains 1 guanylate kinase-like domain.
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polarit...; I
polarit...; N
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R PIR; A39651, A442849811; -.

R PIR; A39651, BFE.

R FYBASE; FBGN00164, d1g1.

GO; GO:004519; C:apical cortex; IDA.

GO; GO:004519; C:apical protein localization; IMP.

GO; GO:004519; P:actablishment and/or maintenance of pola

GO; GO:004519; P:actablishment and/or maintenance of pola

GO; GO:004519; P:actablishment and/or maintenance of pola

GO; GO:00039; P:actablishment and/or maintenance of pola

GO; GO:00039; P:actablishment and/or maintenance of pola

GO; GO:00039; P:actablishment and/or maintenance of pola

GO; GO:00039; P:actablishment and/or maintenance of pola

GO; GO:00039; P:actablishment and/or maintenance of pola

R DincerPro; IPR00019; Guanylate_kin,

R InterPro; IPR001452; SH3;

R PFEM; PFC0055; Guanylate_kin; 1.

R PFC00; SH3; 1.

R PRODG; SH3; 1.

R SWART; SM00226; SH3; 1.

R SWART; SM00226; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00856; GUANYLATE KINASE 1; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 3.
PROSITE; PS50002; SH3; 1.
PROSITE; PS50002; SH3; 1.
PROSITE; PS50002; SH3 domain; Alternative splicing; Repeat.
DOMAIN 40 126 PDZ 1.
          TISSUE=Embryo;
MEDLINE=91330294; PubMed=1651169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M73529; AAA28468.1; -.
PIR; A39651; A39651.
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181
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                                                                                                                                                                                                                                                                  DNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 VILIIGKTQHLTTSASGGGGGGLSSGQQLSQSQSQLATSQSQSQVHQQQHATPMVNSQST
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                                                                                                                                                          Length 960;
                                                                                                                                                          5.4%; Score 147; DB 1; Length 96.
21.4%; Pred. No. 0.36;
tive 60; Mismatches 207; Indels
                                                                                                       102468 MW; BF87A4262F1B6AD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464 AAEQVGGQSQLVSAQGSQGM-----GGPVGMG 490
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19-OCT-801 (Rel. 40, Last annotation update)
NUBACCHETICAL PE-PGRS family protein RVB40c.
RV1840C OR MI1888 OR MICYIAII.04 OR MICY359.33.
                                                        SH3.
GUANYLATE KINASE.
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SUBFAMILY.
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ID Y278_MYCTU
AC P56877;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 VAAAIADIISDVADIIKGILGEVW-----EFITNALNGLKELWDKLTGWVTGLFSRGWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 AGKNRN----HVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDL
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                                                                                                                                                                                          [2] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. FRAIN-EDC 1551 / Oshkosh, Fleischmann R.D., Alland D., Eisen J.A., Carpenter D., Hickey E., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Peterson J.F., Umayam L.A., Ermolaeva M.D., Salzberg S.L. Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L. Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Delcher A., Otterback T., Weidman J., Khouri H., Gill J., Mikula A., Delcher A., Otterback T., Weidman J., Khouri H., Gill J., Mikula A., Delcher A., Otterback T., Weidman J., Khouri H., Gill J., Mikula A., Delcher A., Otterback T., Weidman J., Khouri H., Gill J., Mikula A., Delcher A., Otterback T., Weidman J., Khouri H., Gill J., Mikula A., Delcher A., Otterback T., Weidman J., Khouri H., Gill J., Mikula A., Delcher A., Otterback T., Weidman J., Khouri H., Gill J., Mikula A., Delcher A., Otterback T., Weidman J., Khouri H., Gill J., Mikula A., Delcher A., Otterback T., Weidman J., Khouri H., Gill J., Mikula A., Delcher A., Otterback T., Weidman J., Khouri H., Gill J., Mikula A., Delcher A., Otterback T., Weidman J., Khouri H., Gill J., Mikula A., Delcher A., Otterback T., Weidman J., Khouri H., Gill J., Mikula A., Delcher A., Otterback T., Weidman J., Khouri H., Gill J., Mikula A., Delcher A., Otterback T., Weidman J., Khouri H., Gill J., Weidman J., Khouri H., Gill J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J.
                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                laboratory strains.";
submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulscon J.B., Taylor K., Whitehead S., Barrell B.G.; Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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PIR; H70663; H70663.
TIGR; MT1888; -.
Tuberculist; Rv1840c; -.
InterPro; IPR000084; PE_region.
Pfam; PR0934; PE; 1.
Hypor, PF0934; PE; 1.
Pypor, PF0834; PE; 1.
Pyporherical protein; Transmembrane; Complete proteome.
TRANSMEM 1.
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POTENTIAL.
; ZEDC8B6C6D28B7F3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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Holroyd
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr Gordon S.V., Egglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A. Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitchead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Whole genome comparison of Mycobacterium tuberculosis clinical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. -: SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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MISSING (IN REF. 2).
R -> G (IN REF. 2).
; 71EBABD417FBA47C CRC64;
                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical PB-PGRS family protein Rv0278c precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterineae; Mycobacteriaceae; Mycobacterium
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EMBL, AE006936, AAK44511.1; ALT_INIT.
PIR, D70835, D70835.
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Pfam; PF00934; PE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D.
                                                                                                                                                                                                                         STANDARD;
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158
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957 AA;
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530
                                                             333 NG 334
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DB 1; Length 957;

Score 146;

5.3%;

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15;
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                                                    257 EFVRPVAVDLTYIPVVGHALSAAFQAP-----FCAG-----AMAVVGGA--LAYLVV 301
                                                                                                                      302 KTLINA--TQLLKLLAKLAELVAAAIADIISDVADIIKGILGEVWEF------ITNA 350
                                                                                                                                                     66 SAQAQÀFHAQFVQALTSGGGAYAAAEAAVSPLLDPIN-----EFFLANTGRPLIGNG 118
                                                                                                                                                                                      351 INGLKELWDKLT-----GWVTGLFSRGWSNLESFFAGVPGLTGATSGLSQVTGLFGAA 403
                                                                                                                                                                                                                         119 ANGAPG-----TGANGGDGGWLIGNGGAGGS-----GAAGVNGGAGGNGGAGGNGGAG 166
                                                                                                                                                                                                                                                           404 GLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAASTR----QALRPRADG 459
                                                                                                                                                                                                                                                                                                                             460 PVGA-----AAEQVGGQ----SQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTK 505
                                                                         module.";
J. Biol. Chem. 268:17377-17383 (1993).
J. Biol. Chem. 268:17377-17383 (1993).
II. Biol. Chem. 268:17377-17383 (1993).
II. BUNCTION: THIS PROTEOGLYCAN IS A MAJOR FUNCTION OF THIS PROTEIN MATRIX OF CARTILAGENOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN IS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO HYALURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION. MAY PLAY A
                                                                                                                                                                                                                                                                                            ĠĹĬĠŊĠĠĀĠĠĀĠĠŶĀŚŚ-----ĠĬĠĠSĠĠĠĠŊĀMĹFĠĀĠĠĀĠĠĀĠĠĸŶĀĹŢĠĠĀĠĠ
                                                                                                                                                                                                                                                                                                                                                                220 AGGAGGNAGLLFGAAGVGGAGGFTNGSALGGAGGAGGAGGLFATGGVGGSGGAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Glant T.T., Adams M.E., Kwok S.X.F., Huang D., Fueloep C.; "Complete coding sequence and deduced amino acid sequence of aggrecan of canine cartilage."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Cartilage,
MEDLINE=93352525; PubMed=8349621;
Fueloep C., Walcz E., Valyon M., Glant T.T.;
"Expression of alternatively spliced epidermal growth factor-like domains in aggrecans of different species. Evidence for a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCI.
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                  88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barry F.P., Neame P.J., Sasse J., Pearson D., "Length variation in the keratan sulfate domain of mammalian
                  17; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1830-2333 FROM N.A.
Adams M.E., Kowk S.X.F., Huang D., Glant T.T., Fullop C.
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
 Pred. No. 0.41;
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MEDLINE=95128522; PubMed=7827755;
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 28.4%;
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                  Conservative
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Best Local Similarity
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EVRL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).

DOMAIN: TWO GLOBULAR DOWAINS, G1 AND G2, COMPRISE THE AMINO
TERMINUS OF THE PROTEOGLYCAN, WHILE ANOTHER GLOBULAR REGION, G3,
MAKES UP THE COOH TERMINUS. G1 CONTAINS LINK DOMAINS AND THUS
CONSISTS OF THREE DISULFIDE-BONDED LOOP STRUCTURES DESIGNATED AS
THE A, B, B' MOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULFATE (KS)
AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G2
AND G3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO KERATAN SULFATE
                435 FGGLPSLAQVHAASTRQALRPRADGP-VGAAAEQ-----VGGQSQLVSAQGSQGMGG-PV
                                                --- PSGEGPEVSASGVEDLSGLSSGESPEASASGVGDLSGLPS
                                                                                                                                                                                                                                      01-AUG-1988 (Rel. 08, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
115-5EP-2003 (Rel. 42, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific proteoglycan core
protein) (CSPCP).
                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAINS, N-LINKED AND O-LINKED OLIGOSACCHARIDES.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 4 link domains.
SIMILARITY: Contains 1 C-type lectin family domain.
SIMILARITY: Contains 1 Sushi (SCR) domain.
SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                         SEQUENCE FROM N.A.
MEDLINE=88087070; PubMed=3693370;
Boege K., Sasaki M., Horigan E., Hassell J.R., Yamada Y.;
"Complete primary structure of the rat cartilage proteoglycan profein deduced from cDNA clones."
J. Biol. Chem. 262:17757-17767(1987).
                                                                                   ---VEADAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Doege K., Sasaki M., Horigan E., Hassell J.R., Yamada Y.
J. Biol. Chem. 263:10040-10040(1988).
                                                                                   488 GMGGMHPSS---GASKGTTTKKYSEGAAAGTEDAERAP-
                                                                                                                                                                                                         PRT; 2124 AA
                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                  1080 VGDLSRL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
REVISION TO 698
                                                                                                                                                                                                                                                                                                                             AGC1 OR AGC
                                                                                                                                                                                                   PGCA_RAT
P07897;
                                                                                                                                                                      RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1020 TSGVGDLSRLPSGEGPEVSASGVEDLSGLPSGEGLEASASGVGDLSGLPSGEGPEASASG 1079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 DGAPI -- NSATAMADALN -- GHHPGDVISVTWQTKSGGTRTGNVTLAEGP----- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GIPNQGGLLY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----IHDQANAVQTTRDILEGAKKGLEFVRPVAVDLTYIPVVGHALSAAFQAPFCAGAMA 290
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                              G1-A.
G1-B.
G1-B.
G2-B.
G2-B.
KS.
CS-1.
CS-1.
G3.
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Pred. No. 1.5
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Matches 127; Conservative
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2096
2105
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22243
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PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
PROSITE; PS00395; IG_LIKE; 1.
PROSITE; PS01290; IG_WHC; 1.
PROSITE; PS01241; LINK; 4.
Glycoprotein; Cartiage; Proteoglycan; Lectin; Signal; Sushi; Repeat; Immunoglobulin domain.
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                                                                                         INCEPPOOL IPPRO0233; ANTIFICEZEII.
INCEPPOOL IPPRO03006; IG-like.
INCEPPOOL IPPRO03006; IG-MHC.
INCEPPOOL IPPRO03006; IG-MHC.
INCEPPOOL IPPRO03039; LINK.
INCEPPOOL IPPRO0334; SGXXSG.
INCEPPOOL IPPRO0334; SGXXSG.
FERN; PPOOLS9; IGCTIN C.
FERN; PPOOLS9; IGCTIN C.
FERN; PPOOLS9; SGXXSG, 55.
FERN; PPOOLS9; SGXXSG, 55.
FERN; PPOOLS9; SGXXSG, 55.
FERN; PPOOLS9; SGXXSG, 55.
FERN; PPOOLS9; LINKMODULE.
FRINTS; PRO1265; LINKMODULE.
PPODON; PPOOLS96; ANTIFREEZEII.
FRODON; PRO00305; ANTIFREEZEII.
FRODON; PRO0031; CCP; 1.
SWART; SMO0044; LINK; 4.
EMBL; M13518; AAA41836.1; -.
EMBL; J03485; AAA21000.1; ALT_SEQ.
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963 DLSGLPSGEEGSETSTSGIEDISVLPTGESPETSASGVGDLSGLPS--GGESLETSASGV 1020
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                                                                                                                                               796 AVPSGTELPSSGDT---SGAPDLSGDFT----GSTDTSG---RLDSSGEPSGGSESGLE 844
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                                                                                          24 AIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIS 83
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STRAIN=H97RY,
PubMed=$634230;
A Goldon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
A Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
A Badcock K., Pedram K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
A Hornsby T., Jagels K., Krogh A., Mclean J., Moule S., Murphy L.,
A Oliver S., Seeger K., Skelton S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
I "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
In Arure 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1075 TSASGIEDI-----SVFPTEAEGLETSASGGYVSGIPSGEDGTETSTSGVEGVSGL
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
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YQ34 MYCTU
ID YQ34, MYCTU
AC P71933;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last. sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical Pe-PoRS femily protein Rv2634c.
GN RV2634C OR MT2712 OR MTCY441.04C.
Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 GGATGLIGSGGFGGAGGAAÁGV-GTTGGVGGSGGVGGVFGNGGFGGAGGLGAAGGVGGAA
SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann W.D., Alland B., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D Gordon S.V., Biglimeier K., Gas S., Barry C.B. III, Tekaia F., Badcock K., Basham D., Erwun D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.
                                                                                                                                                                      "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     514
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                                                                                                                                                                                          laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.2%; Score 142; DB 1; Length 778; llarity 30.2%; Pred. No. 0.55; Conservative 12; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 51 V -> L (IN REF. 2).
63 63 Q -> H (IN REF. 2).
274 274 A -> T (IN REF. 2).
778 AA; 63131 MW; DABZOFES8E499957 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical PE-PGRS family protein Rv3508 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422 SLPALAGIGGGSGFGGLPSLAQVHAASTRQALRPRAD--
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InterPro; IPR00084; PE_region.
Pfam; PF00934; PE; 1.
ProDom; PD001223; PE_region; 1.
Hypothetical protein; Complete proteome.
CONFLICT 51 (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE007103; AAK47026.1; ALT_INIT.
PIR; F70963; F70963.
TIGR; MT2712; -.
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Local Sm.
52; (
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289 MAV------VGGALAYLVVKTLINATQLLKLLAKLAELVAAAIADIISDV--
                                                                                                                                                                           Nature 393:537-544(1998).
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J Cutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from complete genome sequence.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probom; PRO034, PE; 1.
Probom; PR00323; PE region; 1.
Probom; P001223; PE region; 1.
Hypothetical protein; Repeat; Signal; Complete proteome.
Hypothetical protein; Repeat; Hypothetical Proteome.

30 POTENTIAL.

HYPOTHETICAL PE-PGRS FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319 GAG--GOGG--------LGGAGGOGGTGGAGGDGVLG---
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Pred. No. 1
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Tuberculist; Rv3508; InterPro; IPR000084; PE_region.
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J. Biol. Chem. 274:20444-20449(1999), MAJOR COMPONENT OF EXTRACELLULAR MATRIX OF CRATILAGENOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN MATRIX OF CRATILAGES. A MAJOR FUNCTION OF THIS PROTEIN MATRIX OF CRATILAGE. IT BINDS AVIDLY TO HYALURONIC ACID VIA AM AMINO-TERMINAL GLOBULAR REGION. MAY PLAY A REGULATORY ROLE IN THE MATRIX ASSEMBLY OF THE CARTILAGE.

1- SUBCUNIT: Interacts with FBLNI.

1- SUBCLIDIAR DOCATION: Secreted; extracellular matrix (By similarity)

1- DOMAIN: TWO GLOBULAR DOMAINS, GI AND G2, COMPRISE THE AMINO TERMINUS OF THE PROTECCLYON, WHILE ANOTHER GLOBULAR REGION, G3, MAKES UP THE COOH TERMINUS (I CONTAINS LINK DOMAINS AND THUS.

CONSISTS OF THREE DISULFIDE-BONDED LOOP STRUCTURES DESIGNATED AS THE A. B. B. WOTIFS. GI SIMILAR TO G1. THE KRRATAN SULFATE (KS) AND G3.

AND G3.

1- PTW: CONTAINS MOSTIV CHONDROITIN SULFATE, BUT ALSO KERATAN SULFATE CHAINS, N-LINKED AND O-LINGSORACHARIDES.

1- DISEASE: DEFECTS IN AGCI ARE THE CAUSE OF CARTILAGE MATRIX DEFICIENCY (CMD), AN AUTOSOMAL RECESSIVE SYNDORM CHARACTERIZED BY CLEFT PALATE. SHORT LINGS: TALL AND SNOUT. MUTATION IN STEAM CHAILS. SHORT LINGS: TALL AND SNOUT. MUTATION IN STRAIN CONTAINS THE CLOBY AND CLUBET PALATE. SHORT LINGS: TALL AND SNOUT. MUTATION IN STRAIN CHAILS IN THE BEST OF THE PROTEIN (MUTATION IN THE DISPASE OF CAUSE OF THE BUT ALSO.)
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                                                                                        PGCA_MOUSE STANDARD; PRT; 2132 AA.

G61282, 064021.

10.NOV-1997 (Rel. 35, Last sequence update)

11.NOV-1997 (Rel. 35, Last sequence update)

12.SEP-2003 (Rel. 42, Last annotation update)

13.SEP-2003 (Rel. 42, Last annotation update)

14.SEP-2003 (Rel. 42, Last annotation update)

15.SEP-2003 (Rel. 42, Last annotation update)

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SIMILARITY: Contains 4 link domains.
SIMILARITY: Contains 1 EGF-like domain.
SIMILARITY: Contains 1 C-type lectin family domain.
SIMILARITY: Contains 1 C-type lectin family domain.
SIMILARITY: Contains 1 Sushi (SCR) domain.
SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
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MEDLINE=95004579; PubMed=7920633;
Watanabe H., Kimata K., Line S., Strong D., Gao L.-Y., Kozak C.A.,
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MEDLINE=95104847; bubmed=7806222;

Walcz E., Deak F., Erhardt P., Coulter S.N., Fueloep C., Horvath Doege K.J., Glant T.T.;

"Complete coding sequence, deduced primary structure, chromosomal localization, and structural analysis of murine aggrecan.";
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SEQUENCE OF 211-326 FROM N.A.
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Nat. Genet. 7:154-157(1994).
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MEDLINE=98295987, PubMed=9634230;

MEDLINE=98295987, PubMed=9634230;

A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Erown D., Chillingworth T., Connor R.,

Badcock K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Woule S., Murphy L.,

A Plures S., Seeger K., Skelton S., Squares S., Squares R.,

Sulston J.B., Taylor K., Whitehead S., Barrell B.G.;

By Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.',

In Nature 393:537-544(1998).
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann J., Beboy R., Godson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.E., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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Bacteria, Actinobacteridae, Actinomycetales, Corymebacterinee, Mycobacterinee, Mycobacterium.
NCBI_TaxID=1773;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Rv3616G.
RV3616C OR MT3718 OR MTCY07H7B.06.
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P96213 mycobacteri
Q8vka4 mycobacteri
O53896 mycobacteri
Q9cd67 mycobacteri
Q8cgq mycobacteri
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Q9qub5 galleria me
O53631 mycobacteri
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080116 bacteriopha
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Copyright (c) 1993 - 2003 Compugen Ltd.
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MEDLINE-IL28732; PubNed=11234002;
MEDLINE-21128732; PubNed=11234002;
Melels S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraeer A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Ruthers S., Seeger K., Simonds M., Skelton J., Squares R., Barrell B.G.; Moodward J.R.,
                                                                                                                                                                                                                          0;
                                                                                                                                                                              Score 1963; DB 16; Length 392; Pred. No. 2.3e-102;
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
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Smith D.R., Robison K.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                             -> I (IN REF. 2).
82BBA8DD99D6F567 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
Hyporhetical protein ML0405.
ML0405 OR B1620_C2_213 OR MLCL383.01.
Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
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EMBL; 295557; CAB08950.1; -.
EMBL; AE07171; AAK48077.1; -.
TIGR; MT3718; -.
TubercuList; Rv3616c; -.
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387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA
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                                                                                                                                                                Caudron B., Cole S.T.; deduce the genomic organization
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris
Cole S.T., Larglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D. Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd &
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                             Σ
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                             Rajandream
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007175,
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
PEPA OR RV0125 OR MTC1418B.07 OR MT0133.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; DB 16; Length
4e-63;
ches 89; Indels
SEQUENCE OF 231-394 FROM N.A.
Oliver K., Harris D., Parkhill J., Barrell B.G., Rajandr
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein, Transmembrane, Complete proteome.
TRANSMEM 279 299 POTENTIAL.
SEQUENCE 394 AA, 40754 MW, DOE455C74ED7A10C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                506 KYSEGAAAGTEDAERAPVEADAGGGQKVLVRNVV
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                                                                                                     SEQUENCE OF 231-394 FROM N.A.
MEDLINE=93189700; Pubmed=8446027;
ElgImeier K., Honore N., Woods S.A., Caille of an ordered cosmid library to decof Mycobacterium leprae.";
MOL. Microbiol. 7.197-206(1993).
EMBL; AL583918; CAC29913.1;
EMBL; 297179; CAB09940.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 62.9
Matches 248; Conservative
                                                                                                                                                                                                                                                                                                                                                             Leproma; ML0405; -
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Mycobacterium leprae.
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Barrell B.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
                                                                                     SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland B., Gwinn M.L., Haft D., Hickey E.,
Fotoray J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 HTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                 "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
EMBL; 296071; CAB09453.1; --
EMBL; AE006925; AAK44357.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=JD88/107;
BYBDINES-S$5005449; PubMed=7921248;
Cameron R.M., Stevenson K., Inglis N.F., Klausen J., Sharp J.M.;
"Idencification and characterisation of a putative serine protease
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Csborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
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Mycobacterium paratuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 355;
                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50106; PDZ; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Hypothetical protein; Serine protease; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              355 AA; 34926 MW; 16CE9E21A97BF192 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.7%; Score 676; DB 16; 99.2%; Pred. No. 2.8e-30; ive 1; Mismatches 0;
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                                                                                                                                                                                                                                                       TICR, MT0133;

Tuberculist, Rv0125;

Tuberculist, Rv0125;

Tuterpro; IPR001478; Pro.
Interpro; IPR001254; Ser_protease_Try.
Interpro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
Pfam; PR0089; trypsin; 1.
PRINTS; PR00839; V8PROTEASES.C.
PRINTS; PR00839; V8PROTEASES.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 RIGNVILAEGPPA 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 132; Conservative
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SEQUENCE 355 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 VORVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWOTKSGGTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21128732; PubMed=11234002; ...
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Errown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quall M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
expressed in vivo by Mycobacterium avium subsp paratuberculosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                              361 AA; 35709 MW; 30FEF78FD6F3C411 CRC64;
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Nature 409:1007-1011(2001).
-:- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.3%; Score 474.5; DB 2
69.7%; Pred. No. 5.6e-19;
cive 17; Mismatches 22
                                                                                                                                                                                                                                                                                             SMART; SM00228; FULL, 1.
PROSITE; PS50106; PD2; 1.
Hydrolase; Protease; Serine protease; Signal.
38 POTENTIAL.
                     Microbiology 140:1977-1982(1994).
-!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
EMBL, Z23092, CAA80638.1;
-InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00595; PDZ; 1.
Pfam; PF0089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMANT; SM00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 AA
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InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000126; Ser_proteas_V8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probable secreted serine protease.
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Pfam; PF00689; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 69.7'
Matches 92; Conservative
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11 TSNFIWGQLLLLGEGIPDPGDIFNTGSSLFKQISDKMGLAIPGTNWIGQAAEAYLNQNIA 70
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                                                                                                                                                                    RVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDITIES 98295987; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Esgameder K., Gas S., Barry C.B. III, Trakaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy I.,

Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

Sulston J.B., Taylor K., Whitehead S., Squares R.,

"Decripherning the biology of Mycobacterium tuberculosis from the

Complete genome sequence.";
                                                                                                              7 HTAASDNFQLSQGGGFALPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGA
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STANDARD STANDARD SEQUENCE FROM N.A. STRAINS-COT 1551 / Oshkosh; STRAINS-COT 1551 / Alland D., Eisen J.A., Carpenter L., White O., Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L. Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                    ı;
                                                        Query Match
16.8%; Score 460.5; DB 16; Length 354;
Best Local Similarity 66.2%; Pred. No. 3.3e-18;
Matches 88; Conservative 18; Mismatches 26; Indels 1;
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                                                                    .3e-18;
les 26; Indels
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PROSITE; PS50106; PDZ; 1.
Hydrolase; Protease; Serine protease; Complete proteome.
SEQUENCE 354 AA; 35265 MW; 612F23261BC9EA4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laboratory strains.";
Submitted (ARR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; Z83864; CAB06237.1;
EMBL; AE007189; AAK48347.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tuberculist, Rv3864; -.
Hypothetical protein, Complete proteome.
SEQUENCE 402 AA; 42068 MW; B400E0E22D482765 CRC64;
                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Rv3864.
RV3864 OR MTCY01A6.04C OR MT3978.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinom
Corynebacterineae; Mycobacteriaceae; Mycobacterium
WCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                            402 AA
                                                                                                                                                                                                                                                                                                                                                    01-MAY-1997 (TrEMBLrel. 03, Created)
                                                                                                                                                                                                                                                                                                                          PRT;
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Matches 130; Conservative 4
                                                                                                                                                                                                                          127 RTGNVTLAEGPPA 139
                                                                                                                                                                                                                                                  342 LTANVTLAEGPPA 354
                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                  67
                                                                                                                                                                                              282
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                                                                  71 QQLRAQVMGDLDKLTGNMISNQAKYVSDTRDVLRAMKKMIDGVYKVCKGLEKIPLLGHLW 130
217 HVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLTYIPVVGHAL 276
                                                                                                                                         SAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLABLVAAAIADIISDVADII 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAASTRQALRPRADGPVGAA 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 PTWIELAALPDFLGGFAGLPSL-GFGNLLSFASLPTVGQVTATMGQLQQLVAAGGGPSQL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343 ASMGSQQAQLISSQAQQG-----GQQHATLVSDK----KEDEEGVA----EAERAPID 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 TAASDNFQLSQG--GQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVV-DNNGN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CDC 1551 / Oshkosh, Fisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKYSEGAAAGTEDAERAPVE
                                                                                                                                                                                                                                                                                                                                              165 RGILGRLIEMLTTLPKFPGLPGLPSLPDIIDGLWPPKLPDIPIPGLPDIPGLPDFKWPPT
                                                                                                                                                                                                                                                                               337 KGILGEVWEFITN-----ALNGLKELWDKLTG-W-------VTGLFSRGW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 PGSPLFPDLPSFPGFPGFPEFPAIPGFP-ALPGLPSIPNLFPGLPGLGDLLPGVGDLGKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium
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Submitted (APR-2011) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO06985; AAK45259.1; -
TIGR; MT1011; -
TIGR; MT1011; -
TIGR; MT0011; -
TIGR; MT0011; -
TIGR; MT0011; -
TIGR; MT0011; -
TIGR; MT00124; Ser_Drotease_Try.
TIGR; MT00255; PDZ; 1.
THEFPTO; IPR001254; Ser_Drotease_Try.
Fram; PF00095; PDZ; 1.
PRINTS; PR00834; PR0TEASES2C.
SNART; SM00228; PDZ; 1.
PROSITE; PSS0106; PDZ; 1.
SEQUENCE 446 AA; 44484 MW; 54170CBEA8FE872B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     374 ----SNLESF-----FAGVPGLTGATSGLSQVTGLF-GAAGL--
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Last annotation update)
                                                                                                                                                                                                    131 SWELAIPMSGIAMAVVGGALLYLIMTLMNATNL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  446 AA.
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MT1011.
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    388 AGTAASOR 395
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157 TISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAADKYAGKNRN 216

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258 ADSGDAQSGSIGLGFAIPVDQAKRIADELISTG--KATH----ASLGVQVATDKGTPGAK 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 VMDVVAGGAAANAAVPKGVVLTKVDDRLISSADALVAAVRSKAPGDKVSLTYQDQSGSSR 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 AASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGN-GAR
                                                                                                                                                                                                                                                  MEDLINE=21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnill T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simonds M., Skelton J., Squares R., Squares R., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Length 382;
                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leproma; ML0176; -.
InterPro; IPR001478; PDZ.
InterPro; IPR001264; Ser_protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00595; PDZ; 1.
Pfam; PF00899; trypsin; 1.
PRINTS; PR00844; PROTEASES2C.
SMART; SM00228; PDZ; 1.
Hydrolase; Protease; Serine protease; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.9%; Score 188.5; DB 16; Length
39.8%; Pred. No. 0.0065;
tive 19; Mismatches 51; Indels
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Harris D., Taylor K.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                           Squares S., Stevens K., Taylor K., Whitehead S., Woo Barrell B.G.;
"Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-i- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY:
EMBL, ALS83917; CAC29684.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                  (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
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                                                                            Possible secreted serine protease.
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01-MAY-1999 (TrEMBLrel. 10,
01-OCT-2002 (TrEMBLrel. 22,
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MLCB373.28.
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                                                                                                               Mycobacterium leprae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leproma; ML0176;
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                                                         01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89
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                                                              319 TLGADSADAQSGSIGLGFAIPVDQAKRIADELISTGKA-----SHASLGVQVTNDKDTP 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 TAASDNFQLSQG--GQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVV-DNNGN 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-H37Ry
MEDLINE-98255987; PubMed=9634230;
MEDLINE-98255987; PubMed=9634230;
MEDLINE-98255987; PubMed=9634230;
Gordon S.V., Eiglmear K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Hornsby T., Jagels K., Kroph A., McLean J., Moule S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Kroph A., McLean J., Moule S., Murphy L.,
Oliver S., Geeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Deciphering the biology of Mycobacterium tuberculosis from the
                                       GARVORVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tübercülösis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50106; PDZ; 1.
Hydrolase; Protease; Serine protease; Complete proteome.
SEQUENCE 464 AA; 46452 MW; AE93BFCC53E1EC8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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InterPro; IPR001449; Protease2C.
InterPro; IPR00144; Ser_protease_Try.
Pfam; PF00595; PDZ; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                            01-UTM-1998 (TrEMBLrel. 06,
01-MAR-2003 (TrEMBLrel. 23,
Putative serine protease.
RV0983 OR MTV044.11.
                                                                                                                                                                                                                                                                                             (TrEMBLrel. 06,
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                                                                                                                                                       433 GSŘÍVQVÍĽGK 443
                                                                                                                                                                                                                                                        PRELIMINARY;
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Best Local Similarity
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01-MAR-2001 (
01-OCT-2002 (
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                                                                                                                                       Caudron B., Cole S.T.; deduce the genomic organization
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MEDLINE-2161879; PubMed=11823852;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Brottier P., Camus J.C., Cattolico L., Arlat M., Choisne N., Cloudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalan M., Wincker P., Levy M., Kelsenbach J., Boucher C.A.;

Melsenbach J., Boucher C.A.;

Nelsenbach J., Solos C.A.;

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Nelsenbach J., Solos J., Salant Pathogen Ralstonia solanacearum.";

PMEL, Al64682; CAD18245.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Ralstoniaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 188.5; DB 2; Length 452;
; Pred. No. 0.0081;
19; Mismatches 51; Indels 7
                   James K.D., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                   protease,
1; 6CA675EB0911F983 CRC64;
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459 AA, 41117 MW; FE06C4144483ACC9 CRC64,
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 22, Last annotation update)
Putative hemagglutinin-related transmembrane protein.
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Ralstonia solanacearum (Pseudomonas solanacearum).
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Eiglmeier K., Honore N., Woods S.A.,
"Use of an ordered cosmid library to
                                                                                                                                                                                of Mycobacterium leprae.";
Mol. Microbiol. 7:197-206(1993).
EMBL; AL035500; CAB36690.1; -.
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Matches 51, Conservative
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---GMGGMHPSSGASKGTTTKKYSEGAAAGTEDA------ERAPVEADAGG 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 VISALGSVGGTTGG--GTLAPVASITAPVGTVVÄTVGSTLISTGATTPLAPVTGSÄGG 445
                                                                                                                                                                                                                                                                88 ITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSG-GTRTGNVTLAEGPPAEFLVPRG
                                                                                                                                                                                                                           147 SMSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSA
                                                                                                                                                                                                                                                                                                                                                                                                                  ----IGSNPNPIG--TTVASTG----NVVTGVGNTVTSAGTLVGGLGTGQLSPLAPVTTP
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Zurowce M., Kodrik D., Yang C., Sehnal F.;
Lucker M., Kodrik D., Yang C., Sehnal F.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF095239; AAG10393.1;
NOW TER 1468 AA; 122705 MW; 2DAS9E1181BBBJDF CRC64;
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Local Similarity 25.1%; Pred. No. 0.11;
nes 138; Conservative 42; Mismatches 219;
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(TrEMBLrel. 22, Last ann
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                                 GGILYSSLEYFEKALEELAAAFPGDGWLGSAADKYAGKNRNHVNFFQELADLDRQLISLI 235
                                                                                                          ---LASAASGAAGAAPVI-----VIEDGSSAASAAAGSGASGVGGLG 714
                                                                                                                                  294 -GALAYLVVKTLINATQLLKLLAKLABLVAAAIADIISDVADIIKGILGEVWEFITNALN 352
                                                                                                                                                         ------GGIGPIGASSAGASGAGLGGVGAAGTSGLG 751
                                                                                                                                                                                                         GI------GGV-----GASTAGSAGAGLGGIGAGGSSGSSAASAASGASGAGEVIVI 797
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KEDLINE=9829597; PubMed=9634230,

A GOLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Barry C.E. III, Tekaia F.,

A Gordon S.V., Eiglmeler K., Gas S., Barry C.E. III, Tekaia F.,

A Badcock K., Basham D., Brown D., Chillingworth T., Connor K.,

Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Squares R.,

Toomplete genome sequence.";

Toomplete genome sequence.";

REMBL; AL021926; CAA17303.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.2%; Score 169; DB 16; I
25.5%; Pred. No. 0.11;
ative 26; Mismatches 107;
                                                         641 GGIGPNGVS--SASATGSÄÄGSIGSGLCGSGÄ---ÄGSS-
                                                                                                                                                                                                                                                                                                                                                                                                                      496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Embu; Abversi: Tuberculist; RV0109; -. TurierPro; IPR00084; PE_region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00934; PE; 1.
ProDom; PD001223; PE_region; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-OCT-2002 (TrEMBLrel. 22, 05)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                 APVEADAGGG 530
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RV0109 OR MTV031.03C.
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                                                                                                                                                          LGALGPL-
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Best Local S
Matches 83
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293

262 VAVDLTYIPVVGHALS---AAFQAPFCAGAMAVVG---

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                                                                                                                                                ---- QALQTVQQNVLTVVNAP 115
                                                                                                                                                                                                                                                                                                                             392 GLSQVTGLFGAAGL--SASSGLAHADSLASSASLPA----LAGIGGGSGFGGLPSLAQV 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------GGPGGAGGNAIG----LFGSGGTGGMGGVGGMGGVGNGGNAGNGGTA 257
                                                                                                                                                                                                     -KGILGEVWEFITNALNGLKELMDKLTGWVTG----LFSRGWSNLESFFAGVPGLTGATS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94
                               68
GALAYLVVKTLINATQLLKLLAKLABLVAAAIADIISDVADII---
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                                                                                                                                                                                                                                                                                                                                                                            156 GVDQAGGNGGAAGLIGNGGSGGVGGPGIAGSAGGAGGAGGLLFGNGGPGGAGGIGTTGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                              445 HAASTRQALRPRADGPVGAAABQVGCQSQLVSAQGSQGMGGPVGMGCMHPSSGASKGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ABC06923; AAK44341.1; ---
IIGR; MT0118; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAINGED., Eisen J.A., Carpenter L., White O., STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                                 116 TQALLGR--PIİGNGANGLPN----TGQDGGPGGLLFGNGGN----
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Last annotation update)
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                                                                                                                                                69 ALAFHDQFVQALNMGAVCYAAAET-ANATPL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     505 KKYSEGAAAGTEDAERAPVEADAGGG 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 GLFGHĠGAGĠAGGIGSADGGLGGĠĠĠ 283
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ProDom; PD001223; PE region; 1.
SEQUENCE 533 AA; 46785 MW;
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InterPro; IPR000084; PE_region.
Pfam; PF00934; PE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
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378 SFFAGVPGLTGATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIG 430  189GGSGGVDQAGGNGGAAGLIGNGGSGGVGGPGIAGSAGGAGGLLFGNG 238  431 GGSGFGGLPSLAQVHAASTRQALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMG 490  189GGSGGVDQAGGNGGPVGAAAEQVGGQSQLVSAQGSQGMGGPVCMG 490  191 GMLPSSGAGGTGTTGDGGPGCAGGNAIGLFGSGGTGCMGGVGCMG 280  491 GMLPSSGASKGTTTKKYSEGAAAGTEDAERAPVEADAGGG 530  191 GVGNGGNAGNGGTAGLFGHGGAGGAGGIGSADGGLGGGGG 320	BESULT 15  99HVM6  D Q9HVM6  PRELIMINARY; PRT; 1417 AA.  C Q9HVM6  PRELIMINARY; PRT; 1417 AA.  C Q9HVM6  D TO 1. WAR-2001 (TrEMBLrel. 16, Last sequence update)  TO 1. WAR-2001 (TrEMBLrel. 16, Last sequence update)  TO 1. WAR-2003 (TrEMBLrel. 23, Last annotation update)  PA541.  PA541.  B PA541.  B PA541.  NOBILITARID-287;  NOBILITARID-287;  WASILIN-ATCC 15692 / PAO1;  P Studomonadaceae: Pseudomonas.  NOBILITARID-287;  WASILIN-ATCC 15692 / PAO1;  P Studomonadaceae: Pseudomonas.  NOBILITARID-287;  WASILIN-ATCC 15692 / PAO1;  P STAIN-ATCC 15692 / PAO1;  P RELET J. Spencer D.H., Mancock R.E.W., Lory S., Olson M.V.;  P RACT STAIN-ATCC PACTORNO.  P RELET PON PROBER PROPAMETHEINE;  P PROSITE; PSO0012; PHOSPHOPAWETHEINE;  W HYDOCHECICAL PROPER PROPAMETHEINE;  W HYDOCHECICAL PROPER PROPAMETHEINE;  W HYDOCHECICAL PROPER PROPAMETHEINE;  W HYDOCHECICAL PROPER PROPAMETHEINE;  W HYDOCHECICAL PROPER PROPAMETHEINE;  W HYDOCHECICAL PROPER PROPAMETHEINE;  W HYDOCHECICAL PROPER PROPAMETHEINE;  W HYDOCHECICAL PROPER PROPAMETHEINE;  W HYDOCHECICAL PROPER PROPAMETHEINE;  W HYDOCHECICAL PROPER PROPAMETHEINE;  W HYDOCHECICAL PROPER PROPAMETHEINE;  W HYDOCHECICAL PROPER PROPAMETHEINE;  W HYDOCHECICAL PROPER PROPAMETHEINE;  W HYDOCHECICAL PROPER PROPAMETHEINE;  W HYDOCHECICAL PROPER PROPAMETHEINE;  W HYDOCHECICAL PROPER PROPAMETHEINE;  W HYDOCHECICAL PROPER PROPAMETHEINE;  W HYDOCHECICAL PROPAMETHEINE;  W HYDOCHECE 1417 AA; 139958 MW; 212C91605639D CRC64;	Query Match  Best Local Similarity 22.1%; Pred. No. 0.55,  Matches 139; Conservative 77; Mismatches 206; Indels 206; Gaps 31;  19 GGGGRAIPIGGAMAIAG
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